

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LOPEIMGVFKVETWPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	9	2	PC7073
2	4	22.2	15	2	PA0105
3	3	16.7	6	2	I49808
4	3	16.7	6	2	I65546
5	3	16.7	8	2	G33098
6	3	16.7	8	2	A61597
7	3	16.7	8	2	A35180
8	3	16.7	8	2	S53008
9	3	16.7	9	2	S77984
10	3	16.7	10	1	XASNPC
11	3	16.7	10	1	RHAQ1
12	3	16.7	10	2	PT0322
13	3	16.7	10	2	B61218
14	3	16.7	10	2	S74147
15	3	16.7	11	2	A33917
16	3	16.7	11	2	PC4267
17	3	16.7	11	2	S78765
18	3	16.7	11	2	H84082
19	3	16.7	12	2	S07206
20	3	16.7	12	2	C39109
21	3	16.7	12	2	A60757
22	3	16.7	12	2	S36899
23	3	16.7	12	2	A35585
24	3	16.7	12	2	PA0098
25	3	16.7	12	2	A61503
26	3	16.7	12	2	D20907
27	3	16.7	12	2	PQ0786
28	3	16.7	13	1	XAV19B
29	3	16.7	13	2	S39413

30	3	16.7	13	2	H64124
31	3	16.7	13	2	PA0023
32	3	16.7	13	2	H44957
33	3	16.7	14	2	PC2373
34	3	16.7	14	2	PS0371
35	3	16.7	14	2	B56863
36	3	16.7	14	2	PA0015
37	3	16.7	14	2	A61002
38	3	16.7	14	2	A61308
39	3	16.7	14	2	B61308
40	3	16.7	14	2	S39111
41	3	16.7	14	2	S00150
42	3	16.7	14	2	PH1625
43	3	16.7	14	2	PH1627
44	3	16.7	14	2	PH1594
45	3	16.7	14	2	S21747
46	3	16.7	14	2	PA0044
47	3	16.7	15	2	S26791
48	3	16.7	15	2	PA0034
49	3	16.7	15	2	PA0014
50	3	16.7	15	2	PN0173
51	3	16.7	15	2	PA0059
52	3	16.7	15	2	PA0106
53	3	16.7	15	2	PA0080
54	3	16.7	15	2	S10388
55	3	16.7	15	2	S10386
56	3	16.7	15	2	B41436
57	3	16.7	15	2	A32971
58	3	16.7	15	2	FN0662
59	3	16.7	15	2	PH1613
60	3	16.7	15	4	I38032
61	3	16.7	16	2	S03532
62	3	16.7	16	2	D49021
63	3	16.7	16	2	S42237
64	3	16.7	16	2	B44896
65	3	16.7	16	2	S65709
66	3	16.7	16	2	C61414
67	3	16.7	17	2	PN0587
68	3	16.7	17	2	S03531
69	3	16.7	17	2	S50901
70	3	16.7	17	2	A48179
71	3	16.7	17	2	B61414
72	3	16.7	17	2	S59512
73	3	16.7	17	2	S69164
74	3	16.7	17	2	PD0005
75	3	16.7	18	1	DRUPPD
76	3	16.7	18	2	I52651
77	3	16.7	18	2	A25941
78	3	16.7	18	2	A56871
79	3	16.7	18	2	PN0149
80	3	16.7	18	2	I40062
81	3	16.7	18	2	A45590
82	3	16.7	18	2	A32917
83	3	16.7	18	2	G84114
84	3	16.7	18	4	S40664
85	3	16.7	19	2	C21182
86	3	16.7	19	2	S19532
87	3	16.7	19	2	S19613
88	3	16.7	19	2	B46592
89	3	16.7	19	2	S69166
90	3	16.7	20	2	A60728
91	3	16.7	20	2	S13274
92	3	16.7	20	2	S46488
93	3	16.7	20	2	C20554
94	3	16.7	20	2	H49034
95	3	16.7	20	2	S33001
96	3	16.7	20	2	S59494
97	3	16.7	20	2	S18582
98	3	16.7	20	2	T50757
99	3	16.7	20	2	A85645
100	3	16.7	20	2	A05310

hypothetical prote
protein QA300052 -
protein P18 - comm
probable IMP dehyd
hypothetical prote
photosystem I reac
seed storage prote
photosystem II oxy
hemocyanin chain 2
hemocyanin chain 4
Ig heavy chain V r
ovostatin - duck (
Ig H chain V-D-J r
Ig H chain V-D-J r
Ig H chain V-D-J r
glutamate dehydrog
NADH2 dehydrogenas
Ig heavy chain V r
seed storage prote
protein QA300024 -
seed storage prote
protein QF200021 -
protein QF200076 -
translation elonga
Ig heavy chain J r
Ig heavy chain J r
ovostatin - green
heparin-binding le
dystrophin-associa
Ig H chain V-D-J r
hypothetical MN1/T
Ig heavy chain J r
Ig heavy chain J7
hypothetical prote
heat shock protein
major allergen Myr
chymotrypsin [EC 3
tyrosine 3-monooxy
Ig heavy chain J5
chlorophyll a/b-bi
methane monooxygen
chymotrypsin [EC 3
probable integrin
ferredoxin a1 - Ja
very-high-density
pigment-dispersing
brain-derived neur
Ig heavy chain J-H
retinol-binding pr
beta-Gliadine 13 -
shikimate 5-dehydr
beta-pigment-dispe
protein phosphatas
hypothetical prote
INS150A/INS150B mu
4K prothoracicotro
globin - polychaet
globin - polychaet
lactase-phlorizin
ferredoxin b - Jap
cytochrome P450 3A
ferredoxin [2Fe-2S
peptidylprolyl iso
hemocyanin subunit
nuclear antigen EB
hypothetical prote
formate dehydrogen
hypothetical prote
pufK protein [lipo
Amino terminal of
apolipoprotein E -

ALIGNMENTS

RESULT 1
PC7073
ubiquinol-cytochrome-c reductase (EC 1.1.0.2.2) core protein II - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Jun-2002
C;Accession: PC7073
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b

A;Reference number: PC7072
A;Accession: PC7073
A;Molecule type: protein
A;Residues: 1-9 <TSU>
C;Keywords: brain; core protein; oxidoreductase

Query Match 22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 9 PKVK 12
|||
Db 6 PKVK 9

RESULT 2
PA0105
heat shock protein dnaJ type - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0105
R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A;Reference number: PA0051
A;Accession: PA0105
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Keywords: heat shock; stress-induced protein

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 11 VKET 14
|||
Db 1 VKET 4

RESULT 3
I49808
D-SP2.5 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I49808
R;Kurosawa, Y.; Toneygawa, S.
J. Exp. Med. 155, 201-218, 1982
A;Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity D
A;Reference number: I49808; MUID:82099938; PMID:6798155
A;Accession: I49808
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:J00432; NID:G194370; PIDN:AAA37904.1; PID:G450452
C;Genetics:
A;Gene: Igh

Query Match 16.7%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 14 TMV 16
|||
Db 2 TMV 4

RESULT 4
165546
MHC H2-L antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I65546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and th
A;Reference number: I52778; MUID:86106202; PMID:3510743
A;Accession: I65546
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:M12483; NID:G199565; PIDN:AAA39663.1; PID:9554234

Query Match 16.7%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 15 MVP 17
|||
Db 1 MVP 3

RESULT 5
G33058
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: G33058
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: G33058
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 7 GVP 9
|||
Db 1 GVP 3

RESULT 6
A61597
cytochrome P450 AL-1 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: A61597
R;Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A;Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto
A;Reference number: A61597; MUID:91292910; PMID:1676625
A;Accession: A61597
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <SHI>

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 11 VKE 13


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Db          |||
           5 VKE 7

RESULT 7
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C;Accession: A35180
R;Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Vajima, H.; Satoh, M.
J. Biol. Chem. 265: 5809-5815, 1990
A;Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A;Reference number: A35180; MUID:90202830; PMID:2318836
A;Accession: A35180
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <VOS>
C;Keywords: hydrolase

Query Match          16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 GVP 9
           |||
           6 GVP 8

RESULT 8
S53008
citrate synthase - cucurbit
C;Species: Cucurbita sp. (cucurbit)
C;Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C;Accession: S53008
R;Kato, A.; Hayashi, M.; Mori, H.; Nishimura, M.
Plant Mol. Biol. 27: 377-390, 1995
A;Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized
A;Reference number: S53007; MUID:95195164; PMID:7888626
A;Accession: S53008
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <KAT>

Query Match          16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          14 TMV 16
           |||
           4 TMV 6

RESULT 9
S77984
cytochrome-c oxidase (EC 1.9.3.1) chain V1a - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77984
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77984
A;Molecule type: protein
A;Residues: 1-9 <ARN>
A;Experimental source: heart
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match          16.7%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 QPE 4
           |||
           3 QPE 5

Db

RESULT 10
XANNPC
angiotensin-converting enzyme inhibitor - aspic viper
C;Species: Vipera aspis (aspic viper)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
C;Accession: A60377
R;Komori, Y.; Sugihara, H.
Int. J. Biochem. 22: 767-771, 1990
A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from tilapia
A;Reference number: A60377; MUID:90382616; PMID:2169439
A;Accession: A60377
A;Molecule type: protein
A;Residues: 1-10 <KOM>
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match          16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 PKV 11
           |||
           6 PKV 8

Db

RESULT 11
RHAQI
gonadoliberin I - American alligator
N;Alternate names: gonadotropin-releasing hormone I
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: A60066
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swan:
Regul. Pept. 33: 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains
A;Reference number: A60066; MUID:91352338; PMID:1892082
A;Accession: A60066
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match          16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LQP 3
           |||
           7 LQP 9

Db

RESULT 12
PT0322
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0322
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173: 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0322

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A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGX 8
|||
DB 8 MGX 10

RESULT 13
B61218
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
C;Species: Haynaldia villosa, Dasypyrum villosum
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
C;Accession: B61218
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa
A;Reference number: A61218; MUID:91515394; PMID:1859356
A;Accession: B61218
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
|||
DB 8 LQP 10

RESULT 14
S74147
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - pig (fragment)
C;Species: Sus scrofa domestica [domestic pig]
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 03-Jun-2002
C;Accession: S74147
R;Fukuda, A.; Osawa, T.; Hitomi, K.; Uchida, K.
Arch. Biochem. Biophys. 333, 419-426, 1996
A;Title: 4-Hydroxy-2-nonenal cytotoxicity in renal proximal tubular cells: protein modification and role of glutathione
A;Reference number: S74147; MUID:96404942; PMID:8809082
A;Accession: S74147
A;Molecule type: protein
A;Residues: 1-10 <FUK>
A;Experimental source: LLC-PK1 cells (renal tubular epithelial cells)
C;Keywords: NAD; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
|||
DB 2 KVK 4

RESULT 15
A33917
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
C;Accession: A33917
R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989
A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and

A;Reference number: A33917; MUID:89282776; PMID:2543974
A;Accession: A33917
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <SIM>
A;Cross-references: GB:M23652
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; arbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-P; C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
|||
DB 5 KVK 7

RESULT 16
PC4267
ribosomal protein L12.1 - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: PC4267
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A;Reference number: PC4267
A;Accession: PC4267
A;Molecule type: protein
A;Residues: 1-11 <KAM>
A;Experimental source: strain Japonica Nihonbare

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
|||
DB 7 PKV 9

RESULT 17
S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78765
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Molecule type: protein
A;Residues: 1-11 <GRA>
C;Keywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
|||
DB 5 VPK 7

RESULT 18
H84082
hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H84082
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: H84082
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-11 <STO>
 A;Cross-references: GB:AP001518; GB:BA000004; NID:G10175792; PIDN:BAB07183.1; GSPDB:GN00
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH3464

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 11 VKE 13
 |||
 Db 3 VKE 5

RESULT 19
 S07206
 kassinin - Senegal running frog
 C;Species: *Kassina senegalensis* (Senegal running frog)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Sep-2000
 C;Accession: S07206
 R;Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.
 Experientia 33, 857-858, 1977
 A>Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide fro
 A;Reference number: S07206; MUID:77246385; PMID:891753
 A;Accession: S07206
 A;Molecule type: protein
 A;Residues: 1-12 <ANA>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end
 F;12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
 |||
 Db 2 VPK 4

RESULT 20
 C39109
 hypothetical 1.2K protein - hepatitis C virus
 N;Alternate names: hypothetical protein 3
 C;Species: hepatitis C virus
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
 C;Accession: C39109; JQ1586
 R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A>Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
 A;Reference number: A39109; MUID:91156678; PMID:1705704
 A;Accession: C39109
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-12 <HAN>
 A;Cross-references: GB:M58406
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A>Title: Cloning and sequencing of the structural region and expression of putative core
 A;Reference number: JQ1584; MUID:92300349; PMID:11318944
 A;Accession: JQ1586
 A;Molecule type: genomic RNA
 A;Residues: 1-12 <KUM>
 A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GVP 9
 |||
 Db 6 GVP 8

RESULT 21
 A60757
 enterotoxin C-1 - *Staphylococcus aureus* (fragments)
 C;Species: *Staphylococcus aureus*
 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 30-Sep-1993
 C;Accession: A60757
 R;Bohach, G.A.; Handley, J.P.; Schlievert, P.M.
 Infect. Immun. 57, 23-28, 1989
 A>Title: Biological and immunological properties of the carboxyl terminus of staphyl
 A;Reference number: A60757; MUID:89079292; PMID:2909489
 A;Accession: A60757
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <BOH>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 4 KVK 6

RESULT 22
 S36899
 ribosomal protein S6 - *Mycobacterium bovis* (fragment)
 C;Species: *Mycobacterium bovis*
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C;Accession: S36899
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A>Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from *Mycc*
 A;Reference number: S36887; MUID:94009653; PMID:8405418
 A;Accession: S36899
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <OHA>
 C;Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIM 6
 |||
 Db 5 EIM 7

RESULT 23
 A35585
 cytokinin-binding factor 1 - durum wheat
 C;Species: *Triticum durum* (durum wheat)
 C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
 C;Accession: A35585
 R;Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.;
 Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988
 A>Title: Characterization of a benzyladenine binding-site peptide isolated from a whe
 by mass spectrometry; MUID:88320357; PMID:3413067
 A;Reference number: A35585
 A;Accession: A35585
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <BRI>

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
|||
Db 3 LQP 5

RESULT 24

PA0098
ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0098
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0098
A:Molecule type: protein
A:Residues: 1-12 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
|||
Db 6 VPK 8

RESULT 25

AG1503
sterol carrier protein-2-like protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C:Accession: AG1503
R:Reinhart, M.P.; Avart, S.J.; Foglia, T.
Comp. Biochem. Physiol. B 100, 243-248, 1991
A:Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken
A:Reference number: AG1503; PMID:92191564; PMID:1799965
A:Accession: AG1503
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <REI>

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
|||
Db 6 PKV 8

RESULT 26

D20907
Ig kappa-1 chain J4 segment (b95 allotype) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 05-Nov-1999
C:Accession: D20907; D53275
R:Emorine, L.; Max, E.E.
Nucleic Acids Res. 11, 8877-8890, 1983
A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
A:Reference number: A20907; PMID:84169523; PMID:6324107
A:Accession: D20907
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <EMO>
A:Cross-references: GB:X00231; NID:91577; PIDN:CAA25049.1; PID:e8275; PID:91364234
R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275; PMID:91372868; PMID:1909995

A:Accession: D53275

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-12 <AYA>

A:Note: sequence extracted from NCBI backbone (NCBI:56069, NCBIP:56166)

C:Comment: This J4 segment may not be functional because of a short space between the

C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
|||
Db 7 TMV 9

RESULT 27

PQ0786
NADH2 dehydrogenase (EC 1.6.99.3) 26K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 26K chain; NADH-ubiquinone reductase 26K chain
C:Species: mitochondrion Vicia faba (fava bean)
C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
C:Accession: PQ0786
R:Leterme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH-ubiquinone reductase) from fava bean mitochondria
A:Reference number: PQ0775; PMID:94151437; PMID:8108509
A:Accession: PQ0786
A:Molecule type: protein
A:Residues: 1-12 <LET>
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the
ranging from 5K to 75K.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
|||
Db 3 GVP 5

RESULT 28

XAV19B
angiotensin-converting enzyme inhibitor V-9 - jararaca
C:Species: Bothrops jararaca (jararaca)
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C:Accession: A01253
R:Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocoy, O.
Biochemistry 10, 4033-4039, 1971
A:Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca
A:Reference number: A90356; PMID:72118526; PMID:4334402
A:Accession: A01253
A:Molecule type: protein
A:Residues: 1-13 <OND>

A:Note: the structure of the peptide was confirmed by synthesis
C:Comment: This peptide also potentiates bradykinin by inhibiting the kinases that i
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5

```

Db          |||
           9 PEI 11

RESULT 29
S39413
tubulin beta chain - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S39413
R:Ruediger, M.; Weber, K.
Eur. J. Biochem. 218, 107-116, 1993
A:Title: Characterization of the post-translational modifications in tubulin from the ma
A:Reference number: S39412; MUID:94062821; PMID:8243458
A:Accession: S39413
A:Molecule type: protein
A:Residues: 1-13 <RUE>
C:Superfamily: tubulin
C:Keywords: heterodimer; microtubule

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 KET 14
           |||
           11 KET 13

Db

RESULT 30
H64124
hypothetical protein H11460 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 31-Oct-1997
C:Accession: H64124
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: H64124
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-13 <TTGR>
A:Cross-references: GB:U32824; GB:L42023; NID:gi574298; PID:gi574306; TIGR:H11460

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          10 KVK 12
           |||
           2 KVK 4

Db

RESULT 31
PA0023
Protein QA300052 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
C:Accession: PA0023
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A:Reference number: PA0001
A:Accession: PA0023
A:Molecule type: protein
A:Residues: 1-13 <KAW>
A:Experimental source: seed
C:Keywords: pyroglutamic acid; seed
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

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Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 KET 14
           |||
           5 KET 7

Db

RESULT 32
H44957
protein p18 - common tobacco (cv. Samsun NN) (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 30-Sep-1993
C:Accession: H44957
R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
Plant Cell Physiol. 31, 215-221, 1990
A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabac
A:Reference number: A44957
A:Accession: H44957
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <TAK>

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 GVP 9
           |||
           2 GVP 4

Db

RESULT 33
PC2373
probable IMP dehydrogenase (EC 1.1.1.205) [similarity] - Bacillus cereus (strain ts-4
C:Species: Bacillus cereus
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: PC2373
R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulatic
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2373
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MAS>
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homc
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKE 13
           |||
           7 VKE 9

Db

RESULT 34
PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C:Species: Synechococcus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synechococcus sp. PC7002 and Cyanophora paradoxa: cloning
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHT>

```

A;Cross-references: GB:M86238; NID:G154574; PIDN:AAA27351.1; PID:G552030

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
|||
Db 12 LQP 14

RESULT 35

B56863 photosystem I reaction center complex small chain psaE - *Synechococcus* sp. (fragment)

C;Species: *Synechococcus* sp.
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 23-Feb-1996

C;Accession: B56863

R;Hatanaka, H.; Sonoike, K.; Hirano, M.; Katch, S.

Biochim. Biophys. Acta 1141, 45-51, 1993

A;Title: Small subunits of Photosystem I reaction center complexes from *Synechococcus* sp.

A;Reference number: A56863; MUID:93168774; PMID:8382079

A;Accession: B56863

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <HAT>

A;Experimental source: thylakoid membranes

A;Note: sequence extracted from NCBI backbone (NCBIP:125606)

A;Note: the species was designated as *Synechococcus elongatus*

C;Keywords: photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
|||
Db 6 KVK 8

RESULT 36

PA0015 seed storage protein 12S 2 - *Arabidopsis thaliana* (fragment)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997

C;Accession: PA0015

R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JPIPD, July 1994

A;Description: Separation and characterization of *Arabidopsis* proteins by two-dimensional

A;Reference number: PA0001

A;Accession: PA0015

A;Molecule type: protein

A;Residues: 1-14 <KAM>

A;Experimental source: seed

C;Keywords: pyrrolidone carboxylic acid; seed; storage protein

F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
|||
Db 5 GVP 7

RESULT 37

A61002

photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)

N;Alternate names: thylakoid membrane protein

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: A61002

R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.;

Electrophoresis 11, 528-536, 1990

A;Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequencing

A;Reference number: A61002; MUID:91031404; PMID:1699755

A;Accession: A61002

A;Molecule type: protein

A;Residues: 1-14 <BAU>

C;Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
|||
Db 2 GVP 4

RESULT 38

A61308

hemocyanin chain 2 - Sahara scorpion (fragment)

C;Species: *Androctonus australis* (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: A61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in *Androctonus* aust

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: A61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13
|||
Db 2 VKE 4

RESULT 39

B61308

hemocyanin chain 4 - Sahara scorpion (fragment)

C;Species: *Androctonus australis* (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: B61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in *Androctonus* aust

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: B61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13
|||
Db 2 VKE 4

RESULT 40

B39111

Ig heavy chain V region - Pacific hagfish (fragment)

C;Species: *Eptatretus stouti* (Pacific hagfish)

C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996

C;Accession: B39111

R;Varner, J.; Neame, P.; Litman, G.W.

Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991

A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity
 A;Reference number: A39111; MUID:91156684; PMID:2000382
 A;Accession: B39111
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <VAR>
 C;Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
 ||||
 Db 11 QPE 13

RESULT 41

S00150
 ovostatin - duck (fragment)
 N;Alternate names: ovomacroglobulin
 C;Species: Anas platyrhynchos (domestic duck)
 C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
 C;Accession: S00150
 R;Nagase, H.; Harris Jr., E.D.; Brew, K.
 J. Biol. Chem. 261, 1421-1426, 1986
 A;Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).
 A;Reference number: S00150; MUID:86111792; PMID:3511043
 A;Accession: S00150
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <NAG>
 A;Note: part of this sequence, including the amino end of the mature chicken and duck pr

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
 ||||
 Db 10 MVP 12

RESULT 42

PH1625
 Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1625
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1625
 A;Molecule type: DNA
 A;Residues: 1-14 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
 ||||
 Db 9 ETM 11

RESULT 43

PH1627
 Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1627
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1627
 A;Molecule type: DNA
 A;Residues: 1-14 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
 ||||
 Db 9 ETM 11

RESULT 44

PH1594
 Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1594
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1594
 A;Molecule type: DNA
 A;Residues: 1-14 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 ||||
 Db 6 TMV 8

RESULT 45

S21747
 glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) - Pyrococcus furiosus
 C;Species: Pyrococcus furiosus
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C;Accession: S21747
 R;Robb, F.I.; Park, J.B.; Adams, M.W.W.
 Biochim. Biophys. Acta 1120, 267-272, 1992
 A;Title: Characterization of an extremely thermostable glutamate dehydrogenase: a key
 A;Reference number: S21747; MUID:92247806; PMID:1576153
 A;Accession: S21747
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <ROB>
 A;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
 ||||
 Db 1 VKE 3

RESULT 46

PA0044
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 22.5K chain - Arabidopsis thaliana (fra

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 03-Jun-2002
 C;Accession: PA00044
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0044
 A;Molecule type: protein
 A;Residues: 1-14 <KAM>
 A;Experimental source: root
 C;Keywords: NAD; oxidative phosphorylation; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 DB 2 KVK 4

RESULT 47
 S26791
 Ig heavy chain V region (N63P2) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 02-Aug-1996 #text_change 20-Jun-2000
 C;Accession: S26791; S19879
 R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
 Eur. J. Immunol. 22, 241-245, 1992
 A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family
 A;Reference number: S26786; MUID:92111632; PMID:1730251
 A;Accession: S26791
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-15 <MOR>
 A;Cross-references: EMBL:X61022; NID:g32791; PIDN:CAA43356.1; PID:gl335124; EMBL:X61234;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 |||
 DB 9 TMV 11

RESULT 48
 PA0034
 protein QA300024 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0034
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0034
 A;Molecule type: protein
 A;Residues: 1-15 <KAM>
 A;Experimental source: leaf

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 |||
 DB 3 GVP 5

RESULT 49
 PA0014
 seed storage protein 12S 3 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C;Accession: PA0014
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0014
 A;Molecule type: protein
 A;Residues: 1-15 <KAM>
 A;Experimental source: seed
 C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 |||
 DB 5 GVP 7

RESULT 50
 PN0173
 seed storage protein 12S4 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
 C;Accession: PN0173
 R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
 submitted to JIPID, December 1995
 A;Description: Two dimensional electrophoresis of plant proteins and standardization
 A;Reference number: PN0173
 A;Accession: PN0173
 A;Molecule type: protein
 A;Residues: 1-15 <TSU>
 A;Experimental source: seeds

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 |||
 DB 5 GVP 7

RESULT 51
 PA0059
 protein QF200021 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0059
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
 A;Reference number: PA0051
 A;Accession: PA0059
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 |||
 DB 10 GVP 12

RESULT 52

PA0106
 protein QP200076 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0106
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A;Reference number: PA0051
 A;Accession: PA0106
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 11 KVK 13

RESULT 53
 PA0080
 translation elongation factor eEF-2 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0080
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A;Reference number: PA0051
 A;Accession: PA0080
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 C;Keywords: protein biosynthesis

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 |||
 Db 8 GVP 10

RESULT 54
 S10388
 Ig heavy chain J region (clone Re102) - little skate (fragment)
 C;Species: Raja erinacea (little skate)
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
 C;Accession: S10388
 R;Harding, F.A.; Cohen, N.; Litman, G.W.
 Nucleic Acids Res. 18, 1015-1020, 1990
 A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja
 A;Reference number: S08462; MUID:90192082; PMID:2107524
 A;Accession: S10388
 A;Molecule type: DNA
 A;Residues: 1-15 <HAR>
 A;Cross-references: EMBL:X16146; NID:g64284; PIDN:CAA34271.1; PID:gl334773
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 |||
 Db 9 TMV 11

RESULT 55
 S10386

Ig heavy chain J region (clone Re107) - little skate (fragment)
 C;Species: Raja erinacea (little skate)
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
 C;Accession: S10386
 R;Harding, F.A.; Cohen, N.; Litman, G.W.
 Nucleic Acids Res. 18, 1015-1020, 1990
 A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, R
 A;Reference number: S08462; MUID:90192082; PMID:2107524
 A;Accession: S10386
 A;Molecule type: DNA
 A;Residues: 1-15 <HAR>
 A;Cross-references: EMBL:X15124
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 |||
 Db 9 TMV 11

RESULT 56
 B41436
 ovostatin - green seaturtle (fragment)
 C;Species: Chelonia mydas (green seaturtle)
 C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
 C;Accession: B41436
 R;Osada, T.; Sasaki, T.; Ikai, A.
 J. Biochem. 103, 212-217, 1988
 A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobul
 A;Reference number: A41436; MUID:88227890; PMID:2453503
 A;Accession: B41436
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <OSA>

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
 |||
 Db 10 MVP 12

RESULT 57
 A32971
 heparin-binding lectin - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Feb-1997
 C;Accession: A32971
 R;Kohnke-Godt, B.; Gabius, H.J.
 Biochemistry 28, 6531-6538, 1989
 A;Title: Heparin-binding lectin from human placenta: purification and partial molecu
 A;Reference number: A32971; MUID:90001207; PMID:2790011
 A;Accession: A32971
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <KOH>
 C;Keywords: heparin binding

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 8 KVK 10

RESULT 58

PN0662

dystrophin-associated glycoprotein A3a-I - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C;Accession: PN0662
 R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
 A;Reference number: PN0662; MUID:94156881; PMID:8113213
 A;Accession: PN0662
 A;Molecule type: protein
 A;Residues: 1-15 <YOS>
 C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C;Keywords: Glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 |||
 Db 9 GVP 11

RESULT 59

PH1613
 Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1613
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1613
 A;Molecule type: DNA
 A;Residues: 1-15 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 |||
 Db 5 TMV 7

RESULT 60

I38032
 hypothetical MNI/TEL mutant fusion protein type I - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
 C;Accession: I38032
 R;Buijjs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
 Oncogene 10, 1511-1519, 1995
 A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
 A;Reference number: I38031; MUID:95249265; PMID:7731705
 A;Accession: I38032
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-15 <BUI>
 A;Cross-references: EMBL:X85025; NID:g971467; PIDN:CAA59398.1; PID:g971468
 C;Comment: This sequence is the chimeric product of a translocation mutation.
 C;Genetics:
 A;Gene: MNI/ETV6; MNI/TEL
 A;Map position: 22q11/12p13
 C;Keywords: fusion protein

Query Match 16.7%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
 |||
 Db 9 LQP 11

RESULT 61

S03532
 Ig heavy chain J region (JH-7) - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
 C;Accession: S03532
 R;Schwager, J.; Grossberger, D.; du Pasquier, L.
 EMBO J. 7, 2409-2415, 1988
 A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian X.
 A;Reference number: S01158; MUID:89052653; PMID:2903824
 A;Accession: S03532
 A;Molecule type: DNA
 A;Residues: 1-16 <SCH>
 A;Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33046.1; PID:gl334660
 A;Note: the authors translated the codon AAC for residue 1 as Asp
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 |||
 Db 10 TMV 12

RESULT 62

D49021
 Ig heavy chain J7 region - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C;Accession: D49021
 R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
 J. Exp. Med. 171, 1721-1737, 1990
 A;Title: Eleven distinct V-H gene families and additional patterns of sequence varia
 A;Reference number: A47624; MUID:90237760; PMID:2110243
 A;Accession: D49021
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-16 <HAI>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 |||
 Db 10 TMV 12

RESULT 63

S42237
 hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
 C;Species: Staphylococcus aureus
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999
 C;Accession: S42237
 R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
 FEMS Microbiol. Lett. 37, 283-288, 1986
 A;Title: Determination of the complete nucleotide sequence of pNS1, a staphylococcal
 A;Reference number: S42236
 A;Accession: S42237
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-16 <NOG>
 A;Cross-references: EMBL:M16217; NID:gl50832; PIDN:AAA19178.1; PID:g501833

C:Genetics: plasmid pNS1

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
|||
Db 14 VKE 16

RESULT 64

B44896
heat shock protein 18 - Streptomyces albus (fragment)
C:Species: Streptomyces albus
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C:Accession: B44896
R:Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.
J. Bacteriol. 173, 7374-7381, 1991
A:Title: A survey of the heat shock response in four Streptomyces species reveals two groups of heat shock proteins
A:Reference number: A44896; MUID:92041638; PMID:1682303
A:Accession: B44896
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <GUG>
A>Note: sequence extracted from NCBI backbone (NCBIP:65107)

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
|||
Db 14 VKE 16

RESULT 65

S65709
major allergen Myr p I - bulldog ant (Myrmecia pilosula) (fragment)
C:Species: Myrmecia pilosula
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S65709
R:Street, M.D.; Donovan, G.R.; Baldo, B.A.
Biochim. Biophys. Acta 1305, 87-97, 1996
A:Title: Molecular cloning and characterization of the major allergen Myr p II from the bulldog ant
A:Reference number: S65709; MUID:96180991; PMID:8605256
A:Accession: S65709
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <STR>

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
|||
Db 7 PKV 9

RESULT 66

C61414
chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
C:Species: Pseudemys scripta (slider)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C:Accession: C61414
R:Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determination of slider turtle chymotrypsinogen
A:Reference number: A61414; MUID:76146602; PMID:4807189
A:Accession: C61414
A>Status: preliminary

A:Molecule type: protein
A:Residues: 1-16 <BHA>
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
|||
Db 2 GVP 4

RESULT 67

PN0587
tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - Japanese macaque (fragment)
N:Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C:Species: Macaca fuscata (Japanese macaque)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C:Accession: PN0587
R:Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A:Reference number: PN0575; MUID:93371398; PMID:7689834
A:Accession: PN0587

A:Molecule type: genomic RNA
A:Residues: 1-17 <ICH>
A:Cross-references: GB:L14801
A:Experimental source: kidney

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biogenesis.
C:Superfamily: phenylalanine 4-monooxygenase
C:Keywords: biopterin; monooxygenase; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
|||
Db 15 LQP 17

RESULT 68

S03531
Ig heavy chain J5 region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C:Accession: S03531; C49021
R:Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A:Reference number: S01158; MUID:89052653; PMID:2903824
A:Accession: S03531
A:Molecule type: DNA
A:Residues: 1-17 <SCH>
A:Cross-references: EMBL:X14918; NID:G64805; PIDN:CAA33044.1; PID:gl334658
R:Hairst, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation in the immunoglobulin V region: immunoglobulin homology
A:Reference number: A47624; MUID:90237760; PMID:2110243
A:Accession: C49021
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 3-17 <HAI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
|||

Db 11 TWV 13

RESULT 69

S50901
chlorophyll a/b-binding protein lhcb4 - spinach (fragment)
N;Alternate names: light-harvesting complex LHClIIa protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50901
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHClIIa and LHClIc are bound by dicyclohexylphosphoribosylated chlorophyll a/b-binding protein
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50901
A;Molecule type: protein
A;Residues: 1-17 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosynthesis

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
|||
Db 4 LQP 6

RESULT 70

A48179
methane monooxygenase (EC 1.14.13.25) regulatory protein B - Methylococcus capsulatus (Bath)
C;Species: Methylococcus capsulatus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: A48179
R;Pilkington, S.J.; Salmond, G.P.C.; Murrell, J.C.; Dalton, H.
FEMS Microbiol. Lett. 72, 345-348, 1990
A;Title: Identification of the gene encoding the regulatory protein B of soluble methane monooxygenase
A;Reference number: A48179
A;Accession: A48179
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <PIL>
C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMG 7
|||
Db 10 IMG 12

RESULT 71

B61414
chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)
C;Species: Chrysemys picta (painted turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Accession: B61414
R;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined from hemolymph of painted turtle
A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: B61414
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BHA>
C;Keywords: hydrolase; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
|||
Db 2 GVP 4

RESULT 72

S59512
probable integrin alpha3 betal - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-May-1999
C;Accession: S59512
R;McCormick, J.I.; Johnstone, R.M.
Biochem. J. 311, 743-751, 1995
A;Title: Identification of the integrin alpha(3)beta(1) as a component of a partially purified integrin alpha3 beta1 complex
A;Reference number: S59512; MUID:96067588; PMID:7487928
A;Accession: S59512
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <MCC>

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
|||
Db 10 VKE 12

RESULT 73

S69164
ferredoxin al - Japanese radish (fragments)
C;Species: Kaiware daikon (Japanese radish)
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C;Accession: S69164
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Accession: S69164
A;Molecule type: protein
A;Residues: 1-17 <OBA>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
|||
Db 4 KVK 6

RESULT 74

PD0005
very-high-density lipoprotein - sand crayfish (fragment)
N;Alternate names: VLDL
C;Species: Ibacus ciliatus (sand crayfish)
C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: PD0005
R;Komatsu, M.; Ando, S.
Biosci. Biotechnol. Biochem. 62, 459-463, 1998
A;Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand crayfish
A;Reference number: PD0005; MUID:98233268; PMID:9571775
A;Accession: PD0005
A;Molecule type: protein
A;Residues: 1-17 <KOM>
C;Comment: This protein plays an important role in the defense process of crustacea,

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
 |||
 Db 1 LQP 3

RESULT 75
 DRUFPD
 pigment-dispersing hormone - Atlantic sand fiddler crab
 N/Alternate names: PDH
 C/Species: Uca pugilator (Atlantic sand fiddler crab)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
 C/Accession: A25144
 R/Rao, K.R.; Riehm, J.P.; Zahnow, C.A.; Kleinholz, L.H.; Tarr, G.E.; Johnson, L.; Norton
 Proc. Natl. Acad. Sci. U.S.A. 82, 5319-5322, 1985
 A/Title: Characterization of a pigment-dispersing hormone in eyestalks of the fiddler crab
 A/Reference number: A25144
 A/Accession: A25144
 A/Molecule type: protein
 A/Residues: 1-18 <RAO>
 C/Superfamily: pigment-dispersing hormone
 C/Keywords: amidated carboxyl end; neuropeptide
 P/18/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKV 11
 |||
 Db 12 PKV 14

Search completed: November 25, 2003, 19:36:08
 Job time : 13.3488 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKVKETWPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	19	1	LPGE_ECOLI
2	3	16.7	7	1	E105_LITRU
3	3	16.7	8	1	VGLG_HSV2B
4	3	16.7	9	1	COXE_THUOB
5	3	16.7	10	1	BPP_VIPAS
6	3	16.7	10	1	GONI_ALIMI
7	3	16.7	10	1	UPA5_HUMAN
8	3	16.7	11	1	CS15_BACSU
9	3	16.7	12	1	PORD_MBTM
10	3	16.7	12	1	TKN_KASSE
11	3	16.7	13	1	BPPI_BOTJA
12	3	16.7	13	1	E121_LITRU
13	3	16.7	13	1	E122_LITRU
14	3	16.7	15	1	RS6_BACST
15	3	16.7	16	1	FIBA_MELE
16	3	16.7	16	1	FIBA_MUSVI
17	3	16.7	16	1	MMPX_SOLTU
18	3	16.7	16	1	ODPB_SOLTU
19	3	16.7	18	1	AL13_CARMA
20	3	16.7	18	1	DRPH_UCAPU
21	3	16.7	18	1	RL24_PROVU
22	3	16.7	19	1	FIBB_PIG
23	3	16.7	20	1	CS21_STRTR
24	3	16.7	20	1	LECB_IRIHO
25	3	16.7	20	1	PUPK_RHOSH
26	2	11.1	4	1	DCML_PSECH
27	2	11.1	6	1	ASP2_LACSN
28	2	11.1	6	1	E101_LITRU
29	2	11.1	6	1	OVN_IEPDE
30	2	11.1	6	1	UN06_CLOPA
31	2	11.1	7	1	LANC_CARUI
32	2	11.1	7	1	TFPV_PACDA
33	2	11.1	7	1	UF04_MOUSE

34	2	11.1	7	1	WNA3_ACHFU
35	2	11.1	8	1	CKKN_MACEU
36	2	11.1	8	1	FUSS_FUSSO
37	2	11.1	8	1	NPB_BOVIN
38	2	11.1	8	1	PKK3_PERAM
39	2	11.1	8	1	RS7_MYCIT
40	2	11.1	8	1	UH05_RAT
41	2	11.1	8	1	UPA1_HUMAN
42	2	11.1	9	1	AL10_CARMA
43	2	11.1	9	1	BS43_SERPL
44	2	11.1	9	1	CONO_CONGE
45	2	11.1	9	1	FAR3_PENMO
46	2	11.1	9	1	FLA2_TREHY
47	2	11.1	9	1	FRF1_SARBU
48	2	11.1	9	1	LMT3_LOCMI
49	2	11.1	9	1	NEF_HV12B
50	2	11.1	9	1	RT33_BOVIN
51	2	11.1	9	1	SAP_STOVA
52	2	11.1	9	1	TKC1_CALVO
53	2	11.1	9	1	TKL1_LOCM1
54	2	11.1	9	1	TRP4_LEUMA
55	2	11.1	9	1	UF02_MOUSE
56	2	11.1	9	1	ULAD_HUMAN
57	2	11.1	9	1	ULAK_MOUSE
58	2	11.1	9	1	UPA7_HUMAN
59	2	11.1	10	1	COXA_ONCMY
60	2	11.1	10	1	COXH_ONCMY
61	2	11.1	10	1	COXK_ONCMY
62	2	11.1	10	1	FAR6_PANRE
63	2	11.1	10	1	GAJU_HUMAN
64	2	11.1	10	1	LABA_JATMU
65	2	11.1	10	1	LPK2_LOCM1
66	2	11.1	10	1	ODE2_BOVIN
67	2	11.1	10	1	PNEU_HUMAN
68	2	11.1	10	1	PNEU_RAT
69	2	11.1	10	1	PORB_MBTM
70	2	11.1	10	1	RL16_ACHLA
71	2	11.1	10	1	SP34_DICMU
72	2	11.1	10	1	SPI_HALUP
73	2	11.1	10	1	SYK_CAMUP
74	2	11.1	10	1	TKL2_LOCM1
75	2	11.1	10	1	TKL3_LOCM1
76	2	11.1	10	1	TKL4_LOCM1
77	2	11.1	10	1	TRP5_LEUMA
78	2	11.1	10	1	TRP7_LEUMA
79	2	11.1	10	1	TRP8_LEUMA
80	2	11.1	10	1	TRP9_LEUMA
81	2	11.1	10	1	UPA4_HUMAN
82	2	11.1	10	1	UPA8_HUMAN
83	2	11.1	10	1	UPA9_HUMAN
84	2	11.1	10	1	URE3_MORMO
85	2	11.1	10	1	VEG6_BACSU
86	2	11.1	10	1	BPPE_AKHA
87	2	11.1	11	1	COXA_CANFA
88	2	11.1	11	1	HS70_PINPS
89	2	11.1	11	1	MLG_THETS
90	2	11.1	11	1	MORN_HUMAN
91	2	11.1	11	1	RS30_ONCMY
92	2	11.1	11	1	TINI_HOPTI
93	2	11.1	11	1	TKC2_CALVO
94	2	11.1	11	1	TKN1_PSEGU
95	2	11.1	11	1	TKN2_PSEGU
96	2	11.1	11	1	TKN2_PSEGU
97	2	11.1	11	1	TKN2_PSEGU
98	2	11.1	11	1	TKN2_PSEGU
99	2	11.1	11	1	TKN3_PSEGU
100	2	11.1	11	1	TKN3_PSEGU

ALIGNMENTS

RESULT 1

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LPGE ECOLI
ID _LPGE_ECOLI STANDARD; PRT; 19 AA.
AC P33236;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gef leader peptide.
GN GEFL OR B0018.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92048481; PubMed=1943701;
RA Poulsen L.K., Refn A., Molin S., Andersson P.;
RT "The gef gene from Escherichia coli is regulated at the level of
translation."
RN Mol. Microbiol. 5:1639-1648(1991).
RL [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AE000112; AAC73129.1; ALT_TERM.
DR EcoGene; EG12074; gsfL.
SQ Leader peptide; Complete proteome.
KW SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 22.2%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13
DB 13 KVKE 16

RESULT 2
EI05 LITRU
ID EI05 LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=skin secretion;
RA Wahlitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -----

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
DB 4 PEI 6

RESULT 3
VGLG HSV2B STANDARD; PRT; 8 AA.
ID VGLG HSV2B
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON TER 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C86588 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 3 GVP 5

RESULT 4
COXE THUOB STANDARD; PRT; 9 AA.
ID COXE THUOB
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide VIa (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
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CC      MITOCHONDRIAL ELECTRON TRANSPORT.
CC      -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC      -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR      PIR; S77984; S77984.
DR      InterPro; IPR001349; COX6A.
DR      PROSITE; PS01329; COX6A; PARTIAL.
KW      Oxidoreductase; Inner membrane; Mitochondrion.
FT      NON_TER 1 1
FT      NON_TER 9 9
SQ      SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match      16.7%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QPE 4
DB      3 QPE 5

RESULT 5
BPP VIPAS
ID      BPP VIPAS      STANDARD;      PRT;      10 AA.
AC      P31351;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Bradykinin-potentiating peptide (Angiotensin-converting
DE      enzyme inhibitor)
OS      Vipera aspis (Aspic viper).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC      Viperidae; Viperinae; Vipera.
OX      NCBI_TaxID=8706;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RX      MEDLINE=90382616; PubMed=2169439;
RA      Komori Y., Sugihara H.;
RT      "Characterization of a new inhibitor for angiotensin converting
RT      enzyme from the venom of Vipera aspis aspis.";
RL      Int. J. Biochem. 22:767-771(1990).
CC      -!- FUNCTION: This peptide both inhibits the activity of the
CC      angiotensin-converting enzyme and enhances the action of
CC      bradykinin by inhibiting the kinases that inactivate it.
CC      It acts as an indirect hypotensive agent.
CC      PIR; A60377; XASNPC.
DR      Hypotensive agent; Pyrrolidone carboxylic acid.
KW      MOD_RES 1 1
FT      MOD_RES 1 1
FT      MOD_RES 9 9
SQ      SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      6 PKV 8

RESULT 6
GONI ALLMI
ID      GONI ALLMI      STANDARD;      PRT;      10 AA.
AC      P37041; P20407;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gonadoliberin I (Gonadotropin-releasing hormone I) (LH-RH I)
DE      (Luliberin I).
OS      Alligator mississippiensis (American alligator).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC      Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX      NCBI_TaxID=8496;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Brain;
RX      MEDLINE=91352338; PubMed=1882082;
RA      Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA      Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT      "Primary structure of two forms of gonadotropin-releasing hormone
RT      from brains of the American alligator (Alligator mississippiensis).";
RL      Regul. Pept. 33:105-116(1991).
CC      -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the GNRH family.
DR      PIR; A60066; RHA01.
DR      InterPro; IPR002012; GNRH.
DR      Pfam; PF00446; GNRH; 1.
DR      PROSITE; PS00473; GNRH; 1.
KW      Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT      MOD_RES 1 1
FT      MOD_RES 10 10
SQ      SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQP 3
DB      7 LQP 9

RESULT 7
UPA5 HUMAN
ID      UPA5 HUMAN      STANDARD;      PRT;      10 AA.
AC      P30091;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Plasma;
RX      MEDLINE=93092937; PubMed=1459097;
RA      Hughes G.J., Frutiger S., Paquet N., Ravier P., Pasquali C.,
RA      Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA      Hochrasser D.F.;
RT      "Plasma protein map: an update by microsequencing.";
RT      Electrophoresis 13:707-714(1992).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC      -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC      ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC      PROTEIN.
DR      SWISS-2DPAGE; P30091; HUMAN.
FT      NON_TER 1 1
FT      VARIANT 9 9
FT      VARIANT 9 9
FT      NON_TER 10 10
SQ      SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      4 PKV 6

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Query Match      16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VKE 13
Db      8 VKE 10

RESULT 10
TKN_KASSE
ID_TKN_KASSE STANDARD; PRT; 12 AA.
AC P08f11.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OC NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=7746385; PubMed=891753;
RA Anastasi A., Montecucchi P.C., Erspamer V., Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
dodecapeptide from the skin of the African frog Kassina
senegalensis.";
RL Experientia 33:857-858(1977).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07206; S07206.
DR PDB; 1MYU; 16-OCT-02.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
RW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW 3D-structure.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VPK 10
Db      2 VPK 4

RESULT 11
BPPI_BOTJA
ID_BPPI_BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
DE Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxID=8724, 8723;
RN [1]

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RP SEQUENCE.
 RC SPECIES=B.jararaca; TISSUE=Venom;
 RX MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
 RA Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 RT jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=B.insularis; TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01253; XAV19B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1388 MW; 6924FC97D83D6774 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
 |||
 Db 9 PEI 11

RESULT 12
 E121_LITRU STANDARD; PRT; 13 AA.
 ID E121_LITRU STANDARD; PRT; 13 AA.
 AC P82097;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 2.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litori electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 5 KVK 7

RESULT 13
 E122_LITRU STANDARD; PRT; 13 AA.
 ID E122_LITRU STANDARD; PRT; 13 AA.

AC P82098;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 2.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litori electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B957322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 5 KVK 7

RESULT 14
 RS6_BACST STANDARD; PRT; 15 AA.
 ID RS6_BACST STANDARD; PRT; 15 AA.
 AC P59582;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 30S ribosomal protein S6 (BS9) (Fragment).
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=10;
 RX PubMed=4607606;
 RA Yaguchi M., Matheson A.T., Visentin L.P.;
 RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and
 RT structural correspondence of 30 S ribosomal proteins from Escherichia
 RT coli and Bacillus stearothermophilus.";
 RL FEBS Lett. 46:296-300(1974).
 CC -!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
 DR HAMAP; MF_00360; -; 1.
 DR PROSITE; PS01048; RIBOSOMAL S6; PARTIAL.
 KW Ribosomal protein; rRNA-binding.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1974 MW; 18C5E2E851E09572 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIM 6
 |||
 Db 5 EIM 7

RESULT 15

FIBA_MELME STANDARD; PRT; 16 AA.
 ID FIBA_MELME
 AC P14456;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Meles meles (Eurasian badger).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
 OC Meles.
 OC NCBI_TaxID=9662;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals."
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VKE 13
 DB |||
 3 VKE 5

FIBA_MUSVI STANDARD; PRT; 16 AA.
 ID FIBA_MUSVI
 AC P14458;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 OC NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals."
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VKE 13
 DB |||
 3 VKE 5

Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VKE 13
 DB |||
 3 VKE 5

RESULT 17
 MPMX_SOLTU STANDARD; PRT; 16 AA.
 ID MPMX_SOLTU
 AC P80501;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Unidentified mitochondrial matrix protein (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=9707345; PubMed=8919912;
 RA Jansch L., Kruft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria."
 RL Plant J. 9:357-368(1996).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC Mitochondrion.
 KW NON_TER 16 16
 KW SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 VPK 10
 DB |||
 4 VPK 6

RESULT 18
 ODPB_SOLTU STANDARD; PRT; 16 AA.
 ID ODPB_SOLTU
 AC P81419;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
 DE (EC 1.2.4.1) (PDBE1-B) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Romano; TISSUE=Tuber;
 RX MEDLINE=98399821; PubMed=9729464;
 RA Millar A.H., Knorr C., Leaver C.J., Hill S.A.;
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and
 RT identification of catalytic components in potato."
 RL Biochem. J. 334:571-576(1998).
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
 CC multiple copies of three enzymatic components: pyruvate
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
 CC lipoamide dehydrogenase (E3).
 CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-

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CC      acetyldihydroipoamide + CO(2).
CC      -|- COFACTOR: THIAMINE PYROPHOSPHATE.
CC      -|- SUBUNIT: Tetramer of two alpha and two beta subunits (by
CC      similarity).
CC      -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW      Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW      phosphorylation; Mitochondrion.
FT      NON TER 16 16
SQ      SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKE 13
DB      4 VKE 6

RESULT 19
AL13_CARMA
ID      AL13_CARMA STANDARD; PRT; 18 AA.
AC      P81816;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Carcinustatin 13.
OS      Carcinus maenas (Common shore crab) (Green crab).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX      NCBI_TaxID=6759;
RN      [1]
RP      TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX      MEDLINE=98121193; PubMed=9461295;
RA      Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA      Thorpe A.;
RT      Isolation and identification of multiple neuropeptides of the
RT      allatostatin superfamily in the shore crab Carcinus maenas.;
RT      Eur. J. Biochem. 250:727-734(1997).
CC      -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC      -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW      Neuropeptide; Amidation; Multigene family.
FT      MOD RES 18 18
FT      SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;
SQ      SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      11 PKV 13

RESULT 20
DRPH_UCAPU
ID      DRPH_UCAPU STANDARD; PRT; 18 AA.
AC      P08871;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-NOV-1988 (Rel. 09, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Pigment-dispersing hormone (PDH) (Light adapting distal retinal
DE      pigment hormone) (ORPH).
OS      Uca pugnator (Atlantic sand fiddler crab) (Celuca pugnator).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex;
OC      Celuca.
OX      NCBI_TaxID=6772;
RN      [1]
RP      NON TER 1 1
RP      SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;

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RA      Rao K.R., Riehm J.P., Zahnow C.A., Kleinholz L.H., Tarr G.E.,
RA      Johnson L., Norton S., Landau M., Semmes O.J., Sattelsberg R.M.,
RA      Jorenbey W.H., Hintz M.F.;
RT      "Characterization of a pigment-dispersing hormone in eyestalks of the
RT      fiddler crab Uca pugnator.";
RL      Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322(1985).
RN      [2]
RP      SEQUENCE.
RX      MEDLINE=93230895; PubMed=8472537;
RA      Loehr J., Klein J., Webster S.G., Dirksen H.;
RT      "Quantification, immunospecificity purification and sequence analysis of
RT      a pigment-dispersing hormone of the shore crab, Carcinus maenas
RT      (L.).";
RL      Comp. Biochem. Physiol. 104B:699-706(1993).
CC      -|- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT
CC      INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND
CC      THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
CC      -|- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
DR      PIR; A25144; DRUFPD.
KW      Hormone; Amidation.
FT      DOMAIN 6 9
FT      MOD RES 18 18
FT      SEQUENCE 18 AA; 1928 MW; 25D5CE8D016F544E CRC64;
SQ      SEQUENCE 18 AA; 1928 MW; 25D5CE8D016F544E CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      12 PKV 14

RESULT 21
RL24_PROVU
ID      RL24_PROVU STANDARD; PRT; 18 AA.
AC      P20032;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      50S ribosomal protein L24 (fragment).
GN      RPLX.
OS      Proteus vulgaris.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Proteus.
OX      NCBI_TaxID=585;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89125589; PubMed=2464692;
RA      Carretti D.P., Matheakis L.C., Kearney K.R., Vu L., Nomura M.;
RT      "Translational regulation of the spc operon in Escherichia coli.
RT      Identification and structural analysis of the target site for S8
RT      repressor protein.";
RL      J. Mol. Biol. 204:309-329(1988).
CC      -|- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND
CC      IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT
CC      INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.
CC      -|- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
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CC      -----
DR      EMBL; M36264; AAA5661.1; -
DR      InterPro; IPR005825; Ribosomal L24_26.
DR      PROSITE; PS01108; RIBOSOMAL_L24; PARTIAL.
KW      Ribosomal protein.
FT      NON TER 1 1
FT      SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;

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Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 KET 14
      |||
Db      14 KET 16

RESULT 22
FIBB_PIG      STANDARD;      PRT;      19 AA.
AC P14477;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 19 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2200 MW; 09F87E44F4F3863D CRC64;

Query Match      16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
      |||
Db      12 PKV 14

RESULT 23
CS21_STRTR      STANDARD;      PRT;      20 AA.
AC P81621;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 21 kDa cold-shock induced protein (fragment).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE.
RC STRAIN=PB18;
RX MEDLINE=99456673; PubMed=10525839;
RA Ferrin C., Guimont C., Bracquet P., Gaillard J.L.;
RT "Expression of a new cold shock protein of 21.5 kDa and of the major
RT cold shock protein by Streptococcus thermophilus after cold shock.";
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RL Curr. Microbiol. 39:342-347(1999).
CC -!- INDUCTION: By cold shock.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2290 MW; 9C2CA57F266B80AD CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 KET 14
      |||
Db      5 KET 7

RESULT 24
LECB_IRHO      STANDARD;      PRT;      20 AA.
ID -LECB_IRHO
AC P36231;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE N-acetyl-D-galactosamine-binding lectin subunit B (A-disaccharide-
DE binding lectin subunit B) (Fragment).
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OC Iris.
OX NCBI_TaxID=35876;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest, and cv. Prof. Blaauw; TISSUE=Bulb;
RX MEDLINE=94171801; PubMed=8125993;
RA Mo H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;
RT "Isolation and characterization of an
RT N-acetyl-D-galactosamine-binding lectin from Dutch Iris bulbs which
RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal).";
J. Biol. Chem. 269:7666-7673(1994).
CC -!- FUNCTION: GAL / GALNAc-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE
CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES
CC IRRESPECTIVE OF BLOOD GROUP TYPE.
CC -!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.
KW Lectin.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 ETM 15
      |||
Db      10 ETM 12

RESULT 25
PUFK_RHOSH      STANDARD;      PRT;      20 AA.
AC Q53121; O08033;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein pufK.
GN PUFK.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=96349111; PubMed=8760918;
RA Gong L., Kaplan S.;
RT "translational control of puf operon expression in Rhodobacter
```

RT sphaeroides 2.4.1.1; ;
 RL Microbiology 142:2057-2069 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RA McGlynn P.;
 RT "R.sphaeroides genes bchC, bchX, bchY, bchZ and pufO";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=20115911; PubMed=10648776;
 RA Choudhary M., Kaplan S.;
 RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
 sphaeroides 2.4.1.1";
 RL Nucleic Acids Res. 28:862-867 (2000).
 CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF PUF.
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 CC -----
 DR EMBL; S82643; AAB46798.1; -;
 DR EMBL; AJ010302; CAB38751.1; -;
 DR EMBL; AF195122; AAF24301.1; -;
 DR PIR; T50757; T50757.
 KW Transcription regulation.
 SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 MVP 17
 DB 1 MVP 3

RESULT 26
 DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydrotrophic bacteria";
 RL Arch. Microbiol. 152:335-341 (1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 SMALL.
 CC PIR; P10140; P10140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4

SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 MG 7
 DB 1 MG 2

RESULT 27
 ASP2_LACSN STANDARD; PRT; 6 AA.
 ID ASP2_LACSN
 AC P82655;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acid shock protein 2 (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CB1;
 RX MEDLINE=21322712; PubMed=11429463;
 RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;
 RT "The acid-stress response in Lactobacillus sanfranciscensis CB1";
 RL Microbiology 147:1863-1873 (2001).
 CC -!- INDUCTION: Overexpressed in acid environments.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 KE 13
 DB 2 KE 3

RESULT 28
 EI01_LITRU STANDARD; PRT; 6 AA.
 ID EI01_LITRU
 AC P82036;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoides; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 Litoria electrica. Comparison with the skin peptides from Litoria
 rubella";
 RL Aust. J. Chem. 52:639-645 (1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 6
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
||
Db 2 VP 3

RESULT 29

OVN LEPDE STANDARD; PRT; 6 AA.
AC P42585;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (LeD-OVM)
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelini; Leptinotarsa;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;

[1] SEQUENCE AND SYNTHESIS.
RN TISSUE=Head;

RC MEDLINE=91271080; PubMed=2052497;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
stimulating head peptide in the Colorado potato beetle, Leptinotarsa
decemlineata.";
RT Peptides 12:31-36(1991).

RL Peptides 12:31-36(1991).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
OVIDUCT.

CC Neuropeptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 720 MW; 6B07632BDD03000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4
||
Db 5 PE 6

RESULT 30

UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 6 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;

[1] SEQUENCE.
RN STRAIN=W5;

RC MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.

NON TER 6
FT MOD RES 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5
||
Db 5 EI 6

RESULT 31

LANC_CARUI STANDARD; PRT; 7 AA.
ID LANC_CARUI
AC P36360;

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnosin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).

OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;

[1] SEQUENCE.

RP MEDLINE=92321768; PubMed=1622206;
RX Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;

RT "Purification and characterization of a new bacteriocin isolated from
a Carnobacterium sp.";
Appl. Environ. Microbiol. 58:1417-1422(1992).

CC -1- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.

NON TER 7
FT MOD RES 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
||
Db 5 QP 6

RESULT 32

TPFY_PACDA STANDARD; PRT; 7 AA.
ID TPFY_PACDA
AC P83455;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Tryptophyllin-1 (PdT-1).
OS Pachymedusa dactinolor (Giant mexican leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;

[1] SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
PRO-7.

RP TISSUE=Skin secretion;
RC Chen T.B., Orr D.F., Shaw C.;

RT "Pachymedusa dactinolor tryptophyllin-1 (PdT-1): structural
characterization, pharmacological activity and cloning of precursor
cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.

CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular
smooth muscle.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Skin.

DR GO; GO:000576; C:extracellular; NAS.

DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.

KW Amphibian defense peptide; Amidation; Hydroxylation.

FT MOD RES 3 3 7
7 7 7
AMIDATION.

```
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
DB 6 VP 7

RESULT 33
UF04 MOUSE STANDARD; PRT; 7 AA.
AC P3842;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -!- PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
DB 1 PK 2

RESULT 34
WVA3 ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-3.
OC Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica."
RL FEBS Lett. 323:104-108(1993).
DR PIR: S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 12 KE 13
DB 2 KE 3

RESULT 35
CCKN MACEU STANDARD; PRT; 8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials."
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: A43001; A43001.
DR PIR: PQ0012; PQ0012.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD RES 2 2 SULFATION.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG 7
DB 3 MG 4

RESULT 36
FUSS FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verna J., Gangal S.V.;
RL Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.
FT NON TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
```


Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 IM 6
||
Db 2 IM 3

RESULT 37

NPB_BOVIN
ID_NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
CC PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 QP 3
||
Db 4 QP 5

RESULT 38

PK3_PERAM
ID_PK3_PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinnin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).

CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKINNIN FAMILY.
KW Neuropeptide; Amidation; Pyrokinnin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D72C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 8 VP 9
||
Db 2 VP 3

RESULT 39

RS7_MYCIT
ID_RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
DE RPSG.
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC tRNA (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.

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EMBL; L08171; AAA25376.1; -;
PIR; S35538; S35538.
DR HAWAP; MF 00480; -; 1.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; tRNA-binding.
FT INIT MET 0 0 BY SIMILARITY.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 9 PK 10
||
Db 7 PK 8

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RESULT 40
UH09 RAT
ID UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RX Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Junblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4
||
Db 7 PE 8

RESULT 41
UPA1 HUMAN
ID UPA1 HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON TER 1
FT UNSURE 8
FT NON TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
||
Db 6 VP 7

RESULT 42
AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]_TaxID=6759;
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
||
Db 3 QP 4

RESULT 43
BS43 SERPL
ID BS43 SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]_TaxID=82996;
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against Erwinia amylovora, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
DR InterPro; IPR006498; Tail tube.
DR Pfam; PF04985; Phage tube_1.
KW Antibiotic; Bacteriocin.
FT NON TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871B1FB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
||
Db 5 GV 6

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RESULT 44
CONO CONGE STANDARD; PRT; 9 AA.
ID -CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro; IPR000981; Neurhyp_horn.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1037 MW; DAFC276EB4540059 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PK 10
Db 7 PK 8

RESULT 45
FAR3 PENMO STANDARD; PRT; 9 AA.
ID -FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (AQPSMRLPF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RM MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivithangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 2 QP 3

RESULT 46
FAR4 PENMO STANDARD; PRT; 9 AA.
ID -FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLPF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RM MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivithangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 2 QP 3

RESULT 47
FLA2 TREHY STANDARD; PRT; 9 AA.
ID -FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are

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RT composed of two sheath proteins and three core proteins." ;
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
CC FLAB3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2 2
FT UNSURE 8 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ET 14
DB 1 ET 2

RESULT 48
FRF1_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE-CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 1 QP 2

RESULT 49
LMT3_LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria; members of the
RT locustamyotropin peptide family." ;
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 3 QP 4

RESULT 50
NEF_HV128 STANDARD; PRT; 9 AA.
ID NEF_HV128
AC P12481;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).
GN NEF.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3395517;
RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1." ;
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
CC activities. It seems to down-regulate the CD4(T4) antigen.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC
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CC
CC EMBL; J03653; AAA44687.1; -.
DR HIV; J03653; NEFSY1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT NON TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 319CB325A3733878 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;

QY 6 MG 7
||
Db 1 MG 2

RESULT 51
RT33 BOVIN
ID RT33 BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRP633.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C.; Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
J. Biol. Chem. 276:19363-19374(2001).
RL J. Biol. Chem. 276:19363-19374(2001).
CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
(28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
||
Db 5 QP 6

RESULT 52
SAP_STOVA
ID SAP_STOVA STANDARD; PRT; 9 AA.
AC P24047;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Sperm-activating peptide (SAP).
OS Stomopneustes variolaris (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinidea; Euechinoidea; Diadematozoa; Phymosomatoida; Stomechinidae;
OC Stomopneustes.
OX NCBI_TaxID=7663;
RN [1]
RP SEQUENCE, AND DISULFIDE BOND.
RC TISSUE=Egg jelly;
RX Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;
RA "Determination of the amino acid sequence of an intramolecular
RT disulfide linkage-containing sperm-activating peptide by tandem mass
RT spectrometry."
RL FEBS Lett. 294:179-182(1991).
CC -1- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CAMP, CGMP AND CALCIUM LEVELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF

CC GUANYLATE CYCLASE.
FT DISULFID 3 8
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4
||
Db 4 PE 5

RESULT 53
TKL1 CALVO
ID TKL1 CALVO STANDARD; PRT; 9 AA.
AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R.J.,
Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -1- FUNCTION: MYOACTIVE PEPTIDE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59DC1B7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
||
Db 7 GV 8

RESULT 54
TKL1 LOOMI
ID TKL1 LOOMI STANDARD; PRT; 9 AA.
AC P16223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=30184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family."
RL FEBS Lett. 261:397-401(1990).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE

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CC      OVIDUCT AND FOREGUT.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW      Tachykinin; Neuropeptide; Amidation.
FT      MOD RES          9          9
SQ      SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GV 8
      |||
DB      7 GV 8

RESULT 55
TRP4 LEUMA
ID TRP4 LEUMA STANDARD; PRT; 9 AA.
AC P81736;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 4 (LemRP 4).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1] _SEQUENCE
RP SEQUENCE
RC TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MIDGUT.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES          9          9
SQ      SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MG 7
      |||
DB      6 MG 7

RESULT 56
UF02 MOUSE
ID UF02 MOUSE STANDARD; PRT; 9 AA.
AC P3840;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _SEQUENCE
RP SEQUENCE
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

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RT      "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL      Electrophoresis 15:735-745(1994).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
FT      NON TER          9          9
SQ      SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EI 5
      |||
DB      4 EI 5

RESULT 57
ULAD HUMAN
ID ULAD HUMAN STANDARD; PRT; 9 AA.
AC P31929;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] _SEQUENCE
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
FT      SWISS-2DPAGE; P31929; HUMAN.
FT      NON TER          9          9
SQ      SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VK 12
      |||
DB      2 VK 3

RESULT 58
ULAK MOUSE
ID ULAK MOUSE STANDARD; PRT; 9 AA.
AC P9031;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _SEQUENCE
RP SEQUENCE
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

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CC      PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.
DR      SWISS-2DPAGE: P99031; MOUSE.
FT      NON TER          9
SQ      SEQUENCE      9 AA; 1106 MW; E1E842C3240B145A CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 KV 11
      ||
Db      6 KV 7

RESULT 59
UPA7 HUMAN          STANDARD;      PRT;      9 AA.
AC      P30093;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Plasma;
RX      MEDLINE=93092937; PubMed=1459097;
RA      Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA      Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA      Hochstrasser D.F.;
RT      "Plasma protein map: an update by microsequencing.";
RL      Electrophoresis 13:707-714(1992).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
DR      SWISS-2DPAGE; P30093; HUMAN.
FT      NON TER          1 1
FT      UNSURE           5 5
FT      NON TER          9 9
SQ      SEQUENCE      9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PE 4
      ||
Db      4 PE 5

RESULT 60
COXA ONCMY
ID      COXA ONCMY          STANDARD;      PRT;      10 AA.
AC      P80328;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX      NCBI_TaxID=8022;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Liver;
RX      MEDLINE=94237150; PubMed=8181469;
RA      Freund R., Kadenbach B.;
RT      "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT      of cytochrome c oxidase isolated from rainbow trout.";
RL      Eur. J. Biochem. 221:1111-1116(1994).
CC      -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC      CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC      MITOCHONDRIAL ELECTRON TRANSPORT.
CC      -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR      PIR; S43630; S43630.
KW      Oxidoreductase; Inner membrane; Mitochondrion.
FT      NON TER          10 10
SQ      SEQUENCE      10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VP 9
      ||
Db      4 VP 5

RESULT 62
COXK ONCMY
ID      COXK ONCMY          STANDARD;      PRT;      10 AA.
AC      P80332;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).
OS      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX      NCBI_TaxID=8022;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Liver;
RX      MEDLINE=94237150; PubMed=8181469;
RA      Freund R., Kadenbach B.;
RT      "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT      of cytochrome c oxidase isolated from rainbow trout.";
RL      Eur. J. Biochem. 221:1111-1116(1994).

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OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferrocytochrome
c + 2 H2O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11
DB 3 KV 4

RESULT 63
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAFQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRFamide-related
peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 5 QP 6

RESULT 64
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75150968; PubMed=5538385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MIM; I37220; -.
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10
FT PEPTIDE 2 10
SQ SEQUENCE 10 AA; 1004 MW; CFEC6AB02C387D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11
DB 5 KV 6

RESULT 65
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosids I; Malpighiales; Euphorbiaceae; Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY
SEEMS TO BE BASED ON AN INTERACTION WITH C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR
TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
DB 2 GV 3

RESULT 66
LPK2_LOCMI
ID LPK2_LOCMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrrolin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94094539; PubMed=7903606;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustapyrokinin II from
RT Locusta migratoria, another member of the FXPRL-amide peptide
RT family.";
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
CC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
DB 3 VP 4

RESULT 67
ODP2_BOVIN STANDARD; PRT; 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
RT "Primary structure around the lipocate-attachment site on the E2
RT component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydropyrimidine acetyltransferase (E2) and
CC lipocate dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydropyrimidine = CoA + S-
CC acetyldihydropyrimidine.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro; IPR003016; Lipoyl.
DR PROSITE; PS00189; LIPOYL; PARTIAL.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.

FT NON_TER 1 1 LIPOYL.
FT BINDING 5 5
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BECDAAD33AB1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ET 14
DB 2 ET 3

RESULT 68
PNEU_HUMAN STANDARD; PRT; 10 AA.
ID PNEU_HUMAN
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
DR PIR; B33143; B33143.
DR GO; GO:0030103; P:vasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
DB 9 GV 10

RESULT 69
PNEU_RAT STANDARD; PRT; 10 AA.
ID PNEU_RAT
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

```

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GV 8
      |||
DB      9 GV 10

RESULT 70
PORB METTM      STANDARD;      PRT;      10 AA.
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
DE (Fragment).
GN PORB.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + COA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1332 MW; 167011DAF6DB0760 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PE 4
      |||
DB      4 PE 5

RESULT 71
RL16 ACHLA
ID PL16 ACHLA      STANDARD;      PRT;      10 AA.
AC F29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).
GN RPLP.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210505; PubMed=1556079;
RA Lim P.O., Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
RT organism and Acholeplasma laidlawii deduced from two ribosomal protein
RT gene sequences.";
RL J. Bacteriol. 174:2606-2611(1992).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS

```

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LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
(BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; M74771; AAA21914.1; -.
DR PIR; F41839; F41839.
DR InterPro; IPR00114; Ribosomal_L16.
DR PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PK 10
      |||
DB      4 PK 5

RESULT 72
SP34 DICMU
ID SP34 DICMU      STANDARD;      PRT;      10 AA.
AC P81545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Surface protein P34 (Fragment).
GN P34.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE.
RA Schreiner S.J.;
RT "Characterization of a surface protein in macrocysts of Dictyostelium
RT mucoroides.";
RL Submitted (NOV-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -!- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
KW Cell wall.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EI 5
      |||
DB      2 EI 3

RESULT 73
SPI HALRO
ID SPI HALRO      STANDARD;      PRT;      10 AA.
AC Q10997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

```

DE Serine proteinase inhibitor (Fragment).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyruidae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RN SEQUENCE.
RP TISSUE=Hemolymph;
RC MEDLINE=96321313; PubMed=8759295;
RX Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RA "Purification and characterization of a 58,000-Da proteinase
RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia
RT roretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 KV 11
DB 8 KV 9
RESULT 74
SYK CAMUP
ID - SYK CAMUP STANDARD; PRT; 10 AA.
AC Q4646;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE (Fragment).
GN LYSS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=28080;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 43954;
RC MEDLINE=97149302; PubMed=8996110;
RX Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RA "Characterization of Campylobacter upsaliensis fur and its
RT localization in a highly conserved region of the Campylobacter
RT genome";
RL Gene 183:219-224(1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

DR EMBL; L77076; AAB41342.1; --
DR HAMAP; MF_00252; -; 1.
DR InterPro; IPR006195; tRNA_ligase_II.

DR PROSITE; PS50862; AA tRNA LIGASE II; PARTIAL.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Magnesium.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 KE 13
DB 6 KE 7
RESULT 75
TKL2 LOCM1
ID - TKL2 LOCM1 STANDARD; PRT; 10 AA.
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RN SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=90184489; PubMed=2311766;
RX Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RA "Locustatachykinin I and II, two novel insect neuropeptides which
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GV 8
DB 8 GV 9
Search completed: November 25, 2003, 19:28:21
Job time : 6.45515 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33,8023 Seconds
(without alignments)
137,415 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVFKVETMVPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	12	2	Q50019 mycobacteri
2	4	22.2	12	8	Q31851 arabidopsis
3	4	22.2	16	2	O54357 bacillus am
4	4	22.2	18	12	Q919D5 human papil
5	4	22.2	18	12	Q919B3 human papil
6	4	22.2	18	12	Q919B5 human papil
7	4	22.2	18	12	Q919B7 human papil
8	4	22.2	18	12	Q919C5 human papil
9	4	22.2	18	12	Q919D1 human papil
10	4	22.2	18	12	Q919D3 human papil
11	4	22.2	18	12	Q919B9 human papil
12	4	22.2	18	12	Q919A8 human papil
13	4	22.2	18	12	Q919C7 human papil
14	4	22.2	18	12	Q919C9 human papil
15	4	22.2	19	2	Q9R4Q2 pseudomonas
16	4	22.2	19	6	Q9N195 bos taurus

17	3	16.7	8	6	Q95M23	Q95m23 sus scrofa
18	3	16.7	8	13	Q8JJ35	Q8jj35 ficedula hy
19	3	16.7	9	2	Q93E20	Q93e20 streptococc
20	3	16.7	9	4	Q96F97	Q96f97 homo sapien
21	3	16.7	9	10	P82440	P82440 nicotiana t
22	3	16.7	9	13	Q8AYL5	Q8ayl5 carassius a
23	3	16.7	9	13	Q8AUM7	Q8aum7 carassius a
24	3	16.7	10	1	Q50843	Q50843 methanococc
25	3	16.7	10	15	Q86324	Q86324 rous sarcom
26	3	16.7	10	15	Q86325	Q86325 rous sarcom
27	3	16.7	10	15	Q86326	Q86326 rous sarcom
28	3	16.7	11	4	O60614	O60614 homo sapien
29	3	16.7	11	4	Q9NV38	Q9nv38 homo sapien
30	3	16.7	11	7	O19718	O19718 homo sapien
31	3	16.7	11	13	Q8UUP1	Q8uup1 xenopus lae
32	3	16.7	11	16	Q9K7A4	Q9k7a4 bacillus ha
33	3	16.7	12	15	Q9ICES	Q9ice5 human immun
34	3	16.7	13	2	Q31295	Q31295 buchnera ap
35	3	16.7	13	4	Q9UB87	Q9ue87 homo sapien
36	3	16.7	13	8	Q8WEJ9	Q8wej9 ginkgo bilo
37	3	16.7	13	10	Q93380	Q93380 brassica ol
38	3	16.7	13	11	Q88176	Q88176 mus musculu
39	3	16.7	14	1	Q9UWM2	Q9uwm2 pyrocococc
40	3	16.7	14	2	Q55326	Q55326 synchococc
41	3	16.7	14	3	Q8J1G2	Q8j1g2 ashbya goss
42	3	16.7	14	4	Q9P2A2	Q9p2a2 homo sapien
43	3	16.7	14	4	Q16045	Q16045 homo sapien
44	3	16.7	14	6	Q8HYM2	Q8hyu2 felis silve
45	3	16.7	14	10	P82341	P82341 pisum sativ
46	3	16.7	14	12	Q98818	Q98818 murine minu
47	3	16.7	14	13	Q8AXQ7	Q8axq7 xenopus lae
48	3	16.7	15	3	Q9UR63	Q9ur63 emericella
49	3	16.7	15	4	Q9UB41	Q9ue41 homo sapien
50	3	16.7	15	4	Q9UCC7	Q9ucc7 homo sapien
51	3	16.7	15	4	Q9UCY1	Q9ucy1 homo sapien
52	3	16.7	15	6	O46661	O46661 macropus ro
53	3	16.7	15	6	Q9TR64	Q9tr64 oryctolagus
54	3	16.7	15	6	Q9MZ85	Q9mz85 oryctolagus
55	3	16.7	15	8	Q9TH04	Q9th04 gryus americ
56	3	16.7	15	10	Q9AT15	Q9at15 lycopersico
57	3	16.7	15	10	P93515	P93515 arabidopsis
58	3	16.7	15	10	Q9S8N8	Q9s8n8 hordeum vul
59	3	16.7	15	13	Q9PR20	Q9pr20 bothrops ja
60	3	16.7	16	2	Q51950	Q51950 staphylococc
61	3	16.7	16	2	Q9F1S7	Q9f1s7 streptococc
62	3	16.7	16	2	Q9F1S4	Q9f1s4 streptococc
63	3	16.7	16	6	Q9TQZ7	Q9tqz7 bos taurus
64	3	16.7	16	11	Q9QV11	Q9qv11 rattus sp.
65	3	16.7	16	11	Q9QUW8	Q9quw8 cavia (guin
66	3	16.7	16	12	Q88250	Q88250 sendai viru
67	3	16.7	16	12	Q84246	Q84246 sendai viru
68	3	16.7	16	12	Q88249	Q88249 sendai viru
69	3	16.7	16	12	Q99154	Q99154 sendai viru
70	3	16.7	17	1	Q50842	Q50842 methanococc
71	3	16.7	17	1	Q8VME2	Q8vme2 pseudomonas
72	3	16.7	17	2	Q9EUB3	Q9eub3 corynebacte
73	3	16.7	17	4	Q14001	Q14001 homo sapien
74	3	16.7	17	4	Q9UCC6	Q9ucc6 homo sapien
75	3	16.7	17	6	Q9XSG1	Q9xsg1 bos taurus
76	3	16.7	17	6	Q9TQZ5	Q9tqz5 macaca fasc
77	3	16.7	17	6	Q9TR21	Q9tr21 sus scrofa
78	3	16.7	17	7	Q9TNQ0	Q9tnq0 mus sp. bet
79	3	16.7	17	8	Q9T2S2	Q9t2s2 solanum tub
80	3	16.7	17	8	Q9T2H4	Q9t2h4 spinacia ol
81	3	16.7	17	11	Q9JK08	Q9jk08 mus musculu
82	3	16.7	17	12	Q919B0	Q919b0 human papil
83	3	16.7	18	2	Q52411	Q52411 thermophili
84	3	16.7	18	3	Q9F897	Q9f897 emericella
85	3	16.7	18	4	Q9UCF4	Q9ucf4 homo sapien
86	3	16.7	18	5	Q9TWW7	Q9tww7 procambarus
87	3	16.7	18	6	Q95MB1	Q95mb1 equus cabal
88	3	16.7	18	6	Q9TOR0	Q9tor0 sus scrofa
89	3	16.7	18	6	Q9TS26	Q9ts26 sus scrofa

90 Q9S8G8 psophocarpu
 91 P70649 mus sp. syn
 92 P70650 mus sp. syn
 93 Q9JIE9 mus musculus
 94 Q90791 gallus gall
 95 Q8QFT3 gallus gall
 96 O57600 gallus gall
 97 O12692 simian-huma
 98 Q9K610 bacillus ha
 99 Q9RQ37 salmonella
 100 Q9K4X0 planktothri

ALIGNMENTS

RESULT 1

Q50019 PRELIMINARY; PRT; 12 AA.
 AC Q50019
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DE U2266a.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U15182; AAA62981.1; --.
 SQ SEQUENCE 12 AA; 1402 MW; DF569D9F7FD1F5A2 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MGVP 9
 Db 1 MGVP 4

RESULT 2

Q31851 PRELIMINARY; PRT; 12 AA.
 AC Q31851
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia; TIGSUE=Leaf;
 RX MEDLINE=94187724; PubMed=8139555;
 RA Conley T.R., Park S.-C., Kwon H.-B., Peng H.-S., Shih M.-C.;
 RT "Characterization of cis-acting elements in light regulation of the
 RT nuclear gene encoding the A subunit of chloroplast isozymes
 RT glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
 RL Mol. Cell. Biol. 14:2525-2533(1994).
 DR EMBL: L14743; AAA31640.1; --.
 KW Chloroplast.

FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPKV 11
 Db 8 VPKV 11

RESULT 3

O54357 PRELIMINARY; PRT; 16 AA.
 AC O54357
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PTSI system enzyme I (Fragment).
 GN PTSI
 OS Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H;
 RA Nicholson W.L., Fajardo-Cavazos P.;
 RT "DNA repair and the ultraviolet radiation resistance of bacterial
 RT spores: from the laboratory to the environment.";
 RL (In) Pandalai S. (eds.);
 RL RECENT RESEARCH ADVANCES IN MICROBIOLOGY, pp.1-1, Research Signpost,
 RL Tivandrum, India (1998).
 DR EMBL: U60821; AAB97621.1; --.
 FT NON TER 1 1
 SQ SEQUENCE 16 AA; 1873 MW; D38C83850AEF4266 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKET 14
 Db 9 VKET 12

RESULT 4

Q919D5 PRELIMINARY; PRT; 18 AA.
 AC Q919D5
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CCL;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF404692; AAL01341.1; --.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LOPE 4
Db 15 LOPE 18

RESULT 5
Q919B3
ID Q919B3 PRELIMINARY; PRT; 18 AA.
AC Q919B3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404703; AAL01364.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 6
Q919B5
ID Q919B5 PRELIMINARY; PRT; 18 AA.
AC Q919B5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404702; AAL01362.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 7
Q919B7
ID Q919B7 PRELIMINARY; PRT; 18 AA.
AC Q919B7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC10;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404701; AAL01360.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 8
Q919C5
ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404697; AAL01352.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 9
Q919D1
ID Q919D1 PRELIMINARY; PRT; 18 AA.
AC Q919D1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).

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GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16B6CC3;
RA "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404694; AAL01346.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 10
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16B6CC3;
RA "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404693; AAL01344.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 11
Q919B9 ID Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=HPV16B6CC9;
RA "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404700; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 12
Q919A8 ID Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16B6CC15;
RA "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404706; AAL01369.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 13
Q919C7 ID Q919C7 PRELIMINARY; PRT; 18 AA.
AC Q919C7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16B6CC5;
RA "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404696; AAL01350.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

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SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18
|||||

RESULT 14

Q919C9 PRELIMINARY; PRT; 18 AA.

AC Q919C9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10381;
RN [1]_TaxID=10381;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC4;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF04695; AAL01348.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18
|||||

RESULT 15

Q9R4Q2 PRELIMINARY; PRT; 19 AA.

AC Q9R4Q2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein S21 (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE.
RX MEDLINE=95244309; PubMed=7727274;
RA Ochi K.;
RT "Comparative ribosomal protein sequence analyses of a phylogenetically
RT defined genus, Pseudomonas, and its relatives.";
RL Int. J. Syst. Bacteriol. 45:268-273(1995).
DR InterPro; IPR001911; Ribosomal_S21.
DR Pfam; PF01165; Ribosomal_S21; I.
DR PRINTS; PR00976; RIBOSOMLS21.
SQ SEQUENCE 19 AA; 2244 MW; 0475DD42A464271C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13

Db 4 KVKE 7
|||||

RESULT 16

Q9N195 PRELIMINARY; PRT; 19 AA.

AC Q9N195;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Parvalbumin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RA Ariza F., Harrison B., Drinkwater R.;
RT "The Assignment by Linkage Mapping of Five Genes from Human Chromosome
RT 22 to Bovine Chromosome 5, 14 and 17.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217654; AAF26420.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2151 MW; D5EA9D89BC3EE951 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
Db 16 VKET 19
|||||

RESULT 17

Q95M23 PRELIMINARY; PRT; 8 AA.

AC Q95M23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).
GN ATP1A1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_TaxID=9823;
RP SEQUENCE FROM N.A.
RC STRAIN=Pietrain;
RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA Geldermann H., Kopecky M.;
RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and
RT linkage assignments of ATP1A1 and IVL to chromosome 4.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344138; CAC51422.1; -.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
Db 4 KET 6
|||||

RESULT 18


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Q8UJ35
ID Q8UJ35 PRELIMINARY; PRT; 8 AA.
AC Q8UJ35;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Arp-citrate lyase (Fragment).
GN ACL.
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O84;
RA MEDLINE=21918460; PubMed=11918793;
RX Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL: AF454211; AM22897.1; -.
KW Lyase.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 981 MW; 98C77B544681AB02 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
DB 2 ETM 4

RESULT 19
Q93EZ0
ID Q93EZ0 PRELIMINARY; PRT; 9 AA.
AC Q93EZ0;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ScpB (Fragment).
GN ScpB.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O90R;
RX MEDLINE=21424698; PubMed=11532154;
RA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,
RA Lammler C., Podbielski A., Luticken R., Spellerberg B.;
RT "Horizontal gene transfer and host specificity of beta-haemolytic
RT streptococci: the role of a putative composite transposon containing
RT scpB and lmb.";
RL Mol. Microbiol. 41:925-935(2001).
DR EMBL: AF327852; AAL10713.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1146 MW; 543721AB1326C403 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
DB 5 KET 7

RESULT 20

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Q96P97
ID Q96P97 PRELIMINARY; PRT; 9 AA.
AC Q96P97;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Reptin52 protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF401216; AAL02172.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 981 MW; 5CDDAAA681AB1873 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
DB 4 ETM 6

RESULT 21
P82440
ID P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (T-EMBLrel. 14, Created)
DT 01-JUN-2000 (T-EMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE 42 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wolfaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
DB 1 QPE 3

RESULT 22
Q8AYL5
ID Q8AYL5 PRELIMINARY; PRT; 9 AA.
AC Q8AYL5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

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DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two Cyp19 genes differentially expressed
in the brain and ovary of teleost fish";
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR EMBL; AF324897; AAN32618.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1060 MW; C49E7D7272B040D CRC64;

Query Match 16.7%; Score 3; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db 6 LQP 8

RESULT 23
Q8AUM7 PRELIMINARY; PRT; 9 AA.
AC Q8AUM7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two Cyp19 genes differentially expressed
in the brain and ovary of teleost fish";
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR EMBL; AF324895; AAN32616.1; -.
DR EMBL; AF324896; AAN32617.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 961 MW; C49E7D7272B187D CRC64;

Query Match 16.7%; Score 3; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db 6 LQP 8

RESULT 24
Q50843 PRELIMINARY; PRT; 10 AA.
AC Q50843;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE RNA polymerase gene 3', flanking region with AT-rich DNA sequence
(Fragment).
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85230552; PubMed=4006907;
RA Bollschweiler C., Kuehn R., Klein A.;
RT "Non-repetitive AT-rich sequences are found in intergenic regions of
RT Methanococcus voltae DNA";
RL EMBO J. 4:805-809(1985).
DR EMBL; X02517; CAA26353.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1149 MW; 27F22A2772CAA9C8 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
Db 6 VPK 8

RESULT 25
Q86324 PRELIMINARY; PRT; 10 AA.
AC Q86324;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "The U3 region of the long terminal repeat of a subgroup A
RT transformation-defective rous sarcoma virus (tdPH2010) converts a
RT noncytopathic virus to a cytopathic virus";
RL Virus Genes 15:171-180(1997).
DR EMBL; U41726; AAB60580.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
Db 4 QPE 6

RESULT 26
Q86325 PRELIMINARY; PRT; 10 AA.
AC Q86325;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "The U3 region of the long terminal repeat of a subgroup A
RT transformation-defective rous sarcoma virus (tdPH2010) converts a

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RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
DR ENBL: U41727; AAB60581.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPE 4
Db 4 QPE 6

RESULT 27
Q86326 Q86326 PRELIMINARY; PRT; 10 AA.
AC Q86326;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OC NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "The U3 region of the long terminal repeat of a subgroup A
RT transformation-defective rous sarcoma virus (tdpH2010) converts a
RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=82271824; PubMed=6287213;
RA Takeya T., Hanafusa H., Junghans R.P., Ju G., Skalka A.M.;
RT "Comparison between the viral transforming gene (src) of recovered
RT avian sarcoma virus and its cellular homolog.";
RL Mol. Cell. Biol. 1:1024-1037(1981).
DR ENBL: U41729; AAB84421.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPE 4
Db 4 QPE 6

RESULT 28
Q86614 Q86614 PRELIMINARY; PRT; 11 AA.
AC Q86614;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MTG8 related protein (Fragment).
GN MTG8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
DR ENBL: U41727; AAB60581.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPE 4
Db 4 QPE 6

RESULT 29
Q9NY38 Q9NY38 PRELIMINARY; PRT; 11 AA.
AC Q9NY38;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Heavy metal-responsive transcription factor (Fragment).
GN MTF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA Georgiev O., Schaffner W.;
RT "Characterization of the mouse gene for the heavy metal-responsive
RT transcription factor MTF-1.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL: AJ251881; CAB71327.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
Db 4 MVP 6

RESULT 30
O19718 O19718 PRELIMINARY; PRT; 11 AA.
AC O19718;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206008; PubMed=3458223;
RA Gregersen P.K., Shen M., Song Q.-L., Merryman P., Degar S., Seki T.,
RA Maccari J., Goldberg D., Murphy H., Schwenzer J., Wang C.Y.,
RA Winchester R.J., Nepom G.T., Silver J.;
RT "Molecular diversity of HLA-DR4 haplotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).

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DR EMBL; M15074; AAA59810.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1143 MW; 4E6AADA061B776D7 CRC64;

Query Match 16.7%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db 4 LQP 6

RESULT 31
Q8UUP1 PRELIMINARY; PRT; 11 AA.
AC Q8UUP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis".
RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db 8 LQP 10

RESULT 32
Q9K7A4 PRELIMINARY; PRT; 11 AA.
AC Q9K7A4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BH3464.
GN BH3464.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001518; BAB07183.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 11 AA; 1219 MW; 5F7D35CB7272B13 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
Db 3 VKE 5

RESULT 33
Q9ICE5 PRELIMINARY; PRT; 12 AA.
AC Q9ICE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=546CP-H7, 546CP-E4, and 546CP-F5;
RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from a patient with HIV dementia: evidence for monocyte trafficking into brain.";
RL J. Neurovirol. 0:0-0(2000).
DR EMBL; AF217155; AAF75497.1; -.
DR EMBL; AF217153; AAF75495.1; -.
DR EMBL; AF217154; AAF75496.1; -.
SQ SEQUENCE 12 AA; 1636 MW; 7ED6A2917A24005B CRC64;

Query Match 16.7%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
Db 3 VKE 5

RESULT 34
Q31295 PRELIMINARY; PRT; 13 AA.
AC Q31295;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN LEUA.
OS Buchnera aphidicola.
OG Plasmid pBt1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97386415; PubMed=9244264;
RA Van Ham R.C.H.J., Moya A., Latorre A.;
RT "Putative origin of plasmids carrying the genes involved in leucine biosynthesis in Buchnera aphidicola (endosymbiont of aphids)."; J. Bacteriol. 179:4768-4777(1997).
DR EMBL; Y11966; CAA72696.1; -.
KW Lyase; Plasmid.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1487 MW; 1BD1D3E72A9E2050 CRC64;
```

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKV 11
 ||||
 Db 3 PKV 5

RESULT 35

Q9UE87 Q9UE87 PRELIMINARY; PRT; 13 AA.
 AC Q9UE87;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Transforming growth factor alpha (Fragment).
 GN TGFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9219018; PubMed=2907605;
 RA Jakobovits E.B., Schlokot U., Vannice J.L., Derynck R., Levinson A.D.;
 RT "The human transforming growth factor alpha promoter directs
 RT transcription initiation from a single site in the absence of a TATA
 RT sequence.";
 RL Mol. Cell. Biol. 8:5549-5554(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92168034; PubMed=1791840;
 RA Saeki T., Cristiano A., Lynch M.J., Brattain M., Kim N., Normanno N.,
 RA Kenney N., Ciardiello F., Salomon D.S.;
 RT "Regulation by estrogen through the 5'-flanking region of the
 RT transforming growth factor alpha gene.";
 RL Mol. Endocrinol. 5:1955-1963(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93364904; PubMed=8358733;
 RA Lynch M.J., Pelosi L., Carboni J.M., Merwin J., Coleman K., Wang R.C.,
 RA Lin P.F., Henry D.L., Brattain M.G.;
 RT "Transforming growth factor-beta 1 induces transforming growth factor-
 RT alpha promoter activity and transforming growth factor-alpha secretion
 RT in the human colon adenocarcinoma cell line FET.";
 RL Cancer Res. 53:4041-4047(1993).
 DR EMBL; M96868; AAA79958.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1318 MW; 2C6E4395FCEE36D8 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
 ||||
 Db 1 MVP 3

RESULT 36

Q8WEJ9 Q8WEJ9 PRELIMINARY; PRT; 13 AA.
 AC Q8WEJ9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE NADH dehydrogenase (Fragment).
 GN NAD1.
 OS Ginkgo biloba (Ginkgo).
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

OX NCBI_TaxID=3311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21555473; PubMed=11697913;
 RA Gugerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,
 RA Palmer J.D., Qiu Y.L.;
 RT "The evolutionary split of pinaceae from other conifers: evidence from
 RT an intron loss and a multigene phylogeny.";
 RL Mol. Phylogenet. Evol. 21:167-175(2001).
 DR EMBL; AF227466; AAL38910.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1419 MW; C00F6805F94945BD CRC64;

Query Match 16.7%; Score 3; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
 ||||
 Db 1 MVP 3

RESULT 37

Q39380 Q39380 PRELIMINARY; PRT; 13 AA.
 ID Q39380;
 AC Q39380;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE IFA binding protein (Sp10) (Fragment).
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DOK; TISSUE=Curd surface;
 RA Willis G.;
 RT "An investigation of nuclear lamin homologues in plants: an apparently
 RT non-intermediate filament sequence that bind a polyclonal anti-lamin
 RT antiserum.";
 DR Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X97678; CAA66268.1; -.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1413 MW; D1D4EA3926B42772 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPK 10
 ||||
 Db 6 VPK 8

RESULT 38

O88176 O88176 PRELIMINARY; PRT; 13 AA.
 ID O88176;
 AC O88176;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Neural cell adhesion molecule (Fragment).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 7 LQP 9

RESULT 39
Q9UWM2
ID Q9UWM2 PRELIMINARY; PRT; 14 AA.
AC Q9UWM2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.3) (Fragment).
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE.
RX MEDLINE=92247806; PubMed=1576153;
RA Robb F.T., Park J.B., Adams M.W.;
RT "Characterization of an extremely thermostable glutamate
dehydrogenase: a key enzyme in the primary metabolism of the
hyperthermophilic archaeobacterium, Pyrococcus furiosus.";
RL Biochim. Biophys. Acta 1120:267-272(1992).
SQ SEQUENCE 14 AA; 1684 MW; 1B8EF0500B25D50B CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 1 VKE 3

RESULT 40
Q55326
ID Q55326 PRELIMINARY; PRT; 14 AA.
AC Q55326;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative ORF1 (Fragment).
OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR6;
RX MEDLINE=92201692; PubMed=1551590;
RA Rhie E., Stirewalt V.L., Gasparich G.E., Bryant D.A.;
RT "The psac genes of Synecococcus sp. PCC7002 and Cyanophora paradoxa:
cloning and sequence analysis.";
RL Gene 112:123-128(1992).
DR EMBL; M86238; AAA27351.1; -.
FT NON_TER 14 14

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SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 12 LQP 14

RESULT 41
Q8JIG2
ID Q8JIG2 PRELIMINARY; PRT; 14 AA.
AC Q8JIG2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE YPL156 (Fragment).
GN YPL156.
OS Ashbya gossypii (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberti-Segui C., Dietrich F., Philippsen P.;
RT "Identification of kinesin-related proteins in the filamentous fungus
Ashbya gossypii.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378570; AAN87139.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1646 MW; 8C3A12EB808B1D15 CRC64;

Query Match 16.7%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
DB 3 PKV 5

RESULT 42
Q9P2A2
ID Q9P2A2 PRELIMINARY; PRT; 14 AA.
AC Q9P2A2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Truncated aldo-keto reductase (Fragment).
GN TRUNCATED AKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20138537; PubMed=10672042;
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
RA Watanabe K., Ito S.;
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
three aldo-keto reductase genes.";
RL Genes Cells 5:111-125(2000).
DR EMBL; AB037903; BAA92888.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LQP 3
Db 7 LQP 9

RESULT 43

Q16045 ID Q16045 PRELIMINARY; PRT; 14 AA.
AC Q16045;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE D3 dopamine receptor (fragment).
GN D3R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Blood;
RX MEDLINE=93326145; PubMed=7916609;
RA Nagai Y., Ueno S., Saeiki Y., Soga F., Yanagihara T.;
RT "Expression of the D3 dopamine receptor gene and a novel variant
RT transcript generated by alternative splicing in human peripheral blood
RT lymphocytes.";
RL Biochem. Biophys. Res. Commun. 194:368-374 (1993).
DR EMBL; S63845; AAB27543.2; -;
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db 12 LQP 14

RESULT 44

Q8HYM2 ID Q8HYM2 PRELIMINARY; PRT; 14 AA.
AC Q8HYM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interferon regulatory factor 6 (fragment).
GN IRF6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
RN SEQUENCE FROM N.A.
RP Susott E.E., Rollo W.A., Vento P.J., Ewart S.L.;
RA "Characterization of 8 Feline Type I Markers.";
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459807; AAO15587.1; -;
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1684 MW; C593CC0754F47BB9 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
Db 3 KVK 5

RESULT 45

P82341 ID P82341 PRELIMINARY; PRT; 14 AA.
AC P82341;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT251) (fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
[1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RP STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Paltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341 (2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
Db 6 PEI 8

RESULT 46

Q89818 ID Q89818 PRELIMINARY; PRT; 14 AA.
AC Q89818;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Hypothetical 1.9 kDa protein.
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=LYMPHOTROPIC VARIANT;
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice,
RT MVM(i), and comparison with the DNA sequence of the fibrotropic
RT prototype strain.";
RL J. Virol. 570:656-669 (1986).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=MVM(P);
RX MEDLINE=83143341; PubMed=6298737;
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
RT "The complete DNA sequence of minute virus of mice, an autonomous
RT parvovirus.";
RL Nucleic Acids Res. 11:999-1018 (1983).
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=MVM(P);
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;

RT "DNA sequence of the lymphotropic variant of minute virus of mice,
 RT MVM(i), and comparison with the DNA sequence of the fibrotropic
 RT prototype strain.",
 RL J. Virol. 57:656-669 (1986).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MVM(P);
 RX MEDLINE=87061199; PubMed=3783817;
 RA Morgan W.R., Ward D.C.;
 RT "three splicing patterns are used to excise the small intron common to
 RT all minute virus of mice RNAs.",
 RL J. Virol. 60:1170-1174 (1986).
 DR EMBL; M12032; AAG69571.1; -;
 DR EMBL; J02275; AAG57113.1; -;
 DR EMBL; V01115; CAA24312.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 14 AA; 1927 MW; 12535381F864D1B CRC64;
 Query Match 16.7%; Score 3; DB 12; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PEI 5
 Db ||||
 9 PEI 11
 RESULT 47
 Q8AXO7
 ID Q8AXO7 PRELIMINARY; PRT; 14 AA.
 AC Q8AXO7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mannose-binding lectin-associated serine protease (Fragment).
 GN MASP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,
 RA Matsushita M., Fujita T.;
 RT "Ancient origin and extensive distribution of mannose-binding lectin-
 RT associated serine protease-3 in vertebrate lineage.",
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078909; BAC41345.1; -;
 KW Lectin; Protease.
 FT NON TER 1 1
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1533 MW; 99DD285F40C2B15 CRC64;
 Query Match 16.7%; Score 3; DB 13; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GVP 9
 Db ||||
 2 GVP 4
 RESULT 48
 Q9UR63
 ID Q9UR63 PRELIMINARY; PRT; 15 AA.
 AC Q9UR63;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
 DE isoform (EC 3.2.1.26) (Fragment).
 OS Emericella nidulans (Aspergillus nidulans).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96409246; PubMed=8814228;
 RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
 RT "Purification and partial characterization of the high and low
 RT molecular weight form (S- and F-form) of invertase secreted by
 RT Aspergillus nidulans.",
 RL Biochim. Biophys. Acta 1296:207-218 (1996).
 SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;
 Query Match 16.7%; Score 3; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQP 3
 Db ||||
 1 LQP 3
 RESULT 49
 Q9UE41
 ID Q9UE41 PRELIMINARY; PRT; 15 AA.
 AC Q9UE41;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Collagen.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89325561; PubMed=2753125;
 RA Vikkula M., Paltonen L.;
 RT "Structural analyses of the polymorphic area in type II collagen
 RT gene.",
 RL FEBS Lett. 250:171-174 (1989).
 DR EMBL; X16158; CAA34281.1; -;
 SQ SEQUENCE 15 AA; 1334 MW; D6DC3824197ABEF6 CRC64;
 Query Match 16.7%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GVP 9
 Db ||||
 1 GVP 3
 RESULT 50
 Q9UCC7
 ID Q9UCC7 PRELIMINARY; PRT; 15 AA.
 AC Q9UCC7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Midkine (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94059921; PubMed=8241100;
 RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
 RT "Identification of novel heparin-releasable proteins, as well as the
 RT cytokines midkine and pleiotrophin, in human postheparin plasma.",
 RL Arterioscler. Thromb. 13:1798-1805 (1993).
 SQ SEQUENCE 15 AA; 1527 MW; C34B6B9787474AC CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 7 KVK 9

RESULT 51

Q9UCY1 PRELIMINARY; PRT; 15 AA.
 AC Q9UCY1, (Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Thromboxane A2 receptor isoform alpha (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96193877; PubMed=8613548;
 RA Hirata T., Ushikubi F., Kakizuka A., Okuma M., Narumiya S.;
 RT "Two thromboxane A2 receptor isoforms in human platelets. Opposite
 RT coupling to adenylyl cyclase with different sensitivity to Arg60 to Leu
 RT mutation.";
 RL J. Clin. Invest. 97:949-956(1996).
 SQ SEQUENCE 15 AA; 1656 MW; 5EC77C6E9E97FB78 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
 |||
 Db 4 LQP 6

RESULT 52

O46661 PRELIMINARY; PRT; 15 AA.
 AC O46661, (Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glucose-6-phosphate dehydrogenase (Fragment).
 GN G6PD.
 OS Macropus robustus robustus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=35580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224585; PubMed=9060417;
 RA Loebel D.A., Johnston P.G.;
 RT "Analysis of the intron-exon structure of the G6PD gene of the
 RT wallaroo (Macropus robustus) by polymerase chain reaction.";
 RL Mamm. Genome 8:146-147(1997).
 DR EMBL; U53768; AAC48786.1; -.
 DR InterPro; IPR001282; G6PD.
 DR Pfam; PF00479; G6PD; 1.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1704 MW; 039588640B5E671E CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5' IMG 7

Db 11 IMG 13
 |||

RESULT 53

Q9TR64 PRELIMINARY; PRT; 15 AA.
 AC Q9TR64, (Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleoside diphosphate kinase, NDK, P19=17.143 kDa A subunit
 DE (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95285334; PubMed=7767789;
 RA Weber B., Weber W., Buck F., Hilz H.;
 RT "Isolation of the myc transcription factor nucleoside diphosphate
 RT kinase and the multifunctional enzyme glyceraldehyde-3-phosphate
 RT dehydrogenase by cAMP affinity chromatography.";
 RL Int. J. Biochem. Cell Biol. 27:215-224(1995).
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1820 MW; 2728CDB4FDAE6316 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
 |||
 Db 7 QPE 9

RESULT 54

Q9MZRS PRELIMINARY; PRT; 15 AA.
 AC Q9MZRS, (Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Interleukin 4 variant IL-4int2A (Fragment).
 GN IL-4.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen, and Lymph node;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 RT European rabbit (Oryctolagus cuniculus).";
 RL Cytokine 12:555-565(2000).
 DR EMBL; AF169172; AAF86656.1; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1586 MW; 876C550E85307B55 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
 |||
 Db 12 VPK 14

RESULT 55

Q9TH04
ID Q9TH04 PRELIMINARY; PRT; 15 AA.
AC Q9TH04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus americana (whooping crane).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=9117;
RN [1]_TaxID=9117;
RP SEQUENCE FROM N.A.
RC STRAIN=LMS B3394;
RA Glenn T.C., Stephan W., Braun M.J.;
RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
RT DNA Variation."
RL Conserv. Biol. 0:0-0(1999).
DR EMBL; AF112373; AAD23994.1; -.
KW Mitochondrion.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1759 MW; A7F711A65E9F934F CRC64;

Query Match 16.7%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGW 8
DB 8 MGW 10

RESULT 56
Q9AT15 PRELIMINARY; PRT; 15 AA.
ID Q9AT15
AC Q9AT15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Plasma membrane H₄-ATPase (Fragment).
GN LHAI.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Ewing N.N., Wimmers L.E., Meyer D.J., Chetelat R.T., Bennett A.B.;
RT "Molecular cloning of tomato plasma membrane H₄-ATPase."
RL Life Sci. Adv. Plant Physiol. 94:1874-1881(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Ewing N.N., Bennett A.B.;
RT "Assessment of the number and expression of P-type H(+) -ATPase genes
RT in tomato."
RL Life Sci. Adv. Plant Physiol. 106:547-557(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Dahmani Z., Ewing N.N.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF353103; AAK31206.1; -.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1673 MW; 5F70477FC08C809E CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
DB 13 KET 15

RESULT 57
P93515 PRELIMINARY; PRT; 15 AA.
ID P93515
AC P93515;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Copper amine oxidase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP SEQUENCE FROM N.A.
RX MEDLINE=96227319; PubMed=8654815;
RA Moller S.G., McPherson M.J.;
RT "Molecular and functional studies of copper amine oxidase from
RT Arabidopsis thaliana."
RL Biochem. Soc. Trans. 23:630S-630S(1995).
DR EMBL; S82296; AAB37690.1; -.
DR InterPro; IPR000269; CuNH_oxidase.
DR Pfam; PF01179; Cu_amine_oxid; 1.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1842 MW; 12BF98E1198BC5CE CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
DB 2 MVP 4

RESULT 58
Q9S8N8 PRELIMINARY; PRT; 15 AA.
ID Q9S8N8
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RX MEDLINE=94170739; PubMed=8125056;
RA Flegsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis."
RL Electrophoresis 14:1060-1066(1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 3 LQP 5

RESULT 59

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Q9PRZ0
ID Q9PRZ0 PRELIMINARY; PRT; 15 AA.
AC Q9PRZ0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RN SEQUENCE.
RX MEDLINE=94080171; PubMed=8257916;
RA Machado O.L., Oliveira-Carvalho A.L., Zingali R.B., Carlini C.R.;
RT "Purification, physicochemical characterization and N-terminal-amino
RT acid sequence of a phospholipase A2 from Bothrops jararaca venom.";
RL Braz. J. Med. Biol. Res. 26:163-166(1993).
SQ SEQUENCE 15 AA; 1734 MW; AF893A50F081B0A0 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
Db 6 ETM 8

RESULT 60
Q51950 PRELIMINARY; PRT; 16 AA.
ID Q51950
AC Q51950;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF E.
OS Staphylococcus aureus.
OG Plasmid pNS1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RN SEQUENCE FROM N.A.
RA Nouchi N., Roki T., Sasatsu M., Kono M., Shishido K., Ando T.;
RT "Determination of the complete nucleotide sequence of pNS1, a
RT staphylococcal tetracycline-resistance plasmid propagated in Bacillus
RT subtilis.";
RL FEMS Microbiol. Lett. 37:283-288(1986).
DR EMBL; M16217; AAA19178.1; -.
KW Plasmid.
SQ SEQUENCE 16 AA; 1929 MW; 0F038C3A8B79F3B0 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
Db 14 VKE 16

RESULT 61
Q9FIS7 PRELIMINARY; PRT; 16 AA.
ID Q9FIS7
AC Q9FIS7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamide aminimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN PURH.
OS Streptococcus suis.

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SsuDAT1I restriction-
RT modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045610; BAB20834.1; -.
KW Ligase.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1935 MW; 1FC8D8B8AE391D40 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
Db 5 TMV 7

RESULT 62
Q9FIS4 PRELIMINARY; PRT; 16 AA.
ID Q9FIS4
AC Q9FIS4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamide aminimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN PURH.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SsuDAT1I restriction-
RT modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045612; BAB20838.1; -.
KW Ligase.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1949 MW; 6978D8B8AE391D44 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
Db 5 TMV 7

RESULT 63
Q9TQZ7 PRELIMINARY; PRT; 16 AA.
ID Q9TQZ7
AC Q9TQZ7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Factor H (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96202005; PubMed=8615824;
RA Soames C.J., Day A.J., Sim R.B.;
RT "prediction from sequence comparisons of residues of factor H involved
RT in the interaction with complement component C3b.";
RL Biochem. J. 315:523-531 (1996).
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
Db 10 KET 12

RESULT 64
Q9QV11 PRELIMINARY; PRT; 16 AA.
AC Q9QV11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hepatic glycoген associated protein phosphatase 1 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=95237359; PubMed=7720853;
RA Moorhead G., MacKintosh C., Morrice N., Cohen P.;
RT "Purification of the hepatic glycoген-associated form of protein
RT phosphatase-1 by microcystin-Sepharose affinity chromatography.";
RL FEBS Lett. 362:101-105 (1995).
SQ SEQUENCE 16 AA; 1750 MW; F1CB6485F4B54AE1 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
Db 13 TMV 15

RESULT 65
Q9QUW8 PRELIMINARY; PRT; 16 AA.
AC Q9QUW8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein isomerase-related protein precursor 71.5 kDa isoform
DE (Fragment).
OS Cavia (guinea pigs).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae.
OX NCBI_TaxID=10140;
RN [1]
RP SEQUENCE.
RX MEDLINE=96070119; PubMed=8535285;
RA Bonifacio M.D., Steeves T., Saunders D.M., Sinosich M.J.;
RT "Isolation of ERp72 from guinea pig term placenta using heparin
RT Sepharose affinity chromatography.";
RL Biochem. Mol. Biol. Int. 36:1143-1152 (1995).
SQ SEQUENCE 16 AA; 1880 MW; 21B44A5F5767CB17 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
Db 11 VKE 13

RESULT 66
Q88250 PRELIMINARY; PRT; 16 AA.
ID Q88250;
AC Q88250;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664 (1990).
DR EMBL; M60152; AAA47808.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1648 MW; 049B529F01B29066 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
Db 4 GVP 6

RESULT 67
Q04246 PRELIMINARY; PRT; 16 AA.
ID Q04246;
AC Q04246;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664 (1990).
DR EMBL; M60155; AAA47805.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1634 MW; 73989D9F01B298D0 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
Db 4 GVP 6

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RESULT 68
Q88249 ID Q88249 PRELIMINARY; PRT; 16 AA.
AC Q88249;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCS, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60154; AAA47807.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1649 MW; 049B529F01B298C4 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
Db 4 GVP 6

RESULT 69
Q99154 ID Q99154 PRELIMINARY; PRT; 16 AA.
AC Q99154;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCS, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60153; AAA47806.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
Db 4 GVP 6

RESULT 70
Q50842 ID Q50842 PRELIMINARY; PRT; 17 AA.
AC Q50842;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCS, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60153; AAA47806.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
Db 4 GVP 6

RESULT 71
Q8VME2 ID Q8VME2 PRELIMINARY; PRT; 17 AA.
AC Q8VME2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE ParC protein (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Great A., Lambertson L., Williams P.A., Thomas C.M.;
RT "Complete nucleotide sequence of IncP-9 plasmid pW0.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344068; CAC86875.1; -.
FT NON_TER 17
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C365A999 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
Db 13 LQP 15

RESULT 72
Q9EUB3 ID Q9EUB3 PRELIMINARY; PRT; 17 AA.
AC Q9EUB3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE CmlB (CmlA).
OS Corynebacterium striatum.
OG Plasmid pRP10.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=43770;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=M82B; PLASMIID=PTP10;
RX MEDLINE=20194806; PubMed=10732668;
RA Tauch A., Krieff S., Kalinowski J., Puhler A.;
RT "The 51,409-bp R-plasmid pTP10 from the multidrug-resistant clinical
RT isolate Corynebacterium striatum M82B is composed of DNA segments
RT initially identified in soil bacteria and in plant, animal, and human
RT pathogens.";
RL Mol. Gen. Genet. 263:1-11(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M82B; PLASMIID=PTP10;
RX MEDLINE=98414982; PubMed=9735314;
RA Tauch A., Zheng Z., Puhler A., Kalinowski J.;
RT "Corynebacterium striatum chloramphenicol resistance transposon
RT Tn5564: genetic organization and transposition in Corynebacterium
RT glutamicum.";
RL Plasmid 40:126-139(1998).
DR EMBL; AF024666; AAG03379.1; -.
DR EMBL; AF024666; AAG03369.1; -.
KW Plasmid.
SQ SEQUENCE 17 AA; 1715 MW; 13CA5DE6CA436B0F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 3 GVP 5

RESULT 73
Q14001 PRELIMINARY; PRT; 17 AA.
ID Q14001
AC Q14001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (fragment).
GN CGIPDE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079687; PubMed=8921398;
RA Loebert R.W., Winterpacht A., Seipel B., Zabel B.U.;
RT "Molecular cloning and chromosomal assignment of the human homologue
RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
RT in fat metabolism located at 11p15.1.";
RL Genomics 37:211-218(1996).
DR EMBL; X95522; CAA64776.1; -.
FT NON-TER 17
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 14 LQP 16

RESULT 74
Q9UCC6 PRELIMINARY; PRT; 17 AA.
ID Q9UCC6
AC Q9UCC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

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DE Pleiotrophin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny M.F., Maffi T., Menta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 17 AA; 1925 MW; 442BC8BEFD417ADD CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
DB 9 KVK 11

RESULT 75
Q9XSG1 PRELIMINARY; PRT; 17 AA.
ID Q9XSG1
AC Q9XSG1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMCX (Fragment).
GN SMCX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Polunienko A., Blecher S.;
RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135448; AAD34440.1; -.
FT NON-TER 17
SQ SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
DB 2 PEI 4

Search completed: November 25, 2003, 19:33:59
Job time : 36.8023 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
 (without alignments)
 62.189 Million cell updates/sec

Title: US-09-641-801-21
 Perfect score: 18
 Sequence: 1 LQPEIMGVPKVKTWPK 18

Scoring table: OJGO
 Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :	A_Geneseq 19Jun03.*
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23:	/SIDSL1/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSL1/gcgcdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Ewe colostrinin pe
5	18	100.0	18	23	Colostrinin consti
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Neural cell regula
8	5	27.8	10	21	Retinoblastoma bin
9	5	27.8	11	21	Retinoblastoma bin

10	5	27.8	12	22	AAB87422	Human gene 3 encod
11	5	27.8	14	14	AAR43871	OmpA2-R-7 signal p
12	5	27.8	16	24	ABP82578	G protein-coupled
13	5	27.8	16	24	ABP82609	G protein-coupled
14	4	22.2	4	20	AAW93084	Human erythropoiet
15	4	22.2	4	23	ABG32218	Sheep colostrinin
16	4	22.2	6	14	AAR32746	PK40 TAU/neurofili
17	4	22.2	6	20	AAV27421	PK40 protein kinase
18	4	22.2	6	23	AAW51129	Bovine TAU/neurofi
19	4	22.2	7	14	AAR33359	HPV E7 protein - R
20	4	22.2	7	20	AAV49017	Membrane dipeptida
21	4	22.2	7	21	AAB35822	T7 phage coat prot
22	4	22.2	7	22	AAB72261	Colostrinin derive
23	4	22.2	7	22	AAB72514	Colostrinin peptid
24	4	22.2	7	22	AAB72546	Colostrinin peptid
25	4	22.2	7	22	AAB59317	Ewe colostrinin pe
26	4	22.2	7	23	AAE20243	Colostrinin consti
27	4	22.2	7	23	AAW51050	Colostrinin consti
28	4	22.2	7	23	AAO14592	Neural cell regula
29	4	22.2	8	12	AAR10631	Human Papilloma Vi
30	4	22.2	8	14	AAR33158	HPV E7 protein - R
31	4	22.2	8	19	AAW77186	Pharmaceutically a
32	4	22.2	8	21	AAB35995	Sorbitol dehydroge
33	4	22.2	8	22	ABP14637	HIV A03 super moti
34	4	22.2	8	22	ABP17276	HIV B27 super moti
35	4	22.2	8	22	ABP21662	HIV A03 motif pol
36	4	22.2	8	22	ABP23544	HIV A11 motif pol
37	4	22.2	8	22	AAG62330	Casain-related pep
38	4	22.2	9	12	AAR10635	Human Papilloma Vi
39	4	22.2	9	14	AAR33157	HPV E7 protein - R
40	4	22.2	9	14	AAR33163	HPV E7 protein - R
41	4	22.2	9	14	AAR33170	HPV E7 protein - R
42	4	22.2	9	14	AAR43741	MHC Class I allele
43	4	22.2	9	14	AAR43742	MHC Class I allele
44	4	22.2	9	15	AAR59257	Peptide fragment (
45	4	22.2	9	15	AAR59247	Peptide fragment (
46	4	22.2	9	15	AAR73799	Antigen fragment 1
47	4	22.2	9	15	AAR73800	Antigen fragment 1
48	4	22.2	9	15	AAR73796	Antigen fragment 1
49	4	22.2	9	16	AAR80939	Peptide for increa
50	4	22.2	9	16	AAR78889	HPV16 E7 11-19 cyt
51	4	22.2	9	16	AAR78894	HPV16 E7 12-20 cyt
52	4	22.2	9	16	AAR78851	HPV16 E7 18-193 CY
53	4	22.2	9	16	AAR70601	HIV(B35)POL-9, hum
54	4	22.2	9	16	AAR84331	HPV derived peptid
55	4	22.2	9	17	AAR89363	Immunogenic peptid
56	4	22.2	9	18	AAW39661	HPV16/18 E7 peptid
57	4	22.2	9	18	AAW39662	HPV16/18 E7 peptid
58	4	22.2	9	18	AAW36590	Hepatitis B virus
59	4	22.2	9	18	AAW28811	HPV-16 derived pep
60	4	22.2	9	19	AAW78893	Human papillomavir
61	4	22.2	9	19	AAW54766	Peptide from HPV 1
62	4	22.2	9	19	AAW54767	Peptide from HPV 1
63	4	22.2	9	20	AAV53466	HIV-1 RT protein (
64	4	22.2	9	20	AAV55432	HLA binding plu-1
65	4	22.2	9	20	AAV40315	Amino acid sequenc
66	4	22.2	9	20	AAV26807	HIV-derived lipope
67	4	22.2	9	20	AAV10346	T cell epitope/MHC
68	4	22.2	9	20	AAV10511	HLA Class I motif
69	4	22.2	9	21	AAB33705	MHC class I associ
70	4	22.2	9	21	AAV18492	Peptide substrate
71	4	22.2	9	21	AAV96941	Processed N-termin
72	4	22.2	9	21	AAV66364	HLA-B7-binding HIV
73	4	22.2	9	21	AAV66378	HLA-B8-binding HIV
74	4	22.2	9	22	ABP11796	HIV A01 super moti
75	4	22.2	9	22	ABP16116	HIV A24 super moti
76	4	22.2	9	22	ABP16839	HIV B07 super moti
77	4	22.2	9	22	ABP21667	HIV A03 motif pol
78	4	22.2	9	22	ABP23548	HIV A11 motif pol
79	4	22.2	9	22	ABP24295	HIV A24 motif pol
80	4	22.2	9	22	AAG93801	Human papilloma vi
81	4	22.2	9	22	AAG88611	HER2/NEU DR superm
82	4	22.2	9	22	AAG88725	HER2/NEU DR 3a mot

83 MHC class-I associ
84 HPV 16 E7 A2 MHC-b
85 HPV 16 E7 A2 MHC-b
86 HPV 16 E7 A2 MHC-b
87 HPV strain 16 E7 p
88 HPV E7 peptide whi
89 Polyepitopic pep
90 A polyepitopic pep
91 HPV type 16 L1 pro
92 Immunogenic HIV pe
93 MHC class I molecu
94 MHC class I molecu
95 Human leukocyte an
96 Human leukocyte an
97 Human leukocyte an
98 Human leukocyte an
99 Human leukocyte an
100 Human leukocyte an

ALIGNMENTS

RESULT 1

AAB72266
ID AAB72266 standard; peptide; 18 AA.

XX AC AAB72266;

XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 21.

XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.

XX OS Synthetic.

XX PN WO20011937-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US222818.

XX PR 17-AUG-1999; 99US-0149311.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PA (REGG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2001-202804/20.

XX PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -

XX PS Claim 1; Page 34; 50pp; English.

XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
XX CC a proline rich polypeptide aggregate contained in colostrum. The
XX CC peptides have immune response modulatory activity, and are capable of
XX CC inducing cytokines. Colostrinin and its derived peptides are useful for
XX CC inducing cytokine production, for modulating an immunological response
XX CC and for inducing blood cell proliferation. The peptides are useful in the
XX CC treatment of disorders of the central nervous system, neurological
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,
XX CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
XX CC disorders of the immune system, bacterial and viral infections and
XX CC acquired immunological deficiencies.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETMVPK 18
|||||
DB 1 LQPEIMGVPKVKETMVPK 18
|||||

RESULT 2

AAB72519
ID AAB72519 standard; Peptide; 18 AA.

XX AC AAB72519;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #20.

XX KW Dermatalogical; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -

XX PS Claim 6; Page 25; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative
XX CC stress level in a cell or a patient, comprising contacting the cell with,
XX CC or administering to the patient, an oxidative stress regulator selected
XX CC from colostrinin, or its constituent peptide (e.g. the present peptide),
XX CC to change the level of an oxidising species in the cell. The method can
XX CC be used to treat oxidative damage to skin, by decreasing or preventing an
XX CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETMVPK 18
|||||
DB 1 LQPEIMGVPKVKETMVPK 18
|||||

RESULT 3

AAB72551
ID AAB72551 standard; Peptide; 18 AA.

XX AC AAB72551;

XX DT 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #20.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
XX
DR WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX
PS Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPEIMGVPKVKTWVPK 18
Db 1 LQPEIMGVPKVKTWVPK 18

RESULT 4
AAB59329
ID AAB59329 standard; Peptide; 18 AA.
AC AAB59329;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment C-4.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO200075173-A2.
XX
XX
PD 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from

colostrinin for treating e.g. disorders of the central nervous system
and immune system, viral and bacterial infections, and diseases
characterized by amyloid plaques -
Claim 7; Page 27; 63pp; English.
The present invention provides the sequences of a number of peptides
found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
fragment of colostrum. These peptides can be used in the treatment of
central nervous system disorders such as senile dementia, Parkinson's
disease, Alzheimer's disease, psychosis and neurosis, immune system
disorders such as bacterial and viral infections, to improve the
development of a child's immune system, as a dietary supplement, and to
promote the dissolution of beta-amyloid plaques.
Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPEIMGVPKVKTWVPK 18
Db 1 LQPEIMGVPKVKTWVPK 18

RESULT 5
AAE20248
ID AAE20248 standard; peptide; 18 AA.
AC AAE20248;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #20.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 18
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
PD 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETWVPK 18
 |||||
 Db 1 LQPEIMGVPKVKETWVPK 18

RESULT 6

AA051055
 ID AAMS1055 standard; Peptide; 18 AA.

XX AA051055;

XX 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 103-120).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Modified-site 18
 FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 103-120. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETWVPK 18
 |||||
 Db 1 LQPEIMGVPKVKETWVPK 18

RESULT 7

AA014597

ID AA014597 standard; peptide; 18 AA.

XX AA014597;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 20.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 18
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

```

CC the method of the invention.
XX
SQ Sequence 18 AA;
    Query Match      100.0%; Score 18; DB 23; Length 18;
    Best Local Similarity 100.0%; Pred. No. 2.3e-12;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETWVPK 18
    |||||
Db 1 LQPEIMGVPKVKETWVPK 18

RESULT 8
AAY65836
ID AAY65836 standard; Peptide; 10 AA.
XX
AC AAY65836;
XX
DT 10-FEB-2000 (first entry)
XX
DE Retinoblastoma binding protein 1 isoform I mutant peptide 6.
XX
KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;
KW mutcin.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9958552-A2.
XX
PD 18-NOV-1999.
XX
PF 03-MAY-1999; 99WO-NO00143.
XX
PR 08-MAY-1998; 98NO-0002097.
XX
PA (NHYD ) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
XX
DR WPI; 2000-039064/03.
XX
PT New peptides derived from genes with frameshift mutations, used to
PT develop products for the treatment and prophylaxis of cancers -
XX
PS Claim 13; Page 28; 166pp; English.
XX
CC Peptides AAY6584-Y66142 are fragments of mutant proteins arising from a
CC frameshift mutation in a gene from a cancer cell. The peptides are
CC characterised in that they:
CC (i) are at least 8 amino acids long and a fragment of a mutant protein
CC arising from a frameshift mutation in a gene of a cancer cell;
CC (ii) consist of at least one amino acid of the mutant part of a protein
CC sequence encoded by the gene;
CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal
CC part of the protein sequence preceding the amino terminus of the mutant
CC sequence and may further extend to the carboxyl terminus of the mutant
CC part of the protein as determined by a new stop codon generated by the
CC frameshift mutation; and
CC (iv) induce, either in their full lengths or after processing by an
CC antigen presenting cell (APC), T cell responses.
CC The genes that the peptides are derived from, are characterised as
CC susceptible to frameshift mutation by having a mono nucleoside base
CC repeat sequence of at least 5 residues, or a di-nucleoside base repeat
CC sequence of at least 4 di-nucleoside base units. The peptides are
CC created by the addition or deletion of 1 or 2 nucleoside base residues
CC from the repeat sequence. The novel peptides can elicit T cell responses
CC and toxicity against tumours and cancer cells carrying genes with
CC frameshift mutations. The novel peptides and DNA sequences can be used
CC for the preparation of a composition for the treatment or prophylaxis of
CC cancer.
XX
SQ Sequence 11 AA;
    Query Match      27.8%; Score 5; DB 21; Length 10;
    Best Local Similarity 100.0%; Pred. No. 63;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVKE 13
    |||||
Db 2 PKVKE 6

RESULT 9
AAY65837
ID AAY65837 standard; Peptide; 11 AA.
XX
AC AAY65837;
XX
DT 10-FEB-2000 (first entry)
XX
DE Retinoblastoma binding protein 1 isoform I mutant peptide 7.
XX
KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;
KW mutcin.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9958552-A2.
XX
PD 18-NOV-1999.
XX
PF 03-MAY-1999; 99WO-NO00143.
XX
PR 08-MAY-1998; 98NO-0002097.
XX
PA (NHYD ) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
XX
DR WPI; 2000-039064/03.
XX
PT New peptides derived from genes with frameshift mutations, used to
PT develop products for the treatment and prophylaxis of cancers -
XX
PS Claim 13; Page 28; 166pp; English.
XX
CC Peptides AAY6584-Y66142 are fragments of mutant proteins arising from a
CC frameshift mutation in a gene from a cancer cell. The peptides are
CC characterised in that they:
CC (i) are at least 8 amino acids long and a fragment of a mutant protein
CC arising from a frameshift mutation in a gene of a cancer cell;
CC (ii) consist of at least one amino acid of the mutant part of a protein
CC sequence encoded by the gene;
CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal
CC part of the protein sequence preceding the amino terminus of the mutant
CC sequence and may further extend to the carboxyl terminus of the mutant
CC part of the protein as determined by a new stop codon generated by the
CC frameshift mutation; and
CC (iv) induce, either in their full lengths or after processing by an
CC antigen presenting cell (APC), T cell responses.
CC The genes that the peptides are derived from, are characterised as
CC susceptible to frameshift mutation by having a mono nucleoside base
CC repeat sequence of at least 5 residues, or a di-nucleoside base repeat
CC sequence of at least 4 di-nucleoside base units. The peptides are
CC created by the addition or deletion of 1 or 2 nucleoside base residues
CC from the repeat sequence. The novel peptides can elicit T cell responses
CC and toxicity against tumours and cancer cells carrying genes with
CC frameshift mutations. The novel peptides and DNA sequences can be used
CC for the preparation of a composition for the treatment or prophylaxis of
CC cancer.
XX
SQ Sequence 11 AA;

```

Query Match 27.8%; Score 5; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 69; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

QY 9 PKVKE 13
 DB 2 PKVKE 6

RESULT 10
 AAB87422 ID AAB87422 standard; peptide; 12 AA.
 XX AC AAB87422;
 XX DT 22-MAY-2001 (first entry)
 XX DE Human gene 3 encoded secreted protein fragment, SEQ ID NO:163.
 XX KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnery;
 KW cell culture; chemotaxis; food additive;
 KW binding partner identification.
 XX KW Homo sapiens.
 OS WO200118022-A1.
 XX PN 15-MAR-2001.
 XX PD 31-AUG-2000; 2000WO-US24008.
 XX PF 03-SEP-1999; 99US-0152315.
 XX PR 03-SEP-1999; 99US-0152317.
 XX (HUMA-) HUMAN GENOME SCI INC.
 FA Ni J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;
 XX Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW;
 PI Moore PA, Shi Y, Wei Y, Florence KA;
 XX WPI; 2001-203081/20.
 XX Nucleic acid molecules encoding human secreted proteins, used in
 XX preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 XX Parkinson's diseases and cancers -
 XX Disclosure; Page 18; 607pp; English.

AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted
 protein genes, and AAB87342-AAB87413 represent the proteins they encode.
 AAB87414-AAB87454 represent human secreted protein fragments. The genes
 and their corresponding secreted proteins are useful for preventing,
 treating or ameliorating medical conditions, e.g., by protein or gene
 therapy. Pathological conditions can be diagnosed by determining the
 amount of the new protein in a sample or by determining the presence of
 mutations in the new genes. Specific uses are described for each of the
 52 genes, based on the tissues in which they are most highly expressed,
 and include developing products for the diagnosis or treatment of
 proliferative disorders, cancer, tumours, foetal and developmental
 abnormalities, haematopoietic disorders, diseases of the immune system,
 AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 allergies, neurological disorders (e.g., Alzheimer's disease,
 Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 cardiovascular disorders, angiogenic disorders, kidney disorders,

CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 12 AA;
 SQ Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPKV 11
 DB 1 GVPKV 5

RESULT 11
 AAR43871 ID AAR43871 standard; Protein; 14 AA.
 XX AC AAR43871;
 XX DT 25-MAR-2003 (updated)
 DT 23-DEC-1993 (first entry)
 XX DE OmpA2-R-7 signal peptide.
 XX KW Polypeptide; antibodies; HTLV; AIDS; vaccine.
 XX OS Human T-cell lymphotropic virus.
 XX PN EP52850-A1.
 XX PD 28-JUL-1993.
 XX PF 10-OCT-1985; 93EP-0200929.
 XX PR 10-OCT-1984; 84US-0659339.
 PR 23-JAN-1985; 85US-0693866.
 PR 10-OCT-1985; 85EP-0307260.
 XX (CENZ) CENTOCOR INC.
 XX Chang NT, Gallo RC, Wong-staal F;
 XX WPI; 1993-236543/30.
 DR N-PSDB; AAQ45924.
 XX Cloning and expression of new HTLV-III DNA - used to obtain
 PT polypeptide(s) and antibodies for diagnosis, prevention and
 PT treatment of HTLV-III infection, partic. AIDS
 PS Disclosure; Figure 6a; 31pp; English.

A fragment of DNA approximately 200-500 base pairs in length is
 CC ligated into a recombinant vector (ompA1-R-6; ompA2-R-7 or ompA3-R-3)
 CC and used to transform E.coli. These cells then express a polypeptide
 CC which is immunoreactive with HTLV-III-specific antibody. The
 CC HTLV-III polypeptides can be used for the production
 CC of antibodies, in immunoassays for the detection of HTLV-
 CC III-specific antibodies and in vaccines for the prevention of AIDS.
 CC The antibodies can also be used to detect HTLV-III polypeptides.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)

CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies. Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX SQ Sequence 16 AA;

Query Match 27.8%; Score 5; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVKE 13
 |||||
 Db 8 PKVKE 12

RESULT 14

AAW93084
 ID AAW93084 standard; Protein; 4 AA.

AC AAW93084;

XX 19-MAY-1999 (first entry)

XX Human erythropoietin modified signal peptide N-terminal #3.

XX Erythropoietin; human; EPO; therapy; erythrocyte production; stimulation.

XX Synthetic.

OS Homo sapiens.

XX WO9905268-A1.

XX 04-FEB-1999.

XX 22-JUL-1998; 98WO-EP04590.

XX 10-JUL-1998; 98US-0113692.

PR 23-JUL-1997; 97EP-0112640.

PR 03-DEC-1997; 97DE-1053681.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Auer J, Brandt M, Honold K, Koll H, Stern A;

XX WPI; 1999-142926/12.

DR N-PSDB; AAX22430.

XX New human cells containing erythropoietin gene controlled by
 PT heterologous promoter - for large scale production of pure,
 PT glycosylated erythropoietin

XX Claim 11; Page 32; 70pp; German.

XX This invention describes human cells containing a copy of an endogenous
 CC gene for erythropoietin (EPO) linked to a heterologous promoter,
 CC functional in human cells, and capable of producing at least 200 ng
 CC EPO/million cells/24 hr. The invention also describes a DNA construct for
 CC activating an endogenous EPO gene in a human cell comprising (i) two

CC flanking sequences, homologous to regions (i.e. the 5'-untranslated
 CC region, exon 1 or intron 1) of the human EPO gene locus and capable of
 CC homologous recombination, including in the exon 1 region a modified
 CC sequence encoding Met-X1-X2-X3 where X1 = Gly or Ser; X2 = Ala, Val,
 CC Ile, Ser or Pro; X3 = Pro, Arg, Cys or His; but X1-X2-X3 is not
 CC Gly-Val-His (ii) a positive selection marker gene (iii) a heterologous
 CC expression control sequence and (iv) optionally an amplification gene.
 CC The method of the invention can be used to produce EPO for therapeutic
 CC use (stimulation of erythrocyte production). The new cells make possible
 CC economical, large scale production of pure human EPO, and are
 CC significantly more productive than transformed CHO cells. Altering the
 CC signal sequence and/or the distance between promoter and start signal
 CC optimises EPO expression.

XX SQ Sequence 4 AA;

Query Match 22.2%; Score 4; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9

|||||

Db 1 MGVP 4

RESULT 15

ABG32218

ID ABG32218 standard; peptide; 4 AA.

XX AC ABG32218;

XX 05-NOV-2002 (first entry)

XX Sheep colostrin derived peptide #12.

XX Sheep; colostrin; colostrum; cytokine inducer; antigen; dementia;
 KW central nervous system disorder; neurological disorder; neurosis;
 KW mental disorder; psychosis; neurodegenerative disorder;
 KW Alzheimer's disease; motor neuron disease; immune system disorder;
 KW acquired immunological deficiency; bacterial infection; viral infection;
 KW amyloid plaque; dietary supplement; cachexia; weight loss;
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;
 KW drug addiction; drug withdrawal.

XX Ovis aries.

XX WO200246211-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-GB05376.

XX 06-DEC-2000; 2000GB-0029777.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2002-619016/66.

XX Novel peptides isolated from colostrin polypeptide, useful for
 PT treating viral and bacterial infections, disorders of immune system and
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food
 PT additive -

XX Claim 1; Page 8; 16pp; English.

XX The invention relates to a peptide derived from colostrin (a colostrum
 CC protein known to be a cytokine inducer) substantially entirely consists
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included
 CC are a composition comprising two or more of the peptides in combination
 CC with a carrier, a dietary supplement comprising an orally ingestible
 CC combination of the peptide in combination with a carrier and an antibody

CC which binds to the peptide, and which is obtainable by using peptide as
 CC an antigen. The peptide is useful as a medicament for treating chronic
 CC disorders of central nervous system e.g., neurological disorders and/or
 CC mental disorders such as psychosis and/or neurosis, dementia,
 CC neurodegenerative disorders such as Alzheimer's disease, motor
 CC neuron disease, chronic disorders of immune system, diseases
 CC with bacterial and viral etiology, acquired immunological deficiencies,
 CC chronic bacterial, viral infections. The peptide is also useful for
 CC treating diseases characterised by presence of amyloid plaque. The
 CC peptide is also useful as a dietary supplement for babies, small
 CC children, adults who have been subjected to chemotherapy and/or
 CC adults who have suffered from cachexia or weight loss due to chronic
 CC disease. The peptide is also useful for treating senile dementia,
 CC Parkinson's disease, emotional disturbances and depression. The peptides
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,
 CC after a period of detoxification, and in persons dependent on stimulants.
 CC The present sequence is a colostrin derived peptide of the invention.

XX Sequence 4 AA;
 SQ Query Match 22.2%; Score 4; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 Db 1 PKVK 4

RESULT 16

AAR32746
 ID AAR32746 standard; peptide; 6 AA.

XX AC

XX AAR32746;

XX 25-MAR-2003 (updated)

DT 18-JUN-1993 (first entry)

XX PK40 TAU/neurofilament protein kinase tryptic peptide.

DE Neurodegenerative disease; treatment; diagnosis; Alzheimer's;

KW Kinase inhibitor; paired helical fragments; PHF; tangles; formation.

KW Kinase inhibitor; paired helical fragments; PHF; tangles; formation.

XX Homo sapiens.

XX WO9303148-A2.

XX 18-FEB-1993.

XX 10-JUL-1992; 92WO-US05825.

XX 09-AUG-1991; 91US-0742880.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Ingram VM, Roder HM;

XX WPI; 1993-076505/09.

XX Prepn. contg. isolated, pure non-skeletal associated kinase -

PT used in treatment and diagnosis of neurodegenerative conditions

PT e.g. Alzheimer's disease

XX Example; Page 76; 88pp; English.

XX The sequence is that of a tryptic peptide of TAU/neurofilament

CC protein kinase PK40. Antibodies (monoclonal or polyclonal) specific

CC for PK40 which are capable of binding to and inhibiting the kinase

CC activity of PK 40 may be used to reduce phosphorylation activity in

CC the cell, and to reduce or prevent formation of paired helical

CC fragments (PHF) or tangles. This allows investigation e.g. of the

CC contribution of such phosphorylation activity to cell maintenance

CC and to neurocellular states characteristic of neurodegenerative

CC diseases, partic. Alzheimer's and ageing. The sequence shows a very
 CC close match to the ERK-kinase family proteins and so PK40 can be
 CC considered to be a member of the cell cycle-associated ERK kinase
 CC family.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;
 SQ Query Match 22.2%; Score 4; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEIM 6

Db 2 PEIM 5

XX 26-NOV-1999 (first entry)

XX PK40 protein kinase tryptic peptide.

XX TAU hyper-phosphorylation; adenosine triphosphate; ATP binding site;

KW PK40; TAU kinase; neurofilament protein kinase; Alzheimer's disease;

KW tryptic peptide; ERK-Kinase.

XX Homo sapiens.

XX US9555444-A.

XX 21-SBP-1999.

XX 07-JUN-1995; 95US-0480793.

XX 10-JUL-1992; 92US-0912293.

XX 09-AUG-1991; 91US-0742880.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Roder HM, Ingram VM;

XX WPI; 1999-560501/47.

XX Inhibiting abnormal TAU hyper-phosphorylation in cells for the

PT treatment of Alzheimer's disease -

XX Example 11; Columns 33-34; 19pp; English.

XX The invention relates to a new method for inhibiting abnormal TAU hyper-

CC phosphorylation activity in cells. The method comprises contacting a

CC cell with an inhibitor which binds to an adenosine triphosphate (ATP)

CC binding site on PK40 (a TAU/neurofilament protein kinase) and therefore

CC inhibits the phosphorylation activity of PK40 (which is characteristic of

CC abnormal TAU hyper-phosphorylation in Alzheimer's disease). The method

CC may be used for inhibiting TAU hyper-phosphorylation activity in cells.

CC In particular, it may be used for inhibiting the phosphorylating activity

CC of PK40 which is characteristic of abnormal TAU hyper-phosphorylation in

CC Alzheimer's disease. Sequences AAY27408-422 represent peptides obtained

CC by tryptic digestion of PK40 kinase. Peptides AAY27410-422 has high

CC homology to the ERK-kinase family proteins.

XX Sequence 6 AA;

QY Query Match 22.2%; Score 4; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEIM 6


```

Db          |||||
            2 PEIM 5

RESULT 18
AAM51129
ID AAM51129 standard; Peptide; 6 AA.
XX
AC AAM51129;
XX
DT 06-JUN-2002 (first entry)
XX
DE Bovine TAU/neurofilament protein kinase PK40 tryptic peptide 14.
XX
KW PK40; TAU; neurofilament; protein kinase; enzyme; human;
KW ERK kinase; phosphorylation; ageing; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; brain infarct;
KW neurotropic; neuroprotective; diagnosis; therapy.
XX
OS Bos taurus.
XX
PN US2002025942-A1.
XX
PD 28-FEB-2002.
XX
PF 20-MAR-1998; 98US-0045020.
XX
PR 10-JUL-1992; 92US-0912293.
XX
PR 07-JUN-1995; 95US-0480793.
XX
PR 09-AUG-1991; 91US-0742880.
XX
PA (INGR/) INGRAM V M.
XX (RODE/) RODER H M.
XX
PI Ingram VM, Roder HM;
XX
DR WPI; 2002-255975/30.
XX
PT Preparation for phosphorylating dephosphorylated neurofilament-M,
PT comprises isolated, pure, nonskeletal-associated kinase -
XX
PS Example 11; Page 17; 21pp; English.
XX
CC The present sequence is that of tryptic peptide 14, which is 1 of
CC 15 peptides (see AAM51116-30) obtained by trypsin digestion of a
CC novel TAU/neurofilament protein kinase, termed PK40, isolated from
CC bovine brain. PK40 is capable of phosphorylating completely
CC dephosphorylated (cd) neurofilament-M (NF-M) so as to cause a
CC complete shift on SDS-PAGE of the apparent Kr to that of native
CC NF-M. It also causes a partial shift of cdNF-H. PK40 is capable
CC of causing a complete shift of bovine cdTAU or human TAU isoform
CC expressed in Escherichia coli. Under saturation phosphorylation
CC conditions, PK40 causes a change in the isoform pattern that
CC closely resembles the pattern of human TAU proteins extracted from
CC paired helical filaments. PK40 also phosphorylates both KSP sites
CC of TAU and abolishes the TAU 1 epitope. PK40 was identified using
CC a novel kinase immunoassay of the invention. Peptides 3-15 show
CC homology to ERK1 and ERK2, suggesting that PK40 is a member of the
CC cell cycle-associated ERK kinase family. A novel assay that can be
CC used as a diagnostic test for early Alzheimer's disease measures
CC the level of neuroprotein phosphorylation activity in a human cell
CC by PK40 or PK36. The assay can also be used to diagnose other
CC conditions affected by neuronal degeneration such as Parkinson's
CC disease, Huntington's disease, normal ageing and brain infarcts.
CC An inhibitor of PK40 (e.g. an antibody or ATP) may be useful in the
CC treatment of these conditions.
XX
SQ Sequence 6 AA;
Query Match 22.2%; Score 4; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          |||||
            2 PEIM 5

RESULT 19
AAR33159
ID AAR33159 standard; peptide; 7 AA.
XX
AC AAR33159;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
DE HPV E7 protein - RSG protein binding inhibitor peptide.
XX
KW Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
OS Synthetic.
XX
PN EP531080-A2.
XX
PD 10-MAR-1993.
XX
PF 01-SEP-1992; 92EP-0307905.
XX
PR 04-SEP-1991; 91US-0754829.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Oliff AI, Riemen MW;
XX
DR WPI; 1993-078581/10.
XX
PT New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
PS Claim 7; Page 15; 15pp; English.
XX
CC The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
Query Match 22.2%; Score 4; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          |||||
            2 LQPE 5

RESULT 20
AAV49017
ID AAV49017 standard; Peptide; 7 AA.
XX
AC AAV49017;
XX
DT 20-MAR-2003 (updated)
DT 10-DEC-1999 (first entry)
XX
DE Membrane dipeptidase-binding adrenal gland homing peptide #16.
XX
KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
KW membrane dipeptidase.
XX
OS Synthetic.

```

OS Homo sapiens.
 PN WO9946284-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US05284.
 XX
 PR 13-MAR-1998; 98US-0042107.
 PR 26-FEB-1999; 99US-0258754.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Rajotte D, Pasqualini R, Ruoslahti E;
 DR WPI; 1999-571717/48.
 XX
 PT New peptides which selectively home to organs or tissues, used for,
 PT e.g. identifying target ligands and for therapy of pathological
 PT conditions -
 XX
 PS Claim 65; Page 155; 193pp; English.
 XX
 CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ
 CC or tissue, for identifying a target molecule expressed by an organ or
 CC tissue or for treating an organ or tissue pathology, where the organ or
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences
 CC which are used in the exemplification of the present invention.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 9 PKVK 12
 Db |||||
 1 PKVK 4
 RESULT 22
 AAB35822
 ID AAB35822 standard; peptide; 7 AA.
 XX
 AC AAB35822;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE T7 phage coat protein C-terminus modification K+ peptide.
 XX
 KW Epitope identification; display system; gene delivery; drug delivery;
 KW bacteriophage T7.
 XX
 OS Synthetic.
 XX
 PN WO200065350-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 27-APR-2000; 2000WO-US11270.
 XX
 PR 27-APR-1999; 99US-0131151.
 PR 07-JUN-1999; 99US-0139431.
 XX
 PA (MIRU-) MIRUS CORP.
 XX
 PI Wolff JA;
 XX
 DR WPI; 2000-687379/67.

XX Identifying new peptide ligands that protect phage which delivers drugs
 PT and genes in vivo, by binding to blood proteins, comprises exposing an
 PT epitope display system to blood products -
 XX
 PS Example 1; Page 55; 87pp; English.
 XX
 CC This invention relates to a process comprising exposing an epitope
 CC display system to blood products to identify useful epitopes. The process
 CC is useful for identifying new peptide ligands that protect the display
 CC system e.g. phage, which delivers drugs and genes in vivo. The delivery
 CC system may be inhibited through binding to complement, the process
 CC reveals peptides which may be used to protect the system from this
 CC inhibition. The present sequence represents a peptide which can be used
 CC to modify the C-terminal of a T7 phage coat protein. The peptide protects
 CC against inactivation.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 9 PKVK 12
 Db |||||
 4 PKVK 7
 RESULT 22
 AAB72261
 ID AAB72261 standard; peptide; 7 AA.
 XX
 AC AAB72261;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrin derived cytokine inducing peptide SEQ ID 16.
 XX
 KW Colostrin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22818.
 XX
 PR 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the

PI Georgiades JA;
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOPE 4
 Db | | | |
 4 LOPE 7
 RESULT 26
 AAE20243
 ID AAE20243 standard; peptide; 7 AA.
 XX
 AC AAE20243;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #15.
 DE
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 7 /note= "Optionally C-terminal amide"
 FT
 XX
 XX WO200213850-A1.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2002-269151/31.
 XX
 DR Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 PT
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell

CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOPE 4
 Db | | | |
 4 LOPE 7
 RESULT 27
 AAM51050
 ID AAM51050 standard; Peptide; 7 AA.
 XX
 AC AAM51050;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Colostrinin constituent peptide.
 XX
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 7 /note= "optional C-terminal amidation"
 FT
 XX
 XX WO200213849-A1.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX (REGE-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2002-269150/31.
 XX
 DR Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 PT
 XX Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. The peptide is
 CC classified as having a beta-casein homologue precursor. Methods

CC	are claimed for: inducing a cytokine in a cell by contact with an
CC	immunological regulator, where the cell is present in a cell
CC	culture, a tissue, an organ or an organism, and the cell is
CC	mammalian, including human; modulating an immune response in a cell
CC	by contact with the immunological regulator under conditions
CC	effective to induce a cytokine; modulating an immune response in a
CC	patient by administering an immunological regulator under conditions
CC	effective to induce a cytokine, where the immunological regulator
CC	is administered topically or as part of a dietary supplement, and
CC	where the immune response is specific or non specific, an interferon
CC	response or an antibody response; modulating blood cell proliferation
CC	by contacting blood cells with a blood cell regulator, where the
CC	blood cells are present in a cell culture or an organism, are
CC	mammalian or human, and where the blood cells are increased in
CC	number or differentiated; and a method for modulating blood cell
CC	proliferation in a patent. A claimed cytokine-inducing composition
CC	comprises a pharmaceutical carrier and an active agent such as the
CC	present peptide.
XX	
QQ	
SS	
TT	
UU	
VV	
WW	
XX	
YY	
ZZ	
AA	
BB	
CC	
DD	
EE	
FF	
GG	
HH	
II	
JJ	
KK	
LL	
MM	
NN	
OO	
PP	
QQ	
RR	
SS	
TT	
UU	
VV	
WW	
XX	
YY	
ZZ	
AA	
BB	
CC	
DD	
EE	
FF	
GG	
HH	
II	
JJ	
KK	
LL	
MM	
NN	
OO	
PP	
QQ	
RR	
SS	
TT	
UU	
VV	
WW	
XX	
YY	
ZZ	
AA	
BB	
CC	
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EE	
FF	
GG	
HH	
II	
JJ	
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MM	
NN	
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UU	
VV	
WW	
XX	
YY	
ZZ	
AA	
BB	
CC	
DD	
EE	
FF	
GG	
HH	
II	
JJ	
KK	
LL	
MM	
NN	
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QQ	
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VV	
WW	
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AA	
BB	
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DD	
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FF	
GG	
HH	
II	
JJ	
KK	
LL	
MM	
NN	
OO	
PP	
QQ	
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TT	
UU	
VV	
WW	
XX	
YY	
ZZ	
AA	
BB	
CC	
DD	
EE	
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KK	
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MM	
NN	
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TT	
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YY	
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AA	
BB	
CC	
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RR	
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GG	
HH	
II	
JJ	
KK	
LL	
MM	
NN	
OO	
PP	
QQ	
RR	
SS	
TT	
UU	
VV	</

CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. the present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.

XX
XX
SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
|
|
|
|
Db 4 LOPE 7

RESULT 29

AAR10631
ID AAR10631 standard; Protein; 8 AA.
XX
AC AAR10631;
XX
25-MAR-2003 (updated)
DT 18-APR-1991 (first entry)
XX
XX Human Papilloma Virus-16 "[Gln27]-E7-(20-27)-AMIDE" peptide.
XX
XX papilloma virus; retinoblastoma gene-binding protein; genital warts;
KW cervical cancer.
XX
XX Synthetic.
OS
XX EP412762-A.
FN
XX 13-FEB-1991.
PD
XX
XX 06-AUG-1990; 90EP-0308652.
PF
XX
XX 09-APR-1990; 90US-0506981.
PR
XX 07-AUG-1989; 89US-0390569.
PR
XX
XX (MERI) MERCK & CO INC.
PA
XX (OLIF)/ OLIFF A. I.
XX
PI Oliff AI, Riemen MW;
XX
DR WPI; 1991-045887/07.
XX
XX Papilloma virus and retinoblastoma gene-binding protein
PT
PT inhibitors - involves a specified aminoacid sequence contg. 13
PT residues for treatment of genital warts and cervical cancer
XX
XX Claim 12; Page 11; 11pp: English.

XX
XX The peptide carries an amide group at the C-terminus. The sequence
CC comprises residues 20 to 27 of the deduced HPV-16 E7 protein
CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,
CC Plenum Press, N.Y. 1987) but with Gln replacing Asp at position 27.
CC The peptides are used as screening tools and in the prevention,
CC therapy, prophylaxis and treatment of HPV-induced diseases. They
CC can also be used to raise antibodies either as vaccines or to
CC heighten the immune response to an HPV infection all ready present.
CC See also AAR10628-R10630, AAR10632-7.
CC (Updated on 25-MAR-2003 to correct PA field.)

XX
XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 LOPE 4
Db      ||||
        2 LOPE 5

RESULT 30
AAR33158
ID AAR33158 standard; peptide; 8 AA.
XX
AC AAR33158;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
DE HPV E7 protein - RBG protein binding inhibitor peptide.
XX
KW Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
OS Synthetic.
XX
PN EP531080-A2.
XX
PD 10-MAR-1993.
XX
PF 01-SEP-1992; 92EP-0307905.
XX
PR 04-SEP-1991; 91US-0754829.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Oliff AI, Riemen MW;
XX
DR WPI; 1993-078581/10.
XX
PT New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
PS Claim 7; Page 15; 15pp; English.
XX
CC The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOPE 4
Db      ||||
        2 LOPE 5

RESULT 31
AAW77186
ID AAW77186 standard; peptide; 8 AA.
XX
AC AAW77186;
XX
DT 23-NOV-1998 (first entry)
XX
DE Pharmaceutically active peptide 27.
XX
KW Pharmaceutically active peptide; target; organ; lymphocyte; treatment;
KW pharmaceutical agent; disease; radioactive isotope; imaging agent.
XX
OS Synthetic.
OS Homo sapiens.
XX

PN WO9839469-A1.
XX
PD 11-SEP-1998.
XX
PF 04-MAR-1998; 98WO-US04188.
XX
PR 04-MAR-1997; 97US-0810074.
PR 04-MAR-1997; 97US-0039509.
XX
PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
PI Belkind A, Golan I, Hagai Y, Lazarovits J, Levanon A;
PI Nimrod A, Panet A, Vogel T, Zeelon E;
XX
DR WPI; 1998-495863/42.
XX
PT New peptide(s) binding targets in organs and lymphocytes - for the
PT targetted delivery of toxins, anti-cancer drugs and cardiovascular
PT agents to arteries, veins, placenta, liver
XX
PS Claim 54; Page 97; 114pp; English.
XX
CC Sequences shown in AAW77160 to AAW77214 and AAW79167 represent
CC non-naturally- occurring pharmacuetically active peptides. These novel
CC peptides specifically bind to undetermined and determined targets in
CC various organs and in lymphocytes. The peptides can be used in
CC compositions, where they can be linked to pharmaceutical agents, to treat
CC various diseases and conditions. The peptides or chimeric polypeptides
CC comprising these pharmacuetically active peptides and a second peptide
CC may be labelled with a marker (radioactive isotope, etc) to form an
CC imaging agent. This agent is used to bind an organ so that the organ can
CC be imaged.
XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      ||||
        3 PKVK 6

RESULT 32
AAB35995
ID AAB35995 standard; Protein; 8 AA.
XX
AC AAB35995;
XX
DT 01-MAR-2001 (first entry)
XX
DE Sorbitol dehydrogenase subunit 3 internal peptide.
XX
KW Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol;
KW L-sorbose production; 2-keto-L-gulonic acid.
XX
OS Gluconobacter oxydans.
XX
PN WO200065066-A1.
XX
PD 02-NOV-2000.
XX
PF 23-APR-1999; 99WO-IB00736.
XX
PR 23-APR-1999; 99WO-IB00736.
XX
PA (CHOI/) CHOI E.
PA (RHEE/) RHEE S.
PA (LEEE/) LEE E.
XX
PI Choi E, Rhee S, Lee E;
XX

```

DR WPI; 2000-687351/67.

XX Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule

PT isolated from Gluconobacter suboxydans useful for the fermentative

PT production of 2-keto-L-gulononic acid and L-sorbose from D-sorbitol

XX Example 2; Page 37; 96pp; English.

PS This invention relates to an isolated membrane-bound sorbitol

CC dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes

CC polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH

CC (AA835987 - AA835989). Also included in the invention are two

CC polynucleotide sequences AAC83156 and AAC83157 which contain the subunit

CC coding regions. The sorbitol dehydrogenase polynucleotide sequences are

CC useful for producing L-sorbose from D-sorbitol and for increasing the

CC production of 2-keto-L-gulononic acid by transforming a host cell,

CC especially Gluconobacter with the DNA and selecting the transformed host

CC cell. The present sequence represents the SDH subunit 3 internal

CC peptide.

XX Sequence 8 AA;

SQ Query Match 22.2%; Score 4; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVPK 10

Db |||||

5 GVPK 8

RESULT 33

ABP14637

ID ABP14637 standard; Peptide; 8 AA.

XX AC ABP14637;

XX 15-JUL-2002 (first entry)

XX HIV A03 super motif pol peptide #11.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

OS WO200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

PF 05-OCT-1999; 99US-0412863.

PR (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 168; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

XX invention.

SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12

Db |||||

5 PKVK 8

RESULT 34

ABP17276

ID ABP17276 standard; Peptide; 8 AA.

XX AC ABP17276;

XX 15-JUL-2002 (first entry)

XX HIV B27 super motif pol peptide #10.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

OS WO200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

PF 05-OCT-1999; 99US-0412863.

PR (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 223; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 Db 1 PKVK 4

RESULT 35
 ABP21662
 ID ABP21662 standard; Peptide; 8 AA.

XX AC ABP21662;

DT 15-JUL-2002 (first entry)

XX HIV A03 motif pol peptide #657.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 313; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 Db 5 PKVK 8

RESULT 36
 ABP23544

ID ABP23544 standard; Peptide; 8 AA.

XX AC ABP23544;

XX DT 15-JUL-2002 (first entry)

XX HIV A11 motif pol peptide #486.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 351; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 |||||
 Db 5 PKVK 8

RESULT 37

AAG62330
 ID AAG62330 standard; peptide; 8 AA.

XX AC AAG62330;

XX 24-AUG-2001 (first entry)

XX Casein-related peptide SEQ ID 29.

XX Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.

XX Synthetic.

XX WO200134828-A1.

XX 17-MAY-2001.

XX 10-NOV-2000; 2000WO-JP07930.

XX 11-NOV-1999; 99JP-0321084.

XX (CALV) CALPIS CO LTD.

XX Yamamoto N, Ueno K, Ejiri M;

XX WPI; 2001-343606/36.

XX Production of tripeptides for treating hypertension and stress by
 processing casein with proteinase and peptidase -

XX Example 4; Page 13; 32pp; Japanese.

XX This invention relates to a method for the production of tripeptides. The
 method comprises treating material containing milk casein with a
 CC proteinase to produce intermediate peptide containing ValProPro or
 CC IleProPro with no proline residue any where else in the peptide. Use of
 CC the peptides may result in hypotensive and tranquiliser activity. The
 CC peptide can be used in treatments to lower blood pressure and in the
 CC treatment of stress. The present sequence represents a peptide used in an
 CC example illustrating the method of the invention.

XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 |||||
 Db 5 LOPE 8

RESULT 38

AAR10635
 ID AAR10635 standard; Protein; 9 AA.

XX AC AAR10635;

XX 25-MAR-2003 (updated)

DT 18-APR-1991 (first entry)

XX Human Papilloma Virus-16 "[Gln26]-E7-(20-28)-AMIDE" peptide.

XX papilloma virus; retinoblastoma gene-binding protein; genital warts;
 KW cervical cancer.

XX Synthetic.

XX EP412762-A.

XX 13-FEB-1991.

XX 06-AUG-1990; 90EP-0308652.

XX 09-APR-1990; 90US-0506981.

XX 07-AUG-1989; 89US-0390569.

XX (MERI) MERCK & CO INC.

XX (OLIF/) OLIFF A I.

XX Oliff AI, Riemen MW;

XX WPI; 1991-045887/07.

XX Papilloma virus and retinoblastoma gene-binding protein
 PT inhibitors - involves a specified aminoacid sequence contg. 13
 PT residues for treatment of genital warts and cervical cancer

XX Claim 12; Page 11; 11pp; English.

XX The peptide carries an amide group at the C-terminus. The sequence
 CC comprises residues 20 to 28 of the deduced HPV-16 E7 protein
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2, p.379,
 CC Plenum Press, N.Y. 1987) but with Gln replacing Thr at position 26.
 CC The peptides are used as screening tools and in the prevention,
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They
 CC can also be used to raise antibodies either as vaccines or to
 CC heighten the immune response to an HPV infection all ready present.
 CC See also AAR10628-R10634, AAR10636-7.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 |||||
 Db 2 LOPE 5

RESULT 39

AAR33157
 ID AAR33157 standard; peptide; 9 AA.

XX AC AAR33157;

XX 25-MAR-2003 (updated)

DT 25-JUN-1993 (first entry)

XX HPV E7 protein - RBG protein binding inhibitor peptide.

XX Human papilloma virus; retinoblastoma gene; genital warts;
 KW cervical cancer; treatment.

XX

PT	New polypeptide(s) which inhibit human papilloma virus binding to
PP	REG protein - useful for treating genital warts and cervical cancer
XX	
PS	Claim 7; Page 15; 15pp; English.
XX	
CC	The sequence is that of a peptide which inhibits binding of human
CC	papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC	protein. It can be used in the treatment of conditions caused by HPV,
CC	esp. genital warts and cervical cancer.
CC	(Updated on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 9 AA;
	Query Match 22.2%; Score 4; DB 14; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 LOPE 4
Db	1 LOPE 4
RESULT 41	
AAR33170	
ID	AAR33170 standard; peptide; 9 AA.
XX	
AC	AAR33170;
XX	
AC	
XX	
DT	25-MAR-2003 (updated)
DT	25-JUN-1993 (first entry)
XX	
DE	HPV E7 protein - REG protein binding inhibitor peptide.
XX	
KW	Human papilloma virus; retinoblastoma gene; genital warts;
KW	cervical cancer; treatment.
XX	
OS	Synthetic.
XX	
PN	EP531080-A2.
XX	
PD	10-MAR-1993.
XX	
PF	01-SEP-1992; 92EP-0307905.
XX	
PR	04-SEP-1991; 91US-0754829.
XX	
PA	(MERI) MERCK & CO INC.
XX	
EI	Oloff AI, Riemen MW;
XX	
DR	WPI; 1993-078581/10.
XX	
PT	New polypeptide(s) which inhibit human papilloma virus binding to
PP	REG protein - useful for treating genital warts and cervical cancer
XX	
PS	Claim 7; Page 15; 15pp; English.
XX	
CC	The sequence is that of a peptide which inhibits binding of human
CC	papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC	protein. It can be used in the treatment of conditions caused by HPV,
CC	esp. genital warts and cervical cancer.
CC	(Updated on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 9 AA;
	Query Match 22.2%; Score 4; DB 14; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps

```

RESULT 42
AAR43741
ID AAR43741 standard; peptide; 9 AA.
XX AC
XX AAR43741;
XX AC
XX 25-MAR-2003 (updated)
XX DT 19-MAY-1994 (first entry)
XX DT
XX DE MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.
XX XX
XX Human papilloma virus; major histocompatibility complex; prevention;
XX KW treatment; virus-related diseases; T cell response; cervical; human;
XX KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.
XX XX
XX Synthetic.
XX OS
XX WO9322338-A1.
XX PN
XX 11-NOV-1993.
XX PD
XX PF 04-MAY-1993; 93WO-NL00093.
XX XX
XX 05-MAY-1992; 92EP-0201252.
XX PR 10-DEC-1992; 92EP-0203870.
XX PR 01-FEB-1993; 93EP-0200243.
XX PR 05-MAR-1993; 93EP-0200621.
XX XX
XX (UYLE-) RIJKSUNIV LEIDEN.
XX PA
XX Kast WM, Melief CJM, Sette AD, Sidney JC;
XX PI WPI; 1993-368718/46.
XX DR
XX PF Peptide(s) derived from human papilloma virus - which bind to a
XX XX human major histocompatibility complex Class I molecule, used for
XX PT prevention and treatment of virus-related diseases
XX PT
XX PS Claim 5; Page 51; 64pp; English.
XX XX
XX The sequence is that of a peptide, derived from the E7 protein of
XX CC human papilloma virus (HPV) (residues 11-19), which is able to bind
XX CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell
XX CC response effective against HPV, in partic. a HLA class I-restricted
XX CC CD8+ cytotoxic T cell response. It can be used for prevention and
XX CC treatment of cervical carcinoma and/or adenoma and other HPV-related
XX CC diseases. It can also be used as a screening tool and in diagnostic
XX CC applications.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX CC
XX SQ Sequence 9 AA;
XX XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
XX CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX Qy 1 LQPE 4
XX Db 5 LQPE 8
XX XX
XX RESULT 43
XX AAR43742
XX ID AAR43742 standard; peptide; 9 AA.
XX XX
XX AAR43742;
XX AC
XX 25-MAR-2003 (updated)
XX DT 19-MAY-1994 (first entry)
XX DT
XX XX
XX DE MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.
XX XX

```

```

KW Human papilloma virus; major histocompatibility complex; prevention;
KW KW treatment; virus-related diseases; T cell response; cervical; human;
KW KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.
XX OS
XX Synthetic.
XX OS
XX WO9322338-A1.
XX PN
XX 11-NOV-1993.
XX PD
XX PF 04-MAY-1993; 93WO-NL00093.
XX XX
XX 05-MAY-1992; 92EP-0201252.
XX PR 10-DEC-1992; 92EP-0203870.
XX PR 01-FEB-1993; 93EP-0200243.
XX PR 05-MAR-1993; 93EP-0200621.
XX XX
XX (UYLE-) RIJKSUNIV LEIDEN.
XX PA
XX Kast WM, Melief CJM, Sette AD, Sidney JC;
XX PI WPI; 1993-368718/46.
XX DR
XX PF Peptide(s) derived from human papilloma virus - which bind to a
XX XX human major histocompatibility complex Class I molecule, used for
XX PT prevention and treatment of virus-related diseases
XX PT
XX PS Claim 5; Page 51; 64pp; English.
XX XX
XX The sequence is that of a peptide, derived from the E7 protein of
XX CC human papilloma virus (HPV) (residues 12-20), which is able to bind
XX CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell
XX CC response effective against HPV, in partic. a HLA class I-restricted
XX CC CD8+ cytotoxic T cell response. It can be used for prevention and
XX CC treatment of cervical carcinoma and/or adenoma and other HPV-related
XX CC diseases. It can also be used as a screening tool and in diagnostic
XX CC applications.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX CC
XX SQ Sequence 9 AA;
XX XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
XX CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX Qy 1 LQPE 4
XX Db 4 LQPE 7
XX XX
XX RESULT 44
XX AAR59257
XX ID AAR59257 standard; peptide; 9 AA.
XX XX
XX AAR59257;
XX AC
XX 25-MAR-2003 (updated)
XX DT 10-MAY-1995 (first entry)
XX DT
XX DE Peptide fragment (1.0229) of HPV binds HLA-A2.1.
XX XX
XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
XX KW HIV1; core antigen; surface antigen; pharmaceutical composition;
XX KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
XX KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
XX KW human leukocyte antigen.
XX XX
XX Human papilloma virus.
XX OS
XX WO9420127-A1.
XX PN
XX 15-SEP-1994.
XX PD
XX XX

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PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX
PS Example 5; Page 106; 138pp; English.
XX
XX
CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59246
CC has an IC50 of <0.0003 and the sequence occurs at position 14 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 9 AA;
XX
XX
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 LQPE 4
Db ||||
2 LQPE 5
XX
XX
RESULT 46
AAR73799
ID AAR73799 standard; peptide; 9 AA.
XX
XX
AC AAR73799;
XX
XX
DT 25-MAR-2003 (updated)
DT 19-JUN-1995 (first entry)
XX
XX
DE Antigen fragment 115, from HPV(a) has binding affinity for HLA-2.1.
XX
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
XX
OS Human papilloma virus strain 16(a).
XX
XX
PN WO9420127-A1.
XX
XX
PD 15-SEP-1994.
XX
XX
PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX
PS Disclosure; Page 84; 138pp; English.
XX
XX

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PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX
PS Example 5; Page 106; 138pp; English.
XX
XX
CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257
CC has an IC50 of <0.0003 and the sequence occurs at position 14 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 9 AA;
XX
XX
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 LQPE 4
Db ||||
2 LQPE 5
XX
XX
RESULT 45
AAR59246
ID AAR59246 standard; peptide; 9 AA.
XX
XX
AC AAR59246;
XX
XX
DT 25-MAR-2003 (updated)
DT 04-MAY-1995 (first entry)
XX
XX
DE Peptide fragment (1.0316) of c-ERB2 binds HLA-A2.1.
XX
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9420127-A1.
XX
XX
PD 15-SEP-1994.
XX
XX
PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX

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CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from HPV(a) E7(a)
 CC antigen has a binding value of 1.9000. The peptides of the invention can
 CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 9 AA;
 SQ

Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db |||||
 5 LOPE 8

RESULT 47
 AAR73800
 ID AAR73800 standard; peptide; 9 AA.
 XX AC AAR73800;
 XX
 XX
 DT 25-MAR-2003 (updated)
 DT 19-JUN-1995 (first entry)
 XX
 DE Antigen fragment 116, from HPV has binding affinity for HLA-A2.1.
 XX
 XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus; influenza A; M1.
 XX
 OS Human papilloma virus strain 16.
 XX
 XX WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX
 XX 04-MAR-1994; 94WO-US02353.
 XX
 XX 05-MAR-1993; 93US-0027146.
 PR 04-JUN-1993; 93US-0073205.
 PR 29-NOV-1993; 93US-0159184.
 XX
 XX (CYTE-) CYTEL CORP.
 FA
 XX Grey HM, Kast WM, Sette A, Sidney J;
 PI WPI; 1994-302678/37.
 XX
 DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 84; 138pp; English.
 XX
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7
 CC antigen has a binding value of 0.0130. The peptides of the invention can

CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 9 AA;
 SQ

Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db |||||
 4 LOPE 7

RESULT 48
 AAR73796
 ID AAR73796 standard; peptide; 9 AA.
 XX AC AAR73796;
 XX
 XX
 DT 25-MAR-2003 (updated)
 DT 19-JUN-1995 (first entry)
 XX
 DE Antigen fragment 112, from HPV has binding affinity for HLA-A2.1.
 XX
 XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus; influenza A; M1.
 XX
 OS Human papilloma virus strain 16.
 XX
 XX WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX
 XX 04-MAR-1994; 94WO-US02353.
 XX
 XX 05-MAR-1993; 93US-0027146.
 PR 04-JUN-1993; 93US-0073205.
 PR 29-NOV-1993; 93US-0159184.
 XX
 XX (CYTE-) CYTEL CORP.
 FA
 XX Grey HM, Kast WM, Sette A, Sidney J;
 PI WPI; 1994-302678/37.
 XX
 DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 84; 138pp; English.
 XX
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7
 CC antigen has a binding value of 1.4000. The peptides of the invention can
 CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 9 AA;
 SQ

Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 Db ||||
 5 LQPE 8

RESULT 49
 AAR80939
 ID AAR80939 standard; peptide; 9 AA.
 XX
 AC AAR80939;
 XX
 DT 03-MAY-1996 (first entry)
 XX
 XX Peptide for increasing HLA-A2.1 cell expression.
 XX Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
 KW precursor; major histocompatibility complex; MHC; class I; HLA-A2.1;
 KW binding motif; cytolytic T cell; CTL; induction; peptide loading;
 XX primary immune response.
 XX Synthetic.
 XX
 FN WO9525530-A1.
 XX
 PD 28-SEP-1995.
 XX
 PF 21-MAR-1995; 95WO-US03535.
 XX
 PR 24-MAR-1994; 94US-0217188.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Boon-Falleur T, Kast WM, Melief CUM, Van Der Bruggen P;
 PI Visseren MW;
 XX
 XX WPI; 1995-344456/44.
 XX
 PT New peptide(s) based on tumour rejection antigen precursor MAGE-2 -
 PT which bind HLA-A2 molecules to provoke cytolytic T cell prodn., used
 PT partic. for treating cancers
 XX
 XX Example 3; Page 37; 44pp; English.
 XX
 CC Expression of HLA-A2.1 (T2) cells is increased by incubating T2
 CC cells in medium containing the present peptide. T2 cells will
 CC present the peptide bound to HLA-A2.1 in high amount and are good
 CC antigen presenting cells. The claimed MAGE-2 peptides (see AAR80878-
 CC AAR80888) can induce a similar primary immune response.
 XX
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 Db ||||
 4 LQPE 7

RESULT 50
 AAR78889
 ID AAR78889 standard; peptide; 9 AA.
 XX
 AC AAR78889;
 XX
 DT 25-MAR-2003 (updated)

27-MAR-1996 (first entry)
 XX
 DE HPV16 E7 11-19 cytotoxic T lymphocyte epitope.
 XX
 KW HPV16 E7 11-19; cytotoxic T; CTL; epitope; helper T; HTL; cell;
 KW lymphocyte; antigens; treatment; disease prevention;
 XX
 OS Human papillomavirus.
 XX
 FN WO9522317-A1.
 XX
 PD 24-AUG-1995.
 XX
 PF 16-FEB-1995; 95WO-US02121.
 XX
 PR 16-FEB-1994; 94US-0197484.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;
 XX
 DR WPI; 1995-302545/39.
 XX
 PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 PT bacterial, parasitic or tumour antigens - useful in the treatment
 PT and prevention of diseases associated with the antigen e.g.
 PT hepatitis B
 XX
 PS Example 14; Page 72; 109pp; English.
 XX
 CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to
 CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a
 CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a
 CC lipid conjugated helper T cell inducing peptide. The compsn. is
 CC useful in the treatment and prevention of HPV associated diseases.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 Db ||||
 5 LQPE 8

RESULT 51
 AAR78894
 ID AAR78894 standard; peptide; 9 AA.
 XX
 AC AAR78894;
 XX
 DT 25-MAR-2003 (updated)
 DT 27-MAR-1996 (first entry)
 XX
 DE HPV16 E7 12-20 cytotoxic T lymphocyte epitope.
 XX
 KW HPV16 E7 12-20; cytotoxic T; CTL; epitope; helper T; HTL; cell;
 KW lymphocyte; antigens; treatment; disease prevention;
 XX
 OS Human papillomavirus.
 XX
 FN WO9522317-A1.
 XX
 PD 24-AUG-1995.
 XX
 PF 16-FEB-1995; 95WO-US02121.
 XX
 PR 16-FEB-1994; 94US-0197484.
 XX
 PA (CYTE-) CYTEL CORP.


```

XX AC AAR84331;
XX DT 25-JAN-1996 (first entry)
XX DE HPV derived peptide (h).
XX KW Human papilloma virus; HPV; cytotoxic T-cell; HLA-B35 antigen;
XX KW prevention; treatment; carcinoma; cervix; cervical cancer.
XX OS Synthetic.
XX PN JPO7136289-A.
XX PD 16-MAY-1995.
XX PF 02-NOV-1993; 93JP-0297378.
XX PR 02-NOV-1993; 93JP-0297378.
XX PA (KENB/) KENBARA K.
XX PA (TAKI/) TAKIGUCHI M.
XX DR WPI; 1995-212956/28.
XX PT Human papilloma virus derived peptide(s) of 9-11 amino acids in
XX PT length - which bind with HLA-B35 antigen and are useful in
XX PT prevention and treatment of cervical cancer
XX PS Claim 1; Page 2; 7pp; Japanese.
XX CC The sequences given in AAR84324-35 are synthetic peptides which are
XX CC derived from human papilloma virus. These peptides are represented
XX CC in cytotoxic T-cells by binding with HLA-B35 antigen. They are
XX CC prepared by standard methods of peptide synthesis and may be used
XX CC for the prevention and treatment of carcinoma of the cervix.
XX SQ Sequence 9 AA;
    Query Match 22.2%; Score 4; DB 16; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VPXV 11
Db 1 VPXV 4
    ||||
    ||||
RESULT 55
AAR89363
ID AAR89363 standard; peptide; 9 AA.
XX AC AAR89363;
XX DT 18-SEP-1996 (first entry)
XX DE Immunogenic peptide, based on Y1 analog of 1054.05.
XX KW Immunogenic peptide; supermotif; HLA molecule; CTL response;
XX KW therapeutic; diagnostic; cancer; viral infection; hepatitis B;
XX KW hepatitis C.
XX OS Synthetic.
XX PN WO9603140-A1.
XX PD 08-FEB-1996.
XX PF 21-JUL-1995; 95WO-US09234.
XX PR 30-MAY-1995; 95US-0452843.
XX PR 21-JUL-1994; 94US-0278634.
XX PR 23-NOV-1994; 94US-0344824.

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XX PA (CYTE-) CYTEL CORP.
XX FI Sette A, Sidney J;
XX DR WPI; 1996-116784/12.
XX CC Compn. comprising immunogenic peptide with supermotif allowing more
XX PT than one HLA mol. to bind - used to induce CTL response in patient
XX PT and for in vivo and ex vivo therapeutic and diagnostic applications
XX PS Claim 2; Page 26; 32pp; English.
XX CC The sequences given in AAR89362-82 are immunogenic peptides which were
XX CC use in the composition of the invention. The composition comprises
XX CC an immunogenic peptide of 9-10 residues with a supermotif which
XX CC allows binding of more than one HLA molecule. It pref. comprises
XX CC two conserved residues, a first at the 2nd position from the N-
XX CC terminal is pro, and a 2nd at the C-terminal is Met. These peptides
XX CC are used to induce a CTL response in a patient. They are also
XX CC useful in compositions for in vivo and ex vivo therapeutic and
XX CC diagnostic applications, e.g the treatment of cancer and viral
XX CC infections, e.g. hepatitis B and C.
XX SQ Sequence 9 AA;
    Query Match 22.2%; Score 4; DB 17; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVK 12
Db 2 PKVK 5
    ||||
    ||||
RESULT 56
AAW39661
ID AAW39661 standard; peptide; 9 AA.
XX AC AAW39661;
XX DT 11-JUN-1998 (first entry)
XX DE HPV16/18 E7 peptide (pos. 11-19).
XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX KW disease; anti-tumour; anti-viral.
XX OS Human papillomavirus.
XX PN WO9741440-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-NL00229.
XX PR 23-DEC-1996; 96EP-0203670.
XX PR 26-APR-1996; 96EP-0201145.
XX PA (UYLE-) RIJXSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX PI Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX DR WPI; 1997-549891/50.
XX PT Method of selecting T cell peptide epitope(s) - by measuring the
XX PT stability of HLA class I-peptide complexes on intact B cells
XX PS Example 3; Page 78; 109pp; English.
XX CC Peptides AAW39430-W39734 are used in a novel method for the selection of

```


CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
 CC method involves the identification of peptide sequences capable of
 CC binding to an HLA (human leukocyte antigen) class I molecule and
 CC measuring the binding of this epitope peptide to the HLA class I
 CC peptide. The stability of binding of the peptide and MHC (major
 CC histocompatibility complex) class I molecule is measured on intact human
 CC B cells carrying the MHC molecule at their cell surfaces. The method can
 CC be used to select peptide epitopes for generating vaccines against a
 CC disease associated with the polypeptide, e.g. cancers or AIDS. The
 CC peptide epitopes are especially T-cell peptide epitopes with strong
 CC anti-tumour and anti-viral immune responses. Peptide AAW39661 is derived
 CC from the human papillomavirus E7 protein and is capable of binding to the
 CC human MHC Class I allele HLA-A2.1.

XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 ||||
 Db 5 LOPE 8

RESULT 57
 AAW39662
 ID AAW39662 standard; peptide; 9 AA.

AC AAW39662;

DT 11-JUN-1998 (first entry)

XX HPV16/18 E7 peptide (pos. 12-20).

XX T cell epitope; immune response; human leukocyte antigen; HLA Class I;
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
 KW disease; anti-tumour; anti-viral.

XX Human papillomavirus.

XX WO9741440-A1.

PD 06-NOV-1997.

XX 28-APR-1997; 97WO-NL00229.

XX 23-DEC-1996; 96EP-0203670.

PR 26-APR-1996; 96EP-0201145.

XX (UYLE-) RIJKSUNIV LEIDEN.

PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;

PI WPI; 1997-549891/50.

DR Method of selecting T cell peptide epitope(s) - by measuring the
 XX stability of HLA class I-peptide complexes on intact B cells

XX Example 3; Page 78; 109pp; English.

XX Peptides AAW39430-W39734 are used in a novel method for the selection of
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
 CC method involves the identification of peptide sequences capable of
 CC binding to an HLA (human leukocyte antigen) class I molecule and
 CC measuring the binding of this epitope peptide to the HLA class I
 CC peptide. The stability of binding of the peptide and MHC (major
 CC histocompatibility complex) class I molecule is measured on intact human
 CC B cells carrying the MHC molecule at their cell surfaces. The method can
 CC be used to select peptide epitopes for generating vaccines against a
 CC disease associated with the polypeptide, e.g. cancers or AIDS. The
 CC peptide epitopes are especially T-cell peptide epitopes with strong

CC anti-tumour and anti-viral immune responses. Peptide AAW39662 is derived
 CC from the human papillomavirus E7 protein and is capable of binding to the
 CC human MHC Class I allele HLA-A2.1.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 ||||
 Db 4 LOPE 7

RESULT 58
 AAW36590
 ID AAW36590 standard; peptide; 9 AA.

XX AC AAW36590;

DT 25-MAR-2003 (updated)

DT 09-MAR-1998 (first entry)

XX Hepatitis B virus bulk antigen.

XX Melanoma protein; MAGE-2; tumour rejection antigen precursor; HBV;
 KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell;
 KW CTL; induce; production; Hepatitis B virus.

XX Hepatitis B virus.

XX US5686068-A.

XX 11-NOV-1997.

XX 25-JUL-1996; 96US-0687226.

PR 25-JUL-1996; 96US-0687226.

PR 24-MAR-1994; 94US-0217188.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYLE-) RIJKSUNIV LEIDEN.

XX Boon-Falleur T, Melief CJM, Van Der Bruggen P, Van Der Burg S;

PI Visseren MW;

XX WPI; 1997-558084/51.

DR Induction of cytolytic T cell production in vivo - by administering
 XX MAGE-2 peptide(s)

XX Example 3; Column 9; 24pp; English.

XX This peptide sequence represents a hepatitis B virus reference peptide
 CC used in determining the primary induction of the immune response against
 CC MAGE-2 (a tumour rejection antigen precursor) peptides. Only peptides
 CC AAW36529-39 have the ability to bind to human leukocyte antigen (HLA)
 CC A2.1 molecule with high affinity and are therefore the only candidates of
 CC the MAGE-2 protein to be recognised by human cytolytic T cells (CTL),
 CC because CTL recognise peptides only when bound to HLA molecules.
 CC Production of CTL in a subject can be induced by administering a MAGE-2
 CC peptide (particularly AAW36531, AAW36533 and AAW36537) to a subject who
 CC presents HLA-A2 molecules on cells. The method can be used to treat
 CC subjects in need of additional CTL.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 LQPE 4
Db      ||||
        4 LQPE 7

RESULT 59
AAW28811
ID      AAW28811 standard; peptide; 9 AA.
XX
AC      AAW28811;
XX
DT      25-MAR-2003 (updated)
DT      20-NOV-1997 (first entry)
XX
DE      HPV-16 derived peptide (h), recognised by HLA-B35 antigen.
XX
KW      Human papilloma virus; HPV; cervical cancer; diagnosis; epitope;
KW      human leukocyte antigen; HLA-B35; vaccine; prevention; therapy;
KW      cytotoxic T lymphocyte.
XX
OS      Human papilloma virus type 16.
XX
PN      JP09188695-A.
XX
PD      22-JUL-1997.
XX
PF      02-NOV-1993; 96JP-0220327.
XX
PR      02-NOV-1993; 93JP-0297378.
PR      02-NOV-1993; 93JP-0220327.
XX
PA      (NOKI/) NOKIHARA K.
PA      (TAKI/) TAKIGUCHI M.
XX
DR      WPI; 1997-420579/39.
XX
PT      Synthetic peptide derived from human papilloma virus - is able to
PT      bind to HLA-B35 antigen and is useful in a vaccine for prevention or
PT      treatment of cervical cancer
XX
PS      Claim 6; Page 2; 7pp; Japanese.
XX
CC      The present sequence corresponds to amino acids 88-96 of the L1
CC      antigen of human papilloma virus HPV-16. A synthetic peptide having
CC      this sequence is shown in cytotoxic T cells by combining with HLA-B35
CC      antigen. The peptide can be used in a preventive vaccine and a
CC      therapeutic agent for cervical cancer caused by human papilloma virus.
CC      (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 9 AA;

Query Match      22.2%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VPKV 11
Db      ||||
        1 VPKV 4

RESULT 60
AAW78893
ID      AAW78893 standard; peptide; 9 AA.
XX
AC      AAW78893;
XX
DT      17-NOV-1998 (first entry)
XX
DE      Human papillomavirus 16 E7 protein fragment 11-19.
XX
KW      Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
KW      class II associated peptide; pathogen; gene therapy; genetic disease;
KW      infection; downregulation; immune response.
XX

XX      Human papillomavirus.
OS      Synthetic.
XX
PN      WO9831398-A1.
XX
PD      23-JUL-1998.
XX
PF      22-JAN-1998; 98WO-US01499.
PR      06-JAN-1998; 98US-0003253.
PR      22-JAN-1997; 97US-0787547.
XX
PA      (PANG-) PANGAEA PHARM INC.
XX
PI      Curley JM, Hedley ML, Langer RS, Lunsford LB;
XX      WPI; 1998-427556/36.
XX
PT      New preparations of microparticles - comprising a synthetic polymer
PT      matrix and nucleic acid comprising an expression vector for use in
PT      gene therapy
XX
PS      Disclosure; Page 10; 101pp; English.
XX
CC      A microparticle preparation (MP) has been developed, consisting of
CC      microparticles having a diameter of less than 100 mu m. The MP
CC      comprises: (a) a polymeric matrix (PM) consisting of one or more
CC      synthetic polymers having a solubility in water of less than 1 mg/l; and
CC      (b) an expression vector selected from RNA molecules (at least 50% of
CC      which are closed circles) or circular plasmid DNA (at least 50% of
CC      which are supercoiled). Also described is a MP of at most 20 microns in
CC      diameter, comprising: (a) a PM; and (b) a NAM comprising an expression
CC      control sequence operatively linked to a coding sequence, where the
CC      coding sequence encodes an expression product selected from: (i) a
CC      polypeptide at least 7 amino acids in length, having a sequence identical
CC      to the sequence of: (i) a fragment of a naturally-occurring mammalian
CC      protein; or (ii) a fragment of a naturally-occurring protein from an
CC      infectious agent which infects a mammal; (2) a peptide having a length
CC      and sequence which permits it to bind to an MHC class I or II molecule;
CC      and (3) the polypeptide or the peptide linked to a trafficking sequence.
CC      AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for
CC      use in the present invention. The MPs are highly effective vehicles for
CC      the delivery of polynucleotides into phagocytic cells. They can be used
CC      for gene therapy, e.g. for treating genetic diseases, infections or
CC      tumours or for downregulating an immune response.
XX
SQ      Sequence 9 AA;

Query Match      22.2%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
Db      ||||
        5 LQPE 8

RESULT 61
AAW54766
ID      AAW54766 standard; peptide; 9 AA.
XX
AC      AAW54766;
XX
DT      25-SEP-1998 (first entry)
XX
DE      Peptide from HPV 16 E7 (11-19).
XX
KW      Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
KW      vaccine; treatment.
XX
OS      Synthetic.
XX

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PN WO9813378-A1.
XX
PD 02-APR-1998.
XX
PF 25-SEP-1997; 97WO-NL00536.
XX
PR 26-SEP-1996; 96EP-0202701.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Drijfhout JW, Koning F;
XX
DR WPI; 1998-230631/20.
XX
PT Increasing uptake and presentation of antigen(s) - by adding mannose
PT residue(s) to antigen for increasing T cell response, useful in,
PT e.g. vaccines against viral infection(s)
XX
XX Disclosure; Page 37; 47pp; English.
XX
CC The peptides AAW54559-W54809 are examples of peptides to which at least
CC 1 (preferably 2) mannose can be attached to increase their uptake as
CC antigens by antigen-presenting cells. Uptake of agonist mannoseylated
CC peptides will increase the T cell response, whereas uptake of antagonist
CC peptides blocks the T cell response. Blocking binding of immunogenic
CC autoantigens can be used in treatment of type I diabetes, rheumatoid
CC arthritis, graft rejection etc.; also to induce T-cell non-
CC responsiveness. Vaccines containing mannoseylated antigen are used to
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
CC and parasites.
XX
SQ Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LOPE 4
DB ||||
4 LOPE 7
XX
RESULT 63
AAW53466
ID AAW53466 standard; Peptide; 9 AA.
XX
AC AAY53466;
XX
XX 18-JAN-2000 (first entry)
XX
DE HIV-1 RT protein (aa 185-193) binds HLA-B8.
XX
KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
KW melanoma; malaria; parasite.
XX
OS Synthetic.
OS Human immunodeficiency virus type 1.
XX
XX FR2776926-A1.
XX
XX 08-OCT-1999.
XX
XX 07-APR-1998; 98FR-0004323.
XX
XX 07-APR-1998; 98FR-0004323.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX (INSP ) INST PASTEUR LILLE.
XX
PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
XX WPI; 1999-583113/50.
XX
XX New lipopeptide containing lipid regions and two epitopes, all
XX separated by peptide spacers that impart hydrophilicity, useful in
XX vaccines -
XX
XX Disclosure; Page 21; 35pp; French.
XX
XX The invention relates to the generation of a lipopeptide comprising at
XX least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
XX epitope and at least one lipid residue with (i) the epitopes and lipid
XX portion and (ii) the epitopes, being separated independently by peptide
XX spacers. These spacers comprise sequences of amino acids which carry an
XX overall electrical charge in neutral media to ensure that the
XX lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents

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CC examples of peptide epitopes used to generate the lipopeptides. These are
 CC used in therapeutic or prophylactic compositions and vaccines to induce
 CC specific immune responses against human immunodeficiency, hepatitis B or
 CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX Sequence 9 AA;
 SQ Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 Db ||||
 2 PKVK 5

RESULT 64
 AAY55432
 ID AAY55432 standard; peptide; 9 AA.

XX AC AAY55432;
 XX 17-JAN-2000 (first entry)
 XX DE HLA binding plu-1 peptide.
 XX Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
 KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
 KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9949034-A1.
 XX 30-SEP-1999.
 XX 19-MAR-1999; 99WO-G800866.
 XX 20-MAR-1998; 98GB-0005877.
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

PI Taylor-papadimitriou J;

XX WPI; 1999-591090/50.

PT New nucleic acid encoding the cancer-associated polypeptide plu-1, for
 PT diagnosis, treatment and prevention of cancer, especially of breast and
 PT ovary -

XX Example 2; Fig 12; 173pp; English.

XX The invention relates to a human cancer-associated polypeptide plu-1.
 CC The plu-1 polypeptide can be recombinantly expressed by standard
 CC recombinant methodology. Detection of the plu-1 nucleic acid or the
 CC polypeptide is used for the following: (i) diagnosis (including imaging)
 CC and prognosis of, and determination of susceptibility to, cancer,
 CC specifically ovarian or breast cancer; and (ii) treating cancer (by
 CC inducing an immune response against cancer cells, e.g. as a vaccine, or
 CC by antisense inhibition). Antigens derived from the polypeptide are used
 CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for
 CC subsequent return to the patient for treatment of cancer. The polypeptide
 CC may also be used to identify inhibitors of plu-1 activity. Fragments of
 CC the polypeptide, and antibodies raised against plu-1, are useful as assay
 CC and imaging agents, also therapeutically (to induce an anti-idiotype
 CC response or where conjugated to cytotoxic agents). The plu-1 antigen is
 CC expressed more commonly in breast tumors than some known tumor antigens.
 CC Sequences AAY55320-629 represent predicted peptides from the plu-1
 CC polypeptide which may bind to the human class I alleles B27, A2, A3 and
 CC A11.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 Db ||||
 2 LQPE 5

RESULT 65
 AAY40315
 ID AAY40315 standard; Peptide; 9 AA.

XX AC AAY40315;
 XX 19-NOV-1999 (first entry)
 XX DE Amino acid sequence of a HIV-1 epitope.
 KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
 KW vaccine; tumor; infection; immune response; cytokine profile;
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
 KW autoimmune disease.

XX Human immunodeficiency virus type 1.

XX OS
 XX PN FR2774687-A1.

XX PD 13-AUG-1999.

XX PF 06-FEB-1998; 98FR-0001439.

XX PR 06-FEB-1998; 98FR-0001439.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (INSP) INST PASTEUR LILLE.

XX PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;

XX WPI; 1999-510734/43.

XX New lipopeptide comprising C-terminal interferon-gamma fragment with
 XX attached lipophilic groups, used as interferon mimic, e.g. for treating
 XX cancer or virus infection

XX PS Disclosure; Page 39; 53pp; French.

XX CC AAY40123-Y40379 represent epitopes that are able to activate cytotoxic
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
 CC B epitopes recognized by corresponding antibodies. The epitopes may be
 CC used in the composition of the invention. The specification describes a
 CC lipopeptide that has a peptide part derived from mammalian interferon
 CC gamma (IFNg) and one or more lipophilic parts comprising a linear or
 CC branched, (unsaturated 4-20C hydrocarbyl chain or a steroid. The
 CC lipopeptide mimics the activity of IFNg. Compositions comprising the
 CC lipopeptide are used to treat or prevent any condition that responds
 CC to IFNg, and as adjuvant for vaccines (particularly those directed
 CC against tumors, viral or parasitic infections), to stimulate or
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.
 CC Particular applications are treatment of infections (particularly
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
 CC (particularly of kidney, cutaneous T cells or ovary, chronic
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
 CC diseases.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db ||||
2 PKVK 5

RESULT 66
AAAY26807
ID AAY26807 standard; peptide; 9 AA.
XX
AC AAY26807;
XX
XX 14-SEP-1999 (first entry)
XX
DE HIV-derived lipopeptide epitope #77 for mixed micelles.
XX
KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
KW melanoma; Plasmodium falciparum; malaria.
XX
XX Synthetic.
OS Human immunodeficiency virus type 1.
XX
XX FR2771640-A1.
XX
XX 04-JUN-1999.
XX
XX 03-DEC-1997; 97FR-0015246.
XX
XX 03-DEC-1997; 97FR-0015246.
XX
XX (CNRS) CNRS CENT NAT RECH SCI.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX (INSP) INST PASTEUR LILLE.
XX
XX Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;
XX Tartar A, Wieruszkeski JM;
XX WPI; 1999-349509/30.
XX
XX Immunogenic lipopeptide micelles - comprising lipopeptides
XX containing cytotoxic and helper T-lymphocyte epitopes
XX
XX Disclosure; Page 34; 60pp; French.
XX
XX The invention relates to the generation of mixed micelles or
XX microaggregates for inducing an immune response comprise: (a) a first
XX lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
XX and at least one lipid unit; and (b) a second lipopeptide comprising at
XX least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
XX different from that of the first lipopeptide. This peptide represents
XX an example of a lipopeptide epitope used in the invention and is derived
XX from a human immunodeficiency virus type 1 (HIV-1) protein. The
XX immunogenic lipopeptide micelles are used in vaccines, especially
XX against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma
XX or Plasmodium falciparum malaria.

QY 9 PKVK 12
Db ||||
2 PKVK 5

RESULT 67
AAAY10346
ID AAY10346 standard; peptide; 9 AA.
XX

Query Match 22.2%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db ||||
2 PKVK 5

RESULT 67
AAAY10346
ID AAY10346 standard; peptide; 9 AA.
XX

AC AAY10346;
XX
DT 12-MAY-1999 (first entry)
XX
DE T cell epitope/MHC ligand SEQ ID NO:276.
XX
XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW immunisation; tumour; infectious disease; immunotherapy; cancer;
KW malignant melanoma; viral disease; hepatitis; AIDS.
XX
XX Synthetic.
OS Human papillomavirus.
XX
XX WO9902183-A2.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US14289.
XX
XX 10-DEC-1997; 97US-0988320.
XX
XX 10-JUL-1997; 97CA-2209815.
XX
XX (CTL-) CTL IMMUNOTHERAPIES CORP.
XX
XX Kuendig TM, Simard JUL;
XX
XX WPI; 1999-120514/10.
XX
XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
XX of antigen in the lymphatic system of a mammal so as to provide a
XX sustained CTL response, used to treat, e.g. AIDS
XX
XX Disclosure; Page 34; 199pp; English.
XX
XX The present invention describes a method of inducing and/or sustaining
XX an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
XX method comprises: (a) delivering an antigen to the mammal at a level to
XX induce an immunological CTL response in the mammal; and (b) maintaining
XX the level of the antigen in the mammal's lymphatic system to maintain
XX the immunologic CTL response. The method can be used for the delivery of
XX e.g. a differentiation antigen, a tumour-specific multilineage antigen,
XX an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
XX gene antigen, or a viral antigen. They can be used for the treatment of
XX disease such as cancer, e.g. malignant melanoma or infectious disease,
XX e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
XX to the lymphatic system provides for potent CTL stimulation that takes
XX place in the milieu of the lymphoid organ, and it sustains stimulation
XX that is necessary to keep CTL active, cytotoxic and recirculating
XX through the body. AAY10071 to AAY10639 represent examples of peptide
XX antigens given in the present invention.

QY Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db ||||
4 LQPE 7

RESULT 68
AAAY10511
ID AAY10511 standard; Peptide; 9 AA.
XX
XX AAY10511;
XX
XX 12-MAY-1999 (first entry)
XX
XX HLA Class I motif peptide SEQ ID NO:441.
XX
XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;

KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 XW malignant melanoma; viral disease; hepatitis; AIDS.

OS Synthetic.
 OS Human papillomavirus.

XX WO9902183-A2.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US14289.

XX 10-DEC-1997; 97US-0988320.

XX 10-JUL-1997; 97CA-2209815.

XX (CTL1-) CTL IMMUNOTHERAPIES CORP.

XX Kuendig TM, Simard JUL;

XX WPI; 1999-120514/10.

XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
 of antigen in the lymphatic system of a mammal so as to provide a
 sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 44; 199pp; English.

CC The present invention describes a method of inducing and/or sustaining
 an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 method comprises: (a) delivering an antigen to the mammal at a level to
 induce an immunological CTL response in the mammal; and (b) maintaining
 the level of the antigen in the mammal's lymphatic system to maintain
 the immunologic CTL response. The method can be used for the delivery of
 e.g. a differentiation antigen, a tumour-specific multilinage antigen,
 an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 gene antigen, or a viral antigen. They can be used for the treatment of
 disease such as cancer, e.g. malignant melanoma or infectious disease,
 e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 to the lymphatic system provides for potent CTL stimulation that takes
 place in the milieu of the lymphoid organ, and it sustains stimulation
 that is necessary to keep CTL active, cytotoxic and recirculating
 through the body. AAY10071 to AAY10639 represent examples of peptide
 antigens given in the present invention.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 ||||
 Db 4 LQPE 7

RESULT 69

AAB33705

ID AAB33705 standard; Peptide; 9 AA.

XX AAB33705;

XX 26-JAN-2001 (first entry)

XX MHC class I associated immunogenic peptide SEQ ID 104.

XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..

XX Unidentified.

XX WO200053161-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US06578.

XX 11-MAR-1999; 99US-0266463.

XX 27-MAY-1999; 99US-0321346.

XX (ZYCO-) ZYCOS INC.

XX Lunsford LB, Putnam D, Hedley ML;

XX WPI; 2000-638130/61.

XX Microparticles useful for administering a nucleic acid into the mucosal
 tissue preferably vaginal tissue of an animal, comprises a polymeric
 matrix, a lipid and a nucleic acid molecule -

XX Disclosure; Page 16; 96pp; English.

CC The present invention relates to microparticles which are less than 20
 microns in diameter, which comprise a polymeric matrix, a lipid and a
 nucleic acid molecule. The microparticle is specifically not
 encapsulated in a liposome and does not comprise a cell. The nucleotide
 sequence encodes an expression product that binds to major
 histocompatibility complex (MHC) type I or II molecules. Peptides
 AAB33602-B33647 represent MHC class I associated immunogenic peptides,
 and AAB33648-B33710 represent MHC class II associated immunogenic
 peptides. The peptides are examples of the expression products of the
 nucleotide sequences which can be included in the microparticles of the
 invention. Sequences AAB33711-B33716 represent alternative expression
 products and nuclear localisation signals also used in the invention. The
 microparticles are useful for administering a nucleic acid into the
 mucosal tissue preferably vaginal tissue of an animal.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 ||||
 Db 5 LQPE 8

RESULT 70

AAB18492

ID AAB18492 standard; peptide; 9 AA.

XX AAB18492;

XX 15-JAN-2001 (first entry)

XX Peptide substrate used to test prolyl-tripeptidyl peptidase activity.

XX Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
 KW gingivitis; periodontitis.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "hydrogen attached"

XX WO200052147-A2.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05551.

XX 05-MAR-1999; 99US-0123148.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (TRAV/) TRAVIS J.

PA (POTE/) POTEIPA J.
 PA (BANB/) BANBULA A.
 XX
 PI Travis J, Potempa J, Banbula A;
 XX
 XX WPI; 2000-594181/56.
 DR
 XX Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
 PT for identifying its inhibitor which is useful for protecting an animal
 PT from a periodontal disease such as gingivitis and periodontitis -
 XX
 PS Claim 3; Page 37; 58pp; English.
 XX
 CC The present sequence represents a substrate which was used to test
 CC the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The
 CC prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves
 CC a peptide bond in a target polypeptide having at least 4 amino acids.
 CC This bond is between a proline and an amino acid attached to the
 CC alpha-carboxyl group end of the proline. The polypeptide is useful for
 CC identifying inhibitors. These inhibitors are then useful for reducing
 CC the growth of bacterium or for protecting an animal from a periodontal
 CC disease such as gingivitis and periodontitis caused by Porphyromonas
 CC gingivalis.
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GVPK 10
 Db |||||
 1 GVPK 4
 RESULT 71
 AAY96941
 ID AAY96941 standard; peptide; 9 AA.
 XX
 AC AAY96941;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Processed N-terminal peptide of human IL-1RAIL and IL-1RAIV.
 XX
 KW hIL-1RAIL; human interleukin-1 receptor antagonist-1 long; IL-1lp;
 KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
 KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 KW gene therapy; N-terminal.
 XX
 CS Homo sapiens.
 XX
 PN WO2000039297-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-US30720.
 XX
 PR 23-DEC-1998; 98US-0113430.
 XX
 PR 22-JAN-1999; 99US-0116943.
 PR 13-APR-1999; 99US-0129122.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Pan J;
 XX
 DR WPI; 2000-452395/39.
 XX
 CC Nucleic acids encoding interleukin-1-like polypeptides, useful for
 PT preventing and treating e.g. inflammation, asthma and psoriasis
 XX
 PS Example 14; Page 94; 143pp; English.

XX An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-1lp) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (hIL-1RAI) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-1lp polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patient's production of the polypeptide or to rectify
 CC mutations that lead to the production of in active peptides). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-1lp protein expression and activity which may be use
 CC to treat disorders associated with inappropriate IL-1lp expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVK 12
 Db |||||
 5 PKVK 8
 RESULT 72
 AAY66364
 ID AAY66364 standard; Peptide; 9 AA.
 XX
 AC AAY66364;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 DE HLA-B7-binding HIV-1 Pol peptide #166.
 XX
 KW HIV-1; MHC; major histocompatibility complex; Class I; HLA;
 KW human leukocyte antigen; allele; binding; conserved; genome;
 KW peptide; targeting; toxic; drug; antibody; antigen; antiviral;
 KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;
 KW localisation; quantification; detection; infection; drug resistance;
 KW immune response.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9949893-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US07111.
 XX
 PR 31-MAR-1998; 98US-0052530.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;
 XX
 DR WPI; 2000-038361/03.
 XX
 PT Novel methods for designing molecular conjugate therapeutics which are
 PT used for diagnosis, imaging and treatment against pathogens -
 XX
 PS Example 3; Page 45; 62pp; English.
 XX
 CC AAY66199-Y66413 are peptides derived from conserved portions of the
 CC HIV-1 genome which bind to different HLA alleles of MHC (major
 CC histocompatibility complex) Class I molecules. The peptides are used to
 CC construct targetting antigens comprising one or more peptides bound to

CC the corresponding MHC Class I molecule, which can be used to raise
 CC antibodies. The antibody may then be used as a targeting vehicle to
 CC deliver a potentially toxic drug to its target site of action, rather
 CC than administering it systemically, which may result in adverse side
 CC effects. The invention relates to improved methods for the design of
 CC molecular conjugate therapeutics for the diagnosis and treatment of
 CC infections caused by pathogens with a high mutation rate (such as
 CC HIV-1). This method involves identifying conserved peptide-encoding
 CC regions among the genomes of multiple variants of a pathogen, identifying
 CC the Class I MHC molecules which occur with greatest frequency in a
 CC population of interest (e.g., human sub-populations), and determining
 CC which of the peptides bind to the Class I MHC molecules. The MHC-binding
 CC peptides and the corresponding Class I MHC molecules are selected and
 CC used to construct targeting antigens, which are in turn used to produce
 CC quantifying antibodies. The methods may be used in localisation,
 CC complexing and also to detect and treat viral infection. The methods of
 CC the invention mitigate against the development of viral resistance to
 CC drugs and to the immune response, as well as providing a solution for
 CC targeting toxic compounds to destroy viruses sequestered in sites not
 CC accessible to T cells. In addition, the methods eliminate the virus,
 CC whereas current therapies only arrest viral replication.

SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 ||||
 Db 2 PKVK 5

RESULT 73

AAAY66378
 ID AAY66378 standard; Peptide; 9 AA.

AC AAY66378;

DT 22-FEB-2000 (first entry)

XX HLA-B8-binding HIV-1 Pol peptide #180.

XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;
 KW human leukocyte antigen; allele; binding; conserved; genome;
 KW peptide; targeting; toxic; drug; antibody; antigen; antiviral;
 KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;
 KW localisation; quantification; detection; infection; drug resistance;
 KW immune response.

OS Human immunodeficiency virus type 1.

XX WO9949893-A1.

XX 07-OCT-1999.

XX 31-MAR-1999; 99WO-US07111.

XX 31-MAR-1998; 98US-0052530.

XX (UYBO-) UNIV BOSTON.

XX Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;

XX WPT; 2000-038361/03.

XX Novel methods for designing molecular conjugate therapeutics which are
 PT used for diagnosis, imaging and treatment against pathogens -

XX Example 3; Page 46; 62pp; English.

XX AAY66199-Y66413 are peptides derived from conserved portions of the

CC HIV-1 genome which bind to different HLA alleles of MHC (major
 CC histocompatibility complex) Class I molecules. The peptides are used to
 CC construct targeting antigens comprising one or more peptides bound to
 CC the corresponding MHC Class I molecule, which can be used to raise
 CC antibodies. The antibody may then be used as a targeting vehicle to
 CC deliver a potentially toxic drug to its target site of action, rather
 CC than administering it systemically, which may result in adverse side
 CC effects. The invention relates to improved methods for the design of
 CC molecular conjugate therapeutics for the diagnosis and treatment of
 CC infections caused by pathogens with a high mutation rate (such as
 CC HIV-1). This method involves identifying conserved peptide-encoding
 CC regions among the genomes of multiple variants of a pathogen, identifying
 CC the Class I MHC molecules which occur with greatest frequency in a
 CC population of interest (e.g., human sub-populations), and determining
 CC which of the peptides bind to the Class I MHC molecules. The MHC-binding
 CC peptides and the corresponding Class I MHC molecules are selected and
 CC used to construct targeting antigens, which are in turn used to produce
 CC quantifying antibodies. The methods may be used in localisation,
 CC complexing and also to detect and treat viral infection. The methods of
 CC the invention mitigate against the development of viral resistance to
 CC drugs and to the immune response, as well as providing a solution for
 CC targeting toxic compounds to destroy viruses sequestered in sites not
 CC accessible to T cells. In addition, the methods eliminate the virus,
 CC whereas current therapies only arrest viral replication.

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 ||||
 Db 2 PKVK 5

RESULT 74

ABP11796
 ID ABP11796 standard; Peptide; 9 AA.

AC ABP11796;

XX 15-JUL-2002 (first entry)

XX HIV A01 super motif pol peptide #68.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

XX peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 110; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 ||||
 Db 5 PKVK 8

RESULT 75
 ABP16116
 ID ABP16116 standard; Peptide; 9 AA.
 XX AC ABP16116;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV A24 super motif pol peptide #296.
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX PN WC200124810-A1.
 XX PD 12-APR-2001.
 XX PF 05-OCT-2000; 2000WO-US27766.
 XX PR 05-OCT-1999; 99US-0412863.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WP1; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX Claim 32; Page 198; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 ||||
 Db 5 PKVK 8

Search completed: November 25, 2003, 19:27:08
 Job time : 46.9419 secs

89 4 22.2 16 12 US-10-387-645-6 Sequence 6, Appli
90 4 22.2 16 12 US-10-387-645-7 Sequence 7, Appli
91 4 22.2 16 12 US-10-161-791-344 Sequence 344, App
92 4 22.2 16 12 US-10-350-405-114 Sequence 114, App
93 4 22.2 16 12 US-10-350-405-227 Sequence 227, App
94 4 22.2 17 15 US-10-218-743-10 Sequence 10, Appl
95 4 22.2 17 15 US-10-225-567A-1531 Sequence 1531, Ap
96 4 22.2 18 12 US-09-569-197-8 Sequence 8, Appli
97 4 22.2 18 12 US-10-016-986-173 Sequence 173, App
98 4 22.2 19 12 US-10-029-386-32381 Sequence 32381, A
99 4 22.2 19 15 US-10-225-567A-1545 Sequence 1545, Ap
100 4 22.2 19 15 US-10-163-198-88 Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-21
; Sequence 21, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-21

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOPEIMGVVKVKTMPVK 18
Db 1 LOPEIMGVVKVKTMPVK 18

RESULT 2
US-09-789-561-163
; Sequence 163, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: PZ043PI
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163

; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-163
Query Match 27.8%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GVPKV 11
Db 1 GVPKV 5

RESULT 3
US-08-908-884-22
; Sequence 22, Application US/08908884
; Publication No. US20020138872A1
; GENERAL INFORMATION:
; APPLICANT: Dong et al.
; TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,884
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/023,851
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: 60/035,166
; FILING DATE: January 10, 1997
; APPLICATION NUMBER: 60/046,769
; FILING DATE: May 16, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elbing, Karen L
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/339004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-908-884-22

Query Match 27.8%; Score 5; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VPKVK 12
Db 9 VPKVK 13

RESULT 4
US-09-908-323-22
; Sequence 22, Application US/09908323

```
; Patent No. US20020073447A1
; GENERAL INFORMATION:
; APPLICANT: Dong et al.
; TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,323
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/908,884
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/035,166
; FILING DATE: January 10, 1997
; APPLICATION NUMBER: 60/046,769
; FILING DATE: May 16, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elbing, Karen L.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/339004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-908-323-22

Query Match          27.8%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VPKVK 12
Db      9 VPKVK 13
      |||||
      |||||

RESULT 5
US-10-225-567A-1251
; Sequence 1251, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1251
; LENGTH: 16
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1251

Query Match          27.8%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVKE 13
Db      2 PKVKE 6
      |||||
      |||||

RESULT 6
US-10-225-567A-1282
; Sequence 1282, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1282
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1282

Query Match          27.8%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVKE 13
Db      8 PKVKE 12
      |||||
      |||||

RESULT 7
US-10-280-066-315
; Sequence 315, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET B
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 315
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Eschericia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DG15-20M-4-A9
US-10-280-066-315
```

```
Query Match          27.8%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVPK 10
      |||||
Db      14 MGVPK 18

RESULT 8
US-09-985-357A-12
; Sequence 12, Application US/09985357A
; Patent No. US20020110913A1
; GENERAL INFORMATION:
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation
; FILE REFERENCE: HUBR 1151.1 CON PFF/MAS
; CURRENT APPLICATION NUMBER: US/09/985,357A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/463,380
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/EP98/04590
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: DE 19753681.1
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: EP 97112640
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Wordperfect
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide start coded by
; OTHER INFORMATION: EX5
US-09-985-357A-12
```

```
Query Match          22.2%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9
      |||||
Db      1 MGVP 4
```

```
RESULT 9
US-10-353-767-12
; Sequence 12, Application US/10353767
; Publication No. US20030166275A1
; GENERAL INFORMATION:
; APPLICANT: KOLL
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene
; FILE REFERENCE: HUBR 1151.1 CON PFF/MAS
; CURRENT APPLICATION NUMBER: US/10/353,767
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/985,357A
; PRIOR FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: US 09/463,380
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/EP98/04590
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: DE 19753681.1
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: EP 97112640
```

```
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Wordperfect
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide
; OTHER INFORMATION: start coded by primer
; OTHER INFORMATION: EX5
US-10-353-767-12
```

```
Query Match          22.2%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9
      |||||
Db      1 MGVP 4
```

```
RESULT 10
US-10-302-817A-46
; Sequence 46, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Thermus brockianus
US-10-302-817A-46
```

```
Query Match          22.2%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
      |||||
Db      2 PKVK 5
```

```
RESULT 11
US-09-045-020-14
; Sequence 14, Application US/09045020
; Patent No. US2002025942A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.
; TITLE OF INVENTION: No. US2002025942A1e1 Tau/Neurofilament Protein
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 28 Carleton Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,020
; FILING DATE: 20-Mar-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,793
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 07/912,293
; FILING DATE: July 10, 1992
; APPLICATION NUMBER: 07/742,880
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14
US-09-045-020-14
Query Match 22.2%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEIM 6
Db 2 PEIM 5

RESULT 12
US-10-281-652-16
; Sequence 16, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265, 002201.01
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-16

Query Match 22.2%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 4 LQPE 7

RESULT 13
US-08-344-824-33
; Sequence 33, Application US/08344824

```

```

; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-33

Query Match 22.2%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 2 PKVK 5

RESULT 14
US-08-344-824-118
; Sequence 118, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICANT: Collins, Edward J.
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICANT: Hedley, Mary Lynn
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-344-824-118

Query Match 22.2%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 15
US-08-452-843A-2
; Sequence 2, Application US/08452843A
; Publication No. US20020098197A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 399632001321
; CURRENT APPLICATION NUMBER: US/08/452,843A
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Y1 analog of 1054.05
; US-08-452-843A-2

Query Match 22.2%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 16
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. US20010006639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.

```

```

; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-759-960-17

Query Match 22.2%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 17
US-09-909-460-104
; Sequence 104, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
; US-09-909-460-104

Query Match 22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 5 LOPE 8

RESULT 18
US-09-942-052-33
; Sequence 33, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-33

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 2 LOPE 5

RESULT 19
US-09-942-052-39
; Sequence 39, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-39

Query Match 22.2%; Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 5 LOPE 8

RESULT 20
US-09-942-052-104
; Sequence 104, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-104

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 2 LOPE 5

RESULT 21
US-09-942-052-218
; Sequence 218, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 218
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-218

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|
|
|
|
Db 2 LOPE 5

RESULT 22
US-09-942-052-235
; Sequence 235, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-235

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|
|
|
|
Db 1 LOPE 4

RESULT 23
US-09-942-052-236
; Sequence 236, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-236

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|
|
|
|
Db 6 LOPE 9

RESULT 24
US-09-942-052-312
; Sequence 312, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 312
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-312

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|
|
|
|
Db 5 LOPE 8

RESULT 25
US-09-942-052-339
; Sequence 339, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-339

US-09-942-052-339

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
|
|
|
|
Db 1 LQPE 4

RESULT 26

US-09-942-052-424
; Sequence 424, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR FILING DATE: 2001-08-28
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-424

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
|
|
|
|
Db 1 LQPE 4

RESULT 27

US-09-942-052-548
; Sequence 548, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR FILING DATE: 2001-08-28
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-548

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
|
|
|
|
Db 2 LQPE 5

RESULT 28

US-09-942-052-619
; Sequence 619, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR FILING DATE: 2001-08-28
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 619
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-619

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
|
|
|
|
Db 1 LQPE 4

RESULT 29

US-10-365-908-3
; Sequence 3, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winmett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus

US-10-365-908-3

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 5 LOPE 8

RESULT 30

US-10-365-908-26
; Sequence 26, Application US/10355908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-26

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 1 LOPE 4

RESULT 31

US-10-200-708-634
; Sequence 634, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 634
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-634

Query Match 22.2%; Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 32

US-10-200-708-648
; Sequence 648, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-648

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 33

US-10-200-708-669
; Sequence 669, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-669

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 6 PKVK 9

RESULT 34
US-10-001-546-12
; Sequence 12, Application US/10001546
; Publication No. US20030027766A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: FISK, BRYAN A.
; APPLICANT: IOANNIDES, MARIA G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; FILE REFERENCE: T-LYMPHOCYTES
; CURRENT APPLICATION NUMBER: US/10/001,546
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 08/403,459
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-001-546-12

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 2 LOPE 5

RESULT 35
US-10-128-711-28
; Sequence 28, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, MARIA A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811

; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-128-711-28

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 36
US-10-128-711-66
; Sequence 66, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, MARIA A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-128-711-66
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPE 4
DB 5 LQPE 8
RESULT 37
US-10-128-711-71
; Sequence 71, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
;
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-128-711-71
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPE 4
DB 4 LQPE 7
RESULT 38
US-10-133-210-146
; Sequence 146, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-146
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVK 12
DB 2 PKVK 5
RESULT 39
US-10-133-210-167
; Sequence 167, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 167
```

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-167

Query Match          22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 40
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPARISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-5001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19

Query Match          22.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 41
US-09-922-261-283
; Sequence 283, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-283

Query Match          22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18
Db 1 MVPK 4

RESULT 42
US-09-833-328-10
; Sequence 10, Application US/09833328
; Patent No. US20020136713A1
; GENERAL INFORMATION:
; APPLICANT: Laemmle, Bernhard
; APPLICANT: Schwarz, Hans-Peter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Antoine, Gerhard
; APPLICANT: Kerschbaumer, Rndolf
; APPLICANT: Tagliavacca, Luigina
; APPLICANT: Zimmermann, Klaus
; APPLICANT: Furlan, Miha
; APPLICANT: Turecek, Peter
; APPLICANT: Gerriksen, Helena E.
; TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease /
; FILE REFERENCE: 247.00C1P
; CURRENT APPLICATION NUMBER: US/09/833,328
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/721,254
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human
US-09-833-328-10

Query Match          22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMVP 17
Db 5 TMVP 8

```

RESULT 43
US-09-835-853-22
; Sequence 22, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/704,344
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-835-853-22

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPE 4
Db 5 LQPE 8
RESULT 44
US-09-876-904A-388
; Sequence 388, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMTD DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 388

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: C. elegans Sdc-3 protein.
US-09-876-904A-388
Query Match 22.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 KVKE 13
Db 7 KVKE 10
RESULT 45
US-09-572-404B-1436
; Sequence 1436, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SLC12A2 OR NKCC1 at 281-290 and may intera
; OTHER INFORMATION: Sequence 1435 in this patent.
US-09-572-404B-1436

Query Match 22.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVK 12
Db 4 PKVK 7

RESULT 46
US-10-177-390-33
; Sequence 33, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-177-390-33

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPE 4
Db 5 LQPE 8

RESULT 47
 US-09-942-052-54
 ; Sequence 54, Application US/09942052
 ; Publication No. US20030170626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
 ; FILE REFERENCE: 51158-20028.00
 ; CURRENT APPLICATION NUMBER: US/09/942,052
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: 60/228,432
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 744
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 54
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
 US-09-942-052-54

Query Match 22.2%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 ||||
 Db 2 LQPE 5

RESULT 48
 US-09-942-052-74
 ; Sequence 74, Application US/09942052
 ; Publication No. US20030170626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
 ; FILE REFERENCE: 51158-20028.00
 ; CURRENT APPLICATION NUMBER: US/09/942,052
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: 60/228,432
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 744
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 74
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
 US-09-942-052-74

Query Match 22.2%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 ||||

Db 6 LQPE 9

RESULT 49
 US-09-942-052-256
 ; Sequence 256, Application US/09942052
 ; Publication No. US20030170626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
 ; FILE REFERENCE: 51158-20028.00
 ; CURRENT APPLICATION NUMBER: US/09/942,052
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: 60/228,432
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 744
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 256
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
 US-09-942-052-256

Query Match 22.2%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 ||||
 Db 6 LQPE 9

RESULT 50
 US-09-942-052-257
 ; Sequence 257, Application US/09942052
 ; Publication No. US20030170626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
 ; FILE REFERENCE: 51158-20028.00
 ; CURRENT APPLICATION NUMBER: US/09/942,052
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: 60/228,432
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 744
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 257
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
 US-09-942-052-257

Query Match 22.2%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4


```
Db          1 LOPE 5
          ||||
          2 LOPE 5

RESULT 51
US-09-942-052-360
; Sequence 360, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-360

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LOPE 4
          ||||
          6 LOPE 9

RESULT 52
US-09-942-052-476
; Sequence 476, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 476
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-476

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LOPE 4
          ||||
          6 LOPE 9

RESULT 53
US-09-942-052-573
; Sequence 573, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 573
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-573

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LOPE 4
          ||||
          5 LOPE 8

RESULT 54
US-09-942-052-669
; Sequence 669, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-669

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 LOPE 4
|
|
|
|
Db 5 LOPE 8

RESULT 55
US-09-942-052-688
; Sequence 688, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028-00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 688
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-688

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|
|
|
|
Db 2 LOPE 5

RESULT 56
US-10-200-708-122
; Sequence 122, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-122

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
|
|
|
|
Db 6 PKVK 9

RESULT 57
US-10-200-708-223
; Sequence 223, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 223
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-223

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
|
|
|
|
Db 2 PKVK 5

RESULT 58
US-10-200-708-248
; Sequence 248, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-248

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
|
|
|
|
Db 2 PKVK 5

RESULT 59
US-10-200-708-338
; Sequence 338, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 338
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-338

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db ||||
2 PKVK 5

RESULT 60
US-10-200-708-345
; Sequence 345, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-345

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db ||||
7 PKVK 10

RESULT 61

US-10-200-708-520
; Sequence 520, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 520
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-520

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db ||||
2 PKVK 5

RESULT 62
US-10-200-708-542
; Sequence 542, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-542

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db ||||
7 PKVK 10

RESULT 63
US-10-200-708-635
; Sequence 635, Application US/10200708
; Publication No. US20030180314A1

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; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-635

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      2 PKVK 5

RESULT 64
US-10-200-708-649
; Sequence 649, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 649
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-649

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      2 PKVK 5

RESULT 65
US-10-200-708-670
; Sequence 670, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 670
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-670

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      2 PKVK 5

RESULT 66
US-10-062-710-228
; Sequence 228, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymetric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-062-710-228

Query Match      22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
Db      5 LQPE 8

RESULT 67
US-10-133-210-271
; Sequence 271, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND

```

;; TITLE OF INVENTION: COMPOSITIONS THEREOF
;; FILE REFERENCE: BU-035AX
;; CURRENT APPLICATION NUMBER: US/10/133,210
;; CURRENT FILING DATE: 2002-04-26
;; NUMBER OF SEQ ID NOS: 281
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 271
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-271

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 5 LQPE 8

RESULT 68
US-10-224-286-19
;; Sequence 19, Application US/10224286
;; Publication No. US20030108517A1
;; GENERAL INFORMATION:
;; APPLICANT: Soo Hoo, William
;; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
;; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
;; RESPONSE USING SAME
;; NUMBER OF SEQUENCES: 50
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CAMPBELL & FLORES, LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/224,286
;; FILING DATE: 19-Aug-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/902,516
;; FILING DATE: 29-JUL-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IM 2442
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619)535-9001
;; TELEFAX: (619)535-8949
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-224-286-19

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4

Db 5 LQPE 8

RESULT 69
US-10-054-968-13
;; Sequence 13, Application US/10054968
;; Publication No. US20030119101A1
;; GENERAL INFORMATION:
;; APPLICANT: NEUTEC PHARMA PLC
;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM
;; TITLE OF INVENTION: POSITIVE
;; TITLE OF INVENTION: COCCI
;; FILE REFERENCE: PM 259204
;; CURRENT APPLICATION NUMBER: US/10/054,968
;; CURRENT FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: US/09/214,307
;; PRIOR FILING DATE: 1999-01-04
;; PRIOR APPLICATION NUMBER: PCT/GB97/01830
;; PRIOR FILING DATE: 1997-07-07
;; PRIOR APPLICATION NUMBER: GB9614274.0
;; PRIOR FILING DATE: 1996-07-06
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 13
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-054-968-13

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVPK 10
Db 7 GVPK 10

RESULT 70
US-09-852-910-264
;; Sequence 264, Application US/09852910
;; Publication No. US20030096297A1
;; GENERAL INFORMATION:
;; APPLICANT: Hamm, Heidi
;; APPLICANT: Gilchrist, Annette
;; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Recepto
;; FILE REFERENCE: 2661-101
;; CURRENT APPLICATION NUMBER: US/09/852,910
;; CURRENT FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: US 60/275,472
;; PRIOR FILING DATE: 2001-03-14
;; NUMBER OF SEQ ID NOS: 271
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 264
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(11)
;; OTHER INFORMATION: G11 library peptide
US-09-852-910-264

Query Match 22.2%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVXE 13
Db 4 KVXE 7

; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Pever's Patch And/Or M-cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide ligand
US-10-185-815-26

Query Match 22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMVP 17
|||
Db 7 TMVP 10

Search completed: November 25, 2003, 20:36:59
Job time : 29.8837 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKVKEITWPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

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Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	4	US-09-641-803-21
2	4	22.2	4	4	US-09-385-357A-12
3	4	22.2	4	4	US-09-113-692B-9
4	4	22.2	4	4	US-09-607-277A-9
5	4	22.2	5	2	US-08-760-075A-29
6	4	22.2	5	3	US-09-338-546-29
7	4	22.2	5	4	US-09-659-084-29
8	4	22.2	6	2	US-08-480-793-14
9	4	22.2	6	5	PCT-US92-05825A-14
10	4	22.2	7	3	US-09-458-754-383
11	4	22.2	7	3	US-09-042-107-383
12	4	22.2	7	4	US-09-641-803-16
13	4	22.2	8	3	US-09-296-284-14
14	4	22.2	9	1	US-08-217-188A-62
15	4	22.2	9	1	US-08-687-226-62
16	4	22.2	9	1	US-08-467-083-2
17	4	22.2	9	1	US-08-615-181-79
18	4	22.2	9	1	US-08-787-547-104
19	4	22.2	9	1	US-08-414-417B-2
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23	4	22.2	9	3	US-08-667-725B-62
24	4	22.2	9	3	US-08-466-680B-2
25	4	22.2	9	3	US-09-007-748-62
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33	4	22.2	9	5	PCT-US95-02131-66
34	4	22.2	9	5	PCT-US95-02131-71
35	4	22.2	10	2	US-08-302-516-19
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38	4	22.2	10	3	US-09-338-546-34
39	4	22.2	10	3	US-09-461-697-283
40	4	22.2	10	4	US-09-659-084-34
41	4	22.2	10	4	US-09-847-185-19
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46	4	22.2	11	4	US-09-659-084-1
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48	4	22.2	12	4	US-08-949-059A-31
49	4	22.2	12	6	5460961-8
50	4	22.2	13	1	US-07-610-525-5
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52	4	22.2	14	4	US-08-949-059A-26
53	4	22.2	14	4	US-08-949-059A-27
54	4	22.2	14	4	US-08-949-059A-28
55	4	22.2	15	1	US-07-610-525-4
56	4	22.2	15	1	US-08-097-997A-2
57	4	22.2	15	1	US-08-259-672-11
58	4	22.2	15	1	US-08-459-351-11
59	4	22.2	15	1	US-08-460-533-11
60	4	22.2	15	1	US-08-787-547-44
61	4	22.2	15	2	US-08-553-257A-62
62	4	22.2	15	3	US-08-660-347-3
63	4	22.2	15	3	US-09-041-889-16
64	4	22.2	15	3	US-08-837-058-16
65	4	22.2	15	3	US-08-665-574C-2
66	4	22.2	15	3	US-08-946-994-2
67	4	22.2	15	4	US-09-417-264-16
68	4	22.2	15	4	US-09-441-992-62
69	4	22.2	15	5	PCT-US94-06654-11
70	4	22.2	16	2	US-08-591-438-13
71	4	22.2	16	2	US-08-760-075A-2
72	4	22.2	16	3	US-09-011-525-1
73	4	22.2	16	3	US-08-405-647B-11
74	4	22.2	16	3	US-08-602-999A-344
75	4	22.2	16	3	US-08-985-499-11
76	4	22.2	16	3	US-09-204-335-1
77	4	22.2	16	3	US-09-204-335-2
78	4	22.2	16	3	US-09-338-546-2
79	4	22.2	16	4	US-09-659-084-2
80	4	22.2	16	4	US-09-500-124-344
81	4	22.2	16	5	PCT-US96-03180-11
82	4	22.2	16	6	5200320-32
83	4	22.2	17	1	US-07-610-525-3
84	4	22.2	17	1	US-08-445-909A-14
85	4	22.2	17	2	US-08-733-982A-12
86	4	22.2	17	4	US-09-352-078-5
87	4	22.2	17	4	US-09-292-225-10
88	4	22.2	18	1	US-08-259-672-10
89	4	22.2	18	1	US-08-459-351-10
90	4	22.2	18	1	US-08-460-533-10
91	4	22.2	18	1	US-08-451-472-18
92	4	22.2	18	1	US-08-451-472-48
93	4	22.2	18	1	US-08-451-472-68
94	4	22.2	18	3	US-08-075-541D-34
95	4	22.2	18	3	US-08-075-541D-35
96	4	22.2	18	3	US-08-075-541D-45
97	4	22.2	18	5	PCT-US94-06654-10
98	4	22.2	19	1	US-07-610-525-2
99	4	22.2	20	1	US-07-678-974D-6
100	4	22.2	20	2	US-08-484-530-39

Sequence 66, Appl
Sequence 71, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 28, Appl
Sequence 66, Appl
Sequence 71, Appl
Sequence 19, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 13, Appl
Sequence 1, Appl
Sequence 57, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 29, Appl
Sequence 31, Appl
Patent No. 5460961
Sequence 5, Appl
Sequence 36, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 44, Appl
Sequence 62, Appl
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Sequence 16, Appl
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Sequence 2, Appl
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Sequence 2, Appl
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Sequence 344, App
Sequence 11, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 344, App
Sequence 11, Appl
Patent No. 5200320
Sequence 3, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 48, Appl
Sequence 68, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 45, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-21
; Sequence 21, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDGOH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-21
Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPEIMGVVKUKETNVPK 18
| | | | | | | | | | | | | | | | | |
DB 1 LQPEIMGVVKUKETNVPK 18
RESULT 2
US-09-985-357A-12
; Sequence 12, Application US/09985357A
; Patent No. 6544748
; GENERAL INFORMATION:
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation
; FILE REFERENCE: HUBR 1151.1 CON EPF/MAS
; CURRENT APPLICATION NUMBER: US/09/985,357A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/463,380
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/EP98/04590
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: DE 19753681.1
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: EP 97112640
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: wordperfect
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide start coded by
; OTHER INFORMATION: EX5
US-09-985-357A-12
Query Match 22.2%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 MGVP 9
| | | |
DB 1 MGVP 4
RESULT 3
US-09-113-692B-9
; Sequence 9, Application US/09113692B
; Patent No. 6548296
; GENERAL INFORMATION:
; APPLICANT: Stern, Anne
; APPLICANT: Brandt, Michael
; APPLICANT: Honold, Konrad
; APPLICANT: Auer, Johannes
; APPLICANT: Koll, Hans
; APPLICANT: Franze, Reinhard
; APPLICANT: Pessara, Ulrich
; TITLE OF INVENTION: Methods For Identifying Human Cell Lines Useful for
; TITLE OF INVENTION: Endogenous Gene Activation, Isolated Human Cell Lines
; TITLE OF INVENTION: Identified Thereby, And Uses Thereof
; FILE REFERENCE: Hubr 1126
; CURRENT APPLICATION NUMBER: US/09/113,692B
; CURRENT FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP/97 112 640
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: EP/97 121 073
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: EP/97 53 681
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-113-692B-9
Query Match 22.2%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 MGVP 9
| | | |
DB 1 MGVP 4
RESULT 4
US-09-607-277A-9
; Sequence 9, Application US/09607277A
; Patent No. 6555373
; GENERAL INFORMATION:
; APPLICANT: Stern, Anne
; APPLICANT: Brandt, Michael
; APPLICANT: Honold, Konrad
; APPLICANT: Auer, Johannes
; APPLICANT: Koll, Hans
; APPLICANT: Franze, Reinhard
; APPLICANT: Pessara, Ulrich
; TITLE OF INVENTION: Methods For Identifying Human Cell Lines Useful for
; TITLE OF INVENTION: Endogenous Gene Activation, Isolated Human Cell Lines
; TITLE OF INVENTION: Identified Thereby, And Uses Thereof
; FILE REFERENCE: Hubr 1126.1
; CURRENT APPLICATION NUMBER: US/09/607,277A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP/97 112 640
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: EP/97 121 073
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: EP/97 53 681
; PRIOR FILING DATE: 1997-12-03

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; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-607-277A-9

Query Match      22.2%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9      ||||
Db      1 MGVP 4

RESULT 5
US-08-760-075A-29
; Sequence 29, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-760-075A-29

Query Match      22.2%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMGV 8      ||||
Db      2 IMGV 5

RESULT 6
US-09-338-546-29
; Sequence 29, Application US/09338546

```

RESULT 10
US-09-238-754-383
; Sequence 383, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslati, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Ident
; TITLE OF INVENTION: Membrane Dipecti
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/25

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; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 383
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-383

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      1 PKVK 4

RESULT 11
; Sequence 383, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 383
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-383

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      1 PKVK 4

RESULT 12
US-09-641-803-16
; Sequence 16, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-16

Query Match      22.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
Db      4 LQPE 7

RESULT 13
US-09-296-284-14
; Sequence 14, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Bui-Sung
; APPLICANT: Rhee, Sang-Ki
; APPLICANT: Lee, Eun-Hae
; TITLE OF INVENTION: Gluconobacter Suboxydaus Sorbitol Dehydrogenase, Genes
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296,284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-14

Query Match      22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GVPK 10
Db      5 GVPK 8

RESULT 14
US-08-217-188A-62
; Sequence 62, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Pallieur, Thierry
; TITLE OF INVENTION: Isolated tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAG8-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
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```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 15
US-08-687-226-62
; Sequence 62, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-641-801-21.oligo.ra1

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 16
US-08-467-083-2
; Sequence 2, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-467-083-2

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 2 LQPE 5

RESULT 17
US-08-615-181-79
; Sequence 79, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUML, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; US-08-615-181-79
```

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,181
FILING DATE: 04-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01756
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261302/1993
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-796-0 PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-79

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 18
US-08-787-547-104
Sequence 104, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-104

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 19
US-08-414-417B-2
Sequence 2, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-414-417B-2

Query Match 22.2%; Score 4; DB 1; Length 9;

```
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 20
US-08-486-348A-2
; Sequence 2, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-486-348A-2

Query Match 22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 21
US-08-468-545B-2
; Sequence 2, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

```
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-545B-2

Query Match 22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 22
US-08-948-378A-17
; Sequence 17, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948.378A
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
```

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-948-378A-17

Query Match 22.2%; Score 4; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db 5 LQPE 8

RESULT 23

US-08-667-725B-62
 ; Sequence 62, Application US/08667725B

; Patent No. 6063900

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.

; APPLICANT: Visseren, M. J. W.

; APPLICANT: Kast, W. M.

; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Tumor Rejection Antigen

; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/667,725B

; FILING DATE: 21 June 1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6063900man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LJD 5340.1 DIV (081585)

; TELEPHONE: (212) 318-3000

; TELEFAX: (212) 752-5958

; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acid residues

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-667-725B-62

Query Match 22.2%; Score 4; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db 4 LQPE 7

RESULT 24

US-08-466-680B-2

; Sequence 2, Application US/08466680B

; Patent No. 6075122
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,680B
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-466-680B-2

Query Match 22.2%; Score 4; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db 2 LQPE 5

RESULT 25

US-09-007-748-62

; Sequence 62, Application US/09007748

; Patent No. 6147187

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.

; APPLICANT: Visseren, M. J. W.

; APPLICANT: Kast, W. M.

; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Tumor Rejection Antigen

; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,748
FILING DATE: 15 January 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6147187man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-007-748-62

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LOPE 4
| | | |
Db 4 LOPE 7

RESULT 26
US-09-169-425C-17
Sequence 17, Application US/09169425C
Patent No. 6183746
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,425C
FILING DATE: 09-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/061,657
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-169-425C-17

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LOPE 4
| | | |
Db 4 LOPE 7

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LOPE 4
| | | |
Db 5 LOPE 8

RESULT 27
US-08-197-484-28
Sequence 28, Application US/08197484
Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-28

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 PKVK 12
| | | |
Db 2 PKVK 5

RESULT 28
US-08-197-484-66
; Sequence 66, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-66

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 29
US-08-197-484-71
; Sequence 71, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:

; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-71

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 30
US-08-403-459-12
; Sequence 12, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantine G.
; APPLICANT: Fisk, Bryan A.
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403.459
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSC:390/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-459-12

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 2 LOPE 5

RESULT 31
US-09-759-960-17
Sequence 17, Application US/09/759960
Patent No. 6582704
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 'Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-759-960-17

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 5 LOPE 8

RESULT 32
PCT-US95-02121-28
Sequence 28, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-28

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 |||||
 Db 2 PKVK 5

RESULT 33

PCT-US95-02121-66
 ; Sequence 66, Application PC/TUS9502121
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02121
 ; FILING DATE: 16-FEB-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/197,484
 ; FILING DATE: 16-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811
 ; FILING DATE: 26-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/874,491
 ; FILING DATE: 27-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 66:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; PCT-US95-02121-66

Query Match 22.2%; Score 4; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
 |||||
 Db 5 LOPE 8

RESULT 34

PCT-US95-02121-71
 ; Sequence 71, Application PC/TUS9502121
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02121
 ; FILING DATE: 16-FEB-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/197,484
 ; FILING DATE: 16-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811
 ; FILING DATE: 26-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/874,491
 ; FILING DATE: 27-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 71:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; PCT-US95-02121-71

Query Match 22.2%; Score 4; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
 |||||
 Db 4 LOPE 7

RESULT 35

US-08-902-516-19
 ; Sequence 19, Application US/08902516
 ; Patent No. 5891432
 ; GENERAL INFORMATION:
 ; APPLICANT: Soo Hoo, William
 ; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
 ; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
 ; TITLE OF INVENTION: RESPONSE USING SAME
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CAMPBELL & FLORES, LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/902,516
 ; FILING DATE: 29-JUL-1997

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-902-516-19

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQPE 4
Db 5 LQPE 8

RESULT 36
US-08-760-075A-34
Sequence 34, Application US/08760075A
Patent No. 5942429
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-075A-34

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 IMGV 8
Db 5 IMGV 8

RESULT 37
US-08-704-344-22
Sequence 22, Application US/08704344
Patent No. 6218363
GENERAL INFORMATION:
APPLICANT: BASERGA, Renato L.
APPLICANT: RESNICOFF, Mariana
APPLICANT: HUANG, Ziwei
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,344
FILING DATE: 28-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 942-8459
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-704-344-22

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQPE 4
Db 5 LQPE 8

RESULT 38
US-09-338-546-34
Sequence 34, Application US/09338546
Patent No. 6251645
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-338-546-34

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8

Db 5 IMGV 8

RESULT 39

US-09-461-697-283
Sequence 283, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
FILE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 283
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-461-697-283

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18

Db 1 MVPK 4
RESULT 40
US-09-659-084-34
Sequence 34, Application US/09659084
Patent No. 6403299
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
MUELLNER, Stefan
BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/659,084
FILING DATE: 11-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/338,546
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-659-084-34

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8

Db 5 IMGV 8

RESULT 41

US-09-847-185-19
Sequence 19, Application US/09847185
Patent No. 6482407
GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

```

US-08-760-075A-1
; Sequence 1, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-1

Query Match      22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 IMGV 8
Db      5 IMGV 8

RESULT 44
US-09-101-886B-57
; Sequence 57, Application US/09101886B
; Patent No. 6197507
; GENERAL INFORMATION:
; APPLICANT: BERG, THOMAS
; APPLICANT: TOLLERSRUD, OLE K
; APPLICANT: NILSEN, OIVIND
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BARBARA G. ERNST
; STREET: 555 13TH STREET, NW SUITE 701E
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,886B
; FILING DATE: 29-JANUARY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/00109
; FILING DATE: 12-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: not relevant
; ANTI-SENSE: not relevant
; FRAGMENT TYPE: internal
; US-09-101-886B-57

Query Match 22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 IMGV 12

Db 7 PKVK 10

RESULT 45

US-09-338-546-1
; Sequence 1, Application US/09338546
; Patent No. 6251645
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-338-546-1

Query Match 22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 IMGV 8

Db 5 IMGV 8

RESULT 46

US-09-659-084-1
; Sequence 1, Application US/09659084
; Patent No. 6403299
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/659,084
; FILING DATE: 11-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/338,546
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-659-084-1

Query Match 22.2%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 IMGV 8

Db 5 IMGV 8


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RESULT 47
US-08-949-059A-29
; Sequence 29, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-29

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 8 PKVK 11

RESULT 48
US-08-949-059A-31
; Sequence 31, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
```

```
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
US-08-949-059A-31

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 8 PKVK 11

RESULT 49
5460961-8
; Patent No. 5460961
; APPLICANT: DEBY, CAROL/PINCMAIL, JOEL/BOLLEN, ALEX
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; THERAPEUTIC APPLICATION
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,678
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 460,931
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; FILING DATE: 14-FEB-1990
; SEQ ID NO:8;
; LENGTH: 12
5460961-8

Query Match      22.2%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9
Db      1 MGVP 4

RESULT 50
US-07-610-525-5
; Sequence 5, Application US/07610525
; Patent No. 5196512
; GENERAL INFORMATION:
; APPLICANT: BIANCHI Elisabetta
; APPLICANT: PESSI Antonello
; APPLICANT: CORRADIN Giampietro
; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS
; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES
; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHEA & GOULD
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10020-1193
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/610,525
; FILING DATE: 19901108
; CLASSIFICATION: 424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-827-3000
; TELEFAX: 212-840-6702
; TELEX: 423973
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: internal fragment
US-07-610-525-5

Query Match      22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VPKV 11
Db      4 VPKV 7

RESULT 51
US-08-403-459-36
; Sequence 36, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantine G.
; APPLICANT: Fisk, Bryan A.
```

```
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,459
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSC:390/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-403-459-36

Query Match      22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
Db      1 LQPE 4

RESULT 52
US-08-949-059A-26
; Sequence 26, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/949,059A
;; FILING DATE: 10-OCT-1997
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 660081.412
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: cyclic
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 6
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 13
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; US-08-949-059A-26

Query Match 22.2%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 7 PKVK 10

RESULT 53
US-08-949-059A-27
; Sequence 27, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963

;; REFERENCE/DOCKET NUMBER: 660081.412
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: cyclic
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Residue is a D-Lysine"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 6
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 13
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; US-08-949-059A-27

Query Match 22.2%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 7 PKVK 10

RESULT 54
US-08-949-059A-28
; Sequence 28, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

```
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "Residue is a D-Valine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-28
;
; Query Match 22.2%; Score 4; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 2.5e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 9 PKVK 12
; DB 7 PKVK 10
;
; RESULT 55
; US-07-610-525-4
; Sequence 4, Application US/07610525
; Patent No. 5196512
; GENERAL INFORMATION:
; APPLICANT: BIANCHI Elisabetta
; APPLICANT: PESSI Antonello
; APPLICANT: CORRADIN Giampaetro
; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS
; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES
; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHEA & GOULD
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10020-1193
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/610,525
; FILING DATE: 19901108
; CLASSIFICATION: 424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-827-3000
; TELEFAX: 212-840-6702
; TELEX: 423973
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
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; FRAGMENT TYPE: internal fragment
; US-07-610-525-4
;
; Query Match 22.2%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 2.7e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 VPKV 11
; DB 6 VPKV 9
;
; RESULT 56
; US-08-097-997A-2
; Sequence 2, Application US/08097997A
; Patent No. 5728536
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; APPLICANT: Quelle, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; TITLE OF INVENTION: Transduction
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,997A
; FILING DATE: 29-JULY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0370000/SLF/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-097-997A-2
;
; Query Match 22.2%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 2.7e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 10 KVKE 13
; DB 10 KVKE 13
;
; RESULT 57
; US-08-259-672-11
; Sequence 11, Application US/08259672
; Patent No. 5736337
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN
; INTERACTIONS
```

```
;
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,672
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-259-672-11

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 1 LOPE 4

RESULT 59
US-08-459-351-11
; Sequence 11, Application US/08459351
; Patent No. 5763571
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,533
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234002
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-459-351-11

;
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,351
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
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US-08-460-533-11

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
|
|
|
|
Db 1 LOPE 4

RESULT 60

US-08-787-547-44
; Sequence 44, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-44

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPKV 11
|
|
|
|
Db 6 VPKV 9

RESULT 61

US-08-553-257A-62
; Sequence 62, Application US/08553257A
; Patent No. 5994083
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.

; APPLICANT: FELICI, Franco
; APPLICANT: LUZZAGO, Alessandra
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,257A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/IT94/00054
; APPLICATION NUMBER:
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-257A-62

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
|
|
|
|
Db 7 PKVK 10

RESULT 62
US-08-660-347-3
; Sequence 3, Application US/08660347
; Patent No. 6027935
; GENERAL INFORMATION:
; APPLICANT: Purchio, Anthony F.
; APPLICANT: New, Liguio
; APPLICANT: Liu, Kang
; APPLICANT: Kamali, Vafa
; APPLICANT: Naughton, Brian
; TITLE OF INVENTION: No. 6027935el Gene Up-Regulated in
; TITLE OF INVENTION: Regenerating Liver
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,347
FILING DATE: 05-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6261-0151-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6027935e
US-08-660-347-3

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
DB 4 VKET 7

RESULT 63
US-09-041-889-16
Sequence 16, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-041-889-16

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 64
US-08-837-058-16
Sequence 16, Application US/08837058
Patent No. 6074835
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Targan, Stephan R.
APPLICANT: Eggena, Mark
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Histone H1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-837-058-16

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 65

```

US-08-665-574C-2
; Sequence 2, Application US/08665574C
; Patent No. 6136595
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,574C
; FILING DATE: 18-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,997
; FILING DATE: 29-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-665-574C-2

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 10 KVKE 13

RESULT 66
US-08-946-994-2
; Sequence 2, Application US/08946994
; Patent No. 6210654
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; APPLICANT: Quelle, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; TITLE OF INVENTION: Transduction
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600

```

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,994
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,574
; FILING DATE: 18-JUN-1996
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,997
; FILING DATE: 29-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-946-994-2

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 10 KVKE 13

RESULT 67
US-09-417-264-16
; Sequence 16, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:

```



```
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,889
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-417-264-16

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 4 PKVK 7

RESULT 68
US-09-441-992-62
; Sequence 62, Application US/09441992
; Patent No. 6541210
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; MOLECOLARE P. ANGELETTI S.p.A.
; FELICI, Franco
; LUZZAGO, Alessandra
; NICOSIA, Alfredo
; MONACI, Paolo
; CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; OR DIAGNOSTIC REAGENTS AND IMMUNOGENS OR
; DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Brody and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/441,992
; FILING DATE: 18-Nov. 6541210-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/553,257
; FILING DATE: <Unknown>
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brody, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-441-992-62

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 7 PKVK 10

RESULT 69
PCT-US94-06654-11
; Sequence 11, Application PC/TUS9406654
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06654
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US94-06654-11

Query Match 22.2%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 1 LOPE 4

RESULT 70
US-08-591-438-13
; Sequence 13, Application US/08591438
```

```
;
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-441-992-62
```

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 7 PKVK 10

```
RESULT 69
PCT-US94-06654-11
; Sequence 11, Application PC/TUS9406654
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06654
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US94-06654-11
```

Query Match 22.2%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 1 LOPE 4

RESULT 70
US-08-591-438-13
; Sequence 13, Application US/08591438

```
; Patent No. 5939063
; GENERAL INFORMATION:
; APPLICANT: Vadas, Mathew A.
; APPLICANT: Lopez, Angel F.
; APPLICANT: Shannon, Mary F.
; TITLE OF INVENTION: HAEMOPOIETIC GROWTH FACTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,438
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio Esq., Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-591-438-13

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
Db 3 VKET 6

RESULT 71
US-08-760-075A-2
; Sequence 2, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A
```

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; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-2

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8
Db 5 IMGV 8

RESULT 72
US-09-011-525-1
; Sequence 1, Application US/09011525
; Patent No. 6020172
; GENERAL INFORMATION:
; APPLICANT: BOTH, GERALD W.
; TITLE OF INVENTION: GENE THERAPY USING OVINE ADENOVIRAL VECTORS
; FILE REFERENCE: Gene Therapy Using Ovine Adenoviral Ve
; CURRENT APPLICATION NUMBER: US/09/011,525
; CURRENT FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00518
; EARLIER FILING DATE: 1996-08-14
; EARLIER APPLICATION NUMBER: AU PN4776
; EARLIER FILING DATE: 1995-08-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Ovine adenovirus
US-09-011-525-1

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18
Db 4 MVPK 7

RESULT 73
US-08-405-647B-11
; Sequence 11, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Sholet, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
; NUMBER OF SEQUENCES: 50
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/405,647B
;; FILING DATE: 17-MAR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677
;; REFERENCE/DOCKET NUMBER: 02307E-068700US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-405-647B-11

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 MVPK 18
Db 6 MVPK 9

RESULT 74
US-08-602-999A-344
; Sequence 344, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 344:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-602-999A-344

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 9 PKVK 12
Db 11 PKVK 14

RESULT 75
US-08-985-499-11
; Sequence 11, Application US/08985499
; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-985-499-11

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 MVPK 18
Db 6 MVPK 9

Db 6 MVEK 9

Search completed: November 25, 2003, 20:29:58
Job time : 15.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMFPKYPVEPTESQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	22.2	14	H64008	hypothetical prote
2	4	22.2	16	PC4371	telomeric and tetr
3	3	16.7	5	PQ0009	angiotensin-conver
4	3	16.7	5	JT0520	Ig kappa chain V-I
5	3	16.7	6	A61049	halo-toxin - Pseud
6	3	16.7	6	I51317	bHLH transcription
7	3	16.7	7	XEYDGD	galactose oxidase
8	3	16.7	7	S33244	neuromodulatory pe
9	3	16.7	8	A32523	peptidyl-di-peptida
10	3	16.7	8	S20162	leghemoglobin III
11	3	16.7	9	PD0443	3-oxoacid CoA-tran
12	3	16.7	10	A60410	beta-neoendorphin
13	3	16.7	10	S65728	hemoglobin, extrac
14	3	16.7	10	A37268	Ig heavy chain C r
15	3	16.7	11	F58501	43.5K bile stone p
16	3	16.7	11	PA0028	protein QA300042 -
17	3	16.7	11	PC4267	ribosomal protein
18	3	16.7	11	PQ0731	unidentified 5.7/3
19	3	16.7	11	I54193	Rhesus blood group
20	3	16.7	11	A54348	N-acetylglucosamin
21	3	16.7	13	PQ0491	self-incompatibili
22	3	16.7	13	A44818	extracellular lipa
23	3	16.7	13	A28953	alpha-conotoxin Si
24	3	16.7	13	S21152	tryptophyllin-rela
25	3	16.7	13	A60458	protocatechuate 3,
26	3	16.7	13	PC2371	probable endopepti
27	3	16.7	13	D56661	S-locus specific g
28	3	16.7	13	B61620	locustamyotropin I
29	3	16.7	13	D61458	Ig kappa chain V-I

30	3	16.7	13	E61458	Ig kappa chain V-I
31	3	16.7	13	PH1772	T cell receptor al
32	3	16.7	14	PT0026	calotropin DI - mu
33	3	16.7	14	E33098	214K exoantigen (v
34	3	16.7	15	PA0024	protein QA300050 -
35	3	16.7	15	PQ0452	32K protein 3306 -
36	3	16.7	15	PA0062	fumarate hydratase
37	3	16.7	15	B61457	alpha-glucosidase
38	3	16.7	15	A36527	juvenile-hormone e
39	3	16.7	15	A49480	major immunophilin
40	3	16.7	15	PT0205	insulin-like growth
41	3	16.7	15	B45115	peptidylprolyl iso
42	3	16.7	16	B42324	casein kinase II (
43	3	16.7	16	C45133	shikimate 5-dehydr
44	3	16.7	16	C53113	Lys-gingipain form
45	3	16.7	17	S05671	hirudin Ia - medic
46	3	16.7	17	S05033	photosystem II pro
47	3	16.7	17	B31769	T-cell receptor de
48	3	16.7	17	G85956	hypothetical prote
49	3	16.7	17	S29264	ovohemerythrin - d
50	3	16.7	18	H64711	hypothetical prote
51	3	16.7	18	S58277	insulin-like growt
52	3	16.7	18	S71592	serine proteinase
53	3	16.7	18	I46653	T-cell receptor de
54	3	16.7	18	A59137	protein Pii - Gold
55	3	16.7	18	EWSMCN	cinnamycin - Strep
56	3	16.7	19	S59485	hyoxyproline-rich
57	3	16.7	19	S43641	carboxylesterase (
58	3	16.7	19	C56661	S-locus specific g
59	3	16.7	19	PQ0492	self-incompatibili
60	3	16.7	19	A61144	probable flagellar
61	3	16.7	19	C39305	neurotoxin Tx3 - s
62	3	16.7	19	I46654	T-cell receptor de
63	3	16.7	19	S69166	ferredoxin b - Jap
64	3	16.7	19	S11611	ribosomal protein
65	3	16.7	20	S06466	T-cell receptor al
66	3	16.7	20	JP0059	ribosomal protein
67	3	16.7	20	PL0145	carbon-monoxide de
68	3	16.7	20	PQ0046	citrate (si)-synth
69	3	16.7	20	S29635	jacalin beta chain
70	3	16.7	20	B30208	hypothetical prote
71	3	16.7	20	S58382	hypothetical prote
72	3	16.7	20	I46652	T-cell receptor de
73	3	16.7	20	A41439	acid ribonuclease
74	3	16.7	20	GKHU	growth-modulating
75	2	11.1	3	A33802	thyrotropin-releas
76	2	11.1	3	A43391	TRH-like tripeptid
77	2	11.1	3	I78890	tyrosine protein k
78	2	11.1	4	A32039	tyrosine-melanocyt
79	2	11.1	4	S53508	starvation-induced
80	2	11.1	4	PT0240	Ig heavy chain CRD
81	2	11.1	4	I54357	schwannomin - mous
82	2	11.1	5	JN0862	peptidyl-di-peptida
83	2	11.1	5	C41225	copper resistance
84	2	11.1	5	E60274	major protein anti
85	2	11.1	5	T14908	hypothetical prote
86	2	11.1	5	PQ0689	photosystem I 10.4
87	2	11.1	5	B37988	acid proteinase li
88	2	11.1	5	JS0319	subesophageal gang
89	2	11.1	5	S53595	hypothetical prote
90	2	11.1	5	S11127	phosphoprotein, bo
91	2	11.1	5	PT0308	Ig heavy chain CRD
92	2	11.1	5	PT0610	T-cell receptor be
93	2	11.1	5	PT0644	T-cell receptor be
94	2	11.1	6	JN0861	peptidyl-di-peptida
95	2	11.1	6	B34835	dnA protein - Pse
96	2	11.1	6	S11556	hydrogensulfite re
97	2	11.1	6	B60110	repetitive protein
98	2	11.1	6	A31263	dihydrofolate redu
99	2	11.1	6	B31263	dihydrofolate redu
100	2	11.1	6		

Ig kappa chain V-I
T cell receptor al
calotropin DI - mu
214K exoantigen (v
protein QA300050 -
32K protein 3306 -
 fumarate hydratase
alpha-glucosidase
juvenile-hormone e
major immunophilin
insulin-like growth
peptidylprolyl iso
casein kinase II (
cytochrome P450c27
shikimate 5-dehydr
Lys-gingipain form
hirudin Ia - medic
photosystem II pro
T-cell receptor de
hypothetical prote
ovohemerythrin - d
hypothetical prote
insulin-like growt
serine proteinase
T-cell receptor de
protein Pii - Gold
cinnamycin - Strep
hyoxyproline-rich
carboxylesterase (
S-locus specific g
self-incompatibili
probable flagellar
neurotoxin Tx3 - s
T-cell receptor de
ferredoxin b - Jap
ribosomal protein
T-cell receptor al
ribosomal protein
carbon-monoxide de
citrate (si)-synth
jacalin beta chain
hypothetical prote
hypothetical prote
T-cell receptor de
acid ribonuclease
growth-modulating
thyrotropin-releas
TRH-like tripeptid
tyrosine protein k
tyrosine-melanocyt
starvation-induced
Ig heavy chain CRD
schwannomin - mous
peptidyl-di-peptida
copper resistance
major protein anti
hypothetical prote
photosystem I 10.4
acid proteinase li
subesophageal gang
hypothetical prote
phosphoprotein, bo
Ig heavy chain CRD
T-cell receptor be
T-cell receptor be
peptidyl-di-peptida
dnA protein - Pse
hydrogensulfite re
repetitive protein
dihydrofolate redu
dihydrofolate redu

ALIGNMENTS

```
RESULT 1
H64008
hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C/Accession: H64008
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64008
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-14 <TIGR>
A;Cross-references: GB:U32731; GB:L42023; NID:91573465; PID:91573478; TIGR:HI0492

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKYP 10
Db 3 PKYP 6

RESULT 2
PC4371
telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C/Accession: PC4371
R;SariG, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4371
A;Molecule type: protein
A;Residues: 1-16 <SAR>
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
Db 5 PVEP 8

RESULT 3
PQ0009
angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N;Alternate names: ficus latex peptide 2
C;Species: Ficus carica (common fig)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C/Accession: PQ0009
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0009
A;Molecule type: protein
A;Residues: 1-5 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 16.7%; Score 3; DB 2; Length 5;
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```
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11
Db 2 YPV 4

RESULT 4
JT0520
Ig kappa chain V-III region (SD1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
C/Accession: JT0520
R;Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A;Title: Clonal diversity in the B cell repertoire of patients with X-linked agammag
A;Reference number: JT0511; MUID:89279157; PMID:2786547
A;Accession: JT0520
A;Molecule type: mRNA
A;Residues: 1-5 <ANK>
A;Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangem
A;Note: a stop codon terminates the sequence in the V region
C;Keywords: heterotetramer; immunoglobulin
F;1-5/Domain: V kappa region <VRE>

Query Match 16.7%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
Db 1 TES 3

RESULT 5
A61049
halo-toxin - Pseudomonas syringae pv. mori
C;Species: Pseudomonas syringae pv. mori
A;Note: host mulberry tree
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C/Accession: A61049
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata,
Chem. Lett. 00, 679-680, 1989
A;Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas
A;Reference number: A61049
A;Accession: A61049
A;Molecule type: protein
A;Residues: 1-6 <KAJ>
A;Note: sequence confirmed by synthesis
C;Comment: This toxin is one of the etiological agents of halo bright disease in mul
C;Keywords: toxin

Query Match 16.7%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFP 7
Db 1 PFP 3

RESULT 6
I51317
bHLH transcription factor inhibitor - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C/Accession: I51317
R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.
Mech. Dev. 50, 119-130, 1995
A;Title: Id gene activity during Xenopus embryogenesis.
A;Reference number: I51316; MUID:95344988; PMID:7619724
A;Accession: I51317
```

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-6 <ZHA>

A;Cross-references: GB:S79038; NID:gl042006; PIDN:AAD14294.1; PID:94261994

C;Genetics:

A;Gene: XIDib

Query Match 16.7%; Score 3; DB 2; Length 6;

Best Local Similarity 100.0%; Pred.No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0;

Qy 12 EPF 14

Db 4 EPF 6

RESULT 7

XEYDGD

galactose oxidase inhibitor - fungus (Cladobotryum dendroides)

C;Species: Cladobotryum dendroides

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993

C;Accession: A01341

R;Avigad, G.; Markus, Z.

Fed. Proc. 31, 447, 1972

A;Reference number: A01341

A;Accession: A01341

A;Molecule type: protein

A;Residues: 1-7 <AVI>

C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, may inactivate the enzyme by binding to its prosthetic copper group.

C;Superfamily: galactose oxidase inhibitor

C;Keywords: copper

Query Match 16.7%; Score 3; DB 1; Length 7;

Best Local Similarity 100.0%; Pred.No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17

Db 5 TES 7

RESULT 8

S33244

neuromodulatory peptide Wwamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

Query Match 16.7%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred.No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEM 4

Db 2 KEM 4

RESULT 9

A32523

peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)

N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I

C;Species: Bos primigenius taurus (cattle)

C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 11-May-2000

C;Accession: A32523

R;Harris, R.B.

Adv. Exp. Med. Biol. 198, 513-521, 1986

A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-conver

A;Reference number: A32523; MUID:87123961; PMID:3028071

A;Accession: A32523

A;Molecule type: protein

A;Residues: 1-8 <HAR>

C;Superfamily: mammalian peptidyl-dipeptidase A

C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase

Query Match 16.7%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred.No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16

Db 1 FTE 3

RESULT 10

S20162

leghemoglobin III - Sesbania rostrata (fragment)

C;Species: Sesbania rostrata

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-2000

C;Accession: S20162

R;Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.

Mol. Gen. Genet. 214, 181-191, 1988

A;Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-n

A;Reference number: S08322; MUID:89181515; PMID:3237206

A;Accession: S20162

A;Molecule type: DNA

A;Residues: 1-8 <MET>

A;Cross-references: EMBL:X13504; NID:g21383; PIDN:CAA31858.1; PID:g579482

C;Genetics:

A;Gene: glb3

C;Superfamily: globin; globin homology

C;Keywords: heme; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred.No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16

Db 3 FTE 5

RESULT 11

PD0443

3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C;Accession: PD0443

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0443

A;Molecule type: protein

A;Residues: 1-9 <KAW>

C;Keywords: CoA-transferase

Query Match 16.7%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred.No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVE 12

Db 7 PVE 9

RESULT 12

A60410

beta-neoendorphin / dynorphin precursor - guinea pig
 N:Alternate names: alpha-neoendorphin; proenkephalin B precursor
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000
 C:Accession: A60410
 R:Murphy, R.; Turner, C.A.
 Peptides 11, 65-68, 1990
 A:Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.
 A:Reference number: A60410; MUID:90259864; PMID:2342991
 A:Accession: A60410
 A:Molecule type: protein
 A:Residues: 1-10 <MUR>
 C:Superfamily: proenkephalin
 C:Keywords: neuropeptide; opioid peptide

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
 ||||
 Db 7 KYP 9

RESULT 13

S65728
 hemoglobin, extracellular, chain d1 - earthworm (Lumbricus terrestris) (fragment)
 C:Species: Lumbricus terrestris (common earthworm)
 C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S65728
 R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
 Biochim. Biophys. Acta 1292, 273-280, 1996
 A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
 A:Reference number: S65721; MUID:96176855; PMID:8597573
 A:Accession: S65728
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <FUS>

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 5 TES 7

RESULT 14

A37268
 IG heavy chain C region (129) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C:Accession: A37268
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 265, 6607-6613, 1991
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
 A:Reference number: A38740; MUID:91177923; PMID:1706720
 A:Accession: A37268
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-10 <RUF>

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
 ||||
 Db 1 ESQ 3

RESULT 15

F58501
 43.5K bile stone protein - unidentified bacterium (fragment)
 C:Species: unidentified bacterium
 C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 C:Accession: F58501
 R:Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A:Description: The proteins of kidney and gallbladder stones.
 A:Reference number: A58501
 A:Accession: F58501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <BIN>
 A:Experimental source: human bile with stones
 A:Note: 6-Asn and 8-Ala were also found

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
 ||||
 Db 9 PVE 11

RESULT 16

PA0028
 protein QA300042 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0028
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimens.
 A:Reference number: PA0001
 A:Accession: PA0028
 A:Molecule type: protein
 A:Residues: 1-11 <KAM>
 A:Experimental source: seed
 C:Keywords: seed

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
 ||||
 Db 6 PFP 8

RESULT 17

PC4267
 ribosomal protein L12.1 - rice (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
 C:Accession: PC4267
 R:Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
 submitted to JIPID, April 1997
 A:Reference number: PC4267
 A:Accession: PC4267
 A:Molecule type: protein
 A:Residues: 1-11 <KAW>
 A:Experimental source: strain Japonica Nihonbare

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 4 TES 6

RESULT 18

PQ0731
 unidentified 5.7/35K protein [imported] - rice (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C;Accession: PQ0731
 R;Komatsu, S.; Kajiwar, H.; Hirano, H.
 Theor. Appl. Genet. 86, 935-942, 1993
 A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
 A;Reference number: PQ0696
 A;Accession: PQ0731
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <KOM>

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKY 9
 |||
 Db 6 PKY 8

RESULT 19

154193
 Rhesus blood group CcEe protein - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
 C;Accession: I54193
 R;Charif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.
 Genomics 19, 68-74, 1994
 A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe antigens
 A;Reference number: I54193; MUID:94245182; PMID:8188244
 A;Accession: I54193
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <RES>
 A;Cross-references: GB:S70456; MID:g546795; PIDN:AAD14061.1; PID:g4261761
 C;Genetics:
 A;Gene: GDB:RHCE
 A;Cross-references: GDB:229957; OMIM:111700
 A;Map position: lp36.2-lp34

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYP 10
 |||
 Db 4 KYP 6

RESULT 20

A54348
 N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C;Accession: A54348
 R;Shilatfard, A.; Cummings, R.D.
 Biochemistry 33, 4273-4282, 1994
 A;Title: Purification and characterization of N-acetylglucosamine-6-sulfate sulfatase fr
 A;Reference number: A54348; MUID:94206936; PMID:8155645
 A;Accession: A54348
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <SHI>
 C;Keywords: sulfuric ester hydrolase

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14
 |||
 Db 2 EPF 4

RESULT 21

PQ0491
 self-incompatibility locus glycoprotein delta - wild cabbage (fragment)
 C;Species: Brassica oleracea (wild cabbage)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Oct-1997
 C;Accession: PQ0491
 R;Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
 Plant Cell 5, 75-86, 1993
 A;Title: Expression of a self-incompatibility gene in a self-compatible line of Brass
 A;Reference number: JQ1733; MUID:93177215; PMID:8439745
 A;Accession: PQ0491
 A;Molecule type: protein
 A;Residues: 1-13 <GAU>
 A;Experimental source: stigma, var. acephala P57Si
 C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot
 C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
 |||
 Db 7 TES 9

RESULT 22

A44818
 extracellular lipase - Pseudomonas aeruginosa (fragment)
 C;Species: Pseudomonas aeruginosa
 C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
 C;Accession: A44818
 R;Gilbert, B.J.; Cornish, A.; Jones, C.W.
 J. Gen. Microbiol. 137, 2223-2229, 1991
 A;Title: Purification and properties of extracellular lipase from Pseudomonas aerugin
 A;Reference number: A44818; MUID:92085040; PMID:1748875
 A;Accession: A44818
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-13 <GIL>
 A;Experimental source: strain PB3285
 A;Note: sequence extracted from NCBI backbone (NCBIP:70395)
 C;Superfamily: Pseudomonas triacylglycerol lipase

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYP 10
 |||
 Db 7 KYP 9

RESULT 23

A28953
 alpha-conotoxin SI - cone shell (Conus striatus)
 C;Species: Conus striatus (striated cone)
 C;Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
 C;Accession: A28953
 R;Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.
 Biochemistry 27, 7102-7105, 1988
 A;Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.
 A;Reference number: A28953; MUID:89062448; PMID:3196703
 A;Accession: A28953
 A;Molecule type: protein
 A;Residues: 1-13 <ZAF>
 A;Note: this sequence was confirmed by chemical synthesis

C;Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholinesterase activity of the acetylcholine receptor.
 C;Superfamily: alpha-conotoxin
 C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin; 2-7, 3-13/disulfide bonds; #status experimental
 F;13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
 ||||
 Db 9 PKY 11

RESULT 24

S21152
 tryptophyllin-related peptide - two-colored leaf frog
 C;Species: Phyllomedusa bicolor (two-colored leaf frog)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S21152
 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A;Title: Identification and characterization of two dermorphins from skin extracts of the two-colored leaf frog
 A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152
 A;Molecule type: protein
 A;Residues: 1-13 <MIG>
 A;Experimental source: skin
 C;Superfamily: unassigned animal peptides

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
 ||||
 Db 11 YPV 13

RESULT 25

A60458
 protocatechuate 3,4-dioxygenase (EC 1.13.11.13) alpha chain - Moraxella sp. (strain GU2)
 N;Alternate names: protocatechuate oxygenase

C;Species: Moraxella sp.
 C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
 C;Accession: A60458
 R;Sterjades, R.; Belmont, J.
 Appl. Environ. Microbiol. 55, 340-347, 1989
 A;Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Moraxella sp.
 A;Reference number: A60458; MUID:89245845; PMID:2541659

A;Accession: A60458
 A;Molecule type: protein
 A;Residues: 1-13 <STE>
 A;Note: two forms P and G of the alpha subunit yielded identical amino terminal sequence
 C;Keywords: iron; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
 ||||
 Db 11 YPV 13

RESULT 26

PC2371
 probable endopeptidase Clp ATP-binding chain C [similarity] - Bacillus cereus (strain 168)
 N;Contains: adenosinetriphosphatase (EC 3.6.1.3)

C;Species: Bacillus cereus
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C;Accession: PC2371

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
 Biosci. Biotechnol. Biochem. 59, 231-235, 1995
 A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*
 A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2371
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <MAS>

C;Keywords: ATP; hydrolase; nucleotide binding

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
 ||||
 Db 6 FTE 8

RESULT 27

D56661

S-locus specific glycoprotein (allele S3) - wild cabbage (fragment)
 C;Species: Brassica oleracea (wild cabbage)

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C;Accession: D56661

R;Gaude, T.; Denoroy, L.; Dumas, C.

Electrophoresis 12, 646-653, 1991

A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal sequencing of glycoproteins

A;Reference number: A56661; MUID:92090397; PMID:1752245

A;Accession: D56661

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <GAU>

A;Experimental source: stigma extracts, var. acephala

A;Note: sequence extracted from NCBI backbone (NCBI:72300)

C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in the defense of the plant against pathogens

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 7 TES 9

RESULT 28

B61620

locustamytropin IV - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997

C;Accession: B61620

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A;Title: Isolation, identification and synthesis of locustamytropin III and IV, two peptides of the locustamytropin family

A;Reference number: A61620

A;Accession: B61620

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <SCH>

C;Keywords: amidated carboxyl end; neuropeptide

F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6
 ||||
 Db 7 MPF 9

RESULT 29

D61458
Ig kappa chain V-IV region (DEP) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: D61458; PLO158
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein
A:Reference number: A61458; PMID:90039128; PMID:2478651
A:Accession: D61458
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 15 TES 17
|||
Db 5 TES 7

RESULT 30

E61458
Ig kappa chain V-IV region (FUE) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: E61458
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein
A:Reference number: A61458; PMID:90039128; PMID:2478651
A:Accession: E61458
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 15 TES 17
|||
Db 5 TES 7

RESULT 31

PH1772
T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1772
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes

A:Reference number: PH1754; PMID:93301585; PMID:8391057
A:Accession: PH1772
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <POR>

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 11 VEP 13
|||
Db 4 VEP 6

RESULT 32

PT0026
calotropin DI - mudar (fragment)
C:Species: Calotropis gigantea (mudar, madar)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: PT0026
R:Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
Phytochemistry 26, 633-636, 1987
A:Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis gigantea
A:Reference number: PT0026
A:Accession: PT0026
A:Molecule type: protein
A:Residues: 1-14 <BHA>

C:Comment: This enzyme is classified as a plant cysteine protease.
C:Keywords: pyroglutamic acid
F1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 9 YPV 11
|||
Db 5 YPV 7

RESULT 33

E33098
214K exoantigen (version 2) - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: E33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: E33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 9 YPV 11
|||
Db 12 YPV 14

RESULT 34

PA0024
protein QA300050 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0024
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001
A:Accession: PA0024
A:Molecule type: protein
A:Residues: 1-15 <RAM>

A:Experimental source: seed

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 5 PFP 7
|||
Db 6 PFP 8

Db 4 PPT 6

RESULT 35
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pI 5.3.

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPT 7
Db 6 PPT 8

RESULT 36
PA0062
fumarate hydratase (EC 4.2.1.2) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0062
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A:Reference number: PA0051
A:Accession: PA0062
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 5 TES 7

RESULT 37
B61457
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
C:Species: Tetrahymena pyriformis
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C:Accession: B61457
R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purificatio
A:Reference number: A61457; MUID:90095988; PMID:2689637
A:Accession: B61457
A:Molecule type: protein
A:Residues: 1-15 <BAN>
C:Genetics:
A:Genetic code: SGC5
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
Db 11 VEP 13

Db 4 PPT 6

RESULT 38
A36527
juvenile-hormone esterase (EC 3.1.1.59) - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 03-Feb-1994
C:Accession: A36527
R:Venkatesh, K.; Abdel-Aal, Y.A.I.; Armstrong, F.B.; Roe, R.M.
J. Biol. Chem. 265, 21727-21732, 1990
A:Title: Characterization of affinity-purified juvenile hormone esterase from the pl.
A:Reference number: A36527; MUID:91072375; PMID:2254326
A:Accession: A36527
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <VEN>
C:Keywords: carboxylic ester hydrolase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 12 TES 14

RESULT 39
A49480
major immunophilin hsp56 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C:Accession: A49480
R:Yem, A.W.; Reardon, I.M.; Leone, J.W.; Heinrikson, R.L.; Deibel Jr., M.R.
Biochemistry 32, 12571-12576, 1993
A:Title: An active FK506-binding domain of 17,000 daltons is isolated following limi
A:Reference number: A49480; MUID:94072550; PMID:7504525
A:Accession: A49480
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <YEM>
A:Experimental source: thymus
A:Note: sequence extracted from NCBI backbone (NCBIP:142438)

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 7 TES 9

RESULT 40
PT0205
insulin-like growth factor-binding protein, bone - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 08-Dec-1994
C:Accession: PT0205; A33175
R:Bautista, C.M.; Baylink, D.J.; Mohan, S.
Biochem. Biophys. Res. Commun. 176, 756-763, 1991
A:Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from
A:Reference number: PT0205; MUID:91222244; PMID:1709017
A:Accession: PT0205
A:Molecule type: protein
A:Residues: 1-15 <BAU>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

```

Db          7 VEP 9
|||
RESULT 41
B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N/Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP
C/Species: Homo sapiens (man)
C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C/Accession: B45115
R/Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton, D.
J. Biol. Chem. 267, 21753-21760, 1992
A/Title: Characterization of high molecular weight FK-506 binding activities reveals a n
A/Reference number: A45115; MUID:93016131; PMID:1383226
A/Accession: B45115
A/Status: preliminary
A/Molecule type: Protein
A/Residues: 1-15 <WIE>
A/Experimental source: JURKAT cells
A/Note: sequence extracted from NCBI backbone (NCBIP:116748)
C/Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match          16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          15 TES 17
|||
Db          2 TES 4

RESULT 42
B42324
cytochrome P450c27/25 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Mar-1999
C/Accession: B42324
R/Shayig, R.M.; Avadhani, N.G.
J. Biol. Chem. 267, 2421-2428, 1992
A/Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mitoc
ap.
A/Reference number: A42324; MUID:92129322; PMID:1733943
A/Accession: B42324
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-16 <SHA>
A/Note: sequence extracted from NCBI backbone (NCBIN:78408, NCBIP:88990)
C/Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology
C/Keywords: heme; transmembrane protein

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          8 KYP 10
|||
Db          10 KYP 12

RESULT 43
C45133
casein kinase II (EC 2.7.1.1-) alpha chain - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Jun-1996
C/Accession: C45133
R/Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.
J. Biol. Chem. 267, 23789-23796, 1992
A/Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the asso
A/Reference number: A45133; MUID:93054738; PMID:1331100
A/Accession: C45133
A/Status: preliminary
A/Molecule type: protein

A/Residues: 1-16 <OUI>
A/Experimental source: endoplasmic reticulum, pancreas
A/Note: sequence extracted from NCBI backbone (NCBIP:118799)
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protei

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          12 EPF 14
|||
Db          6 EPF 8

RESULT 44
I40065
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C/Species: Buchnera aphidicola
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C/Accession: I40065
R/Rouhbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A/Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (er
A/Reference number: I40065; MUID:95212914; PMID:7535281
A/Accession: I40065
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718
C/Genetics:
A/Gene: aroB
C/Keywords: oxidoreductase

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 FPK 8
|||
Db          9 FPK 11

RESULT 45
C53113
Lys-gingipain form 2, 17K - Porphyromonas gingivalis (fragment)
N/Alternate names: lysine-specific cysteine proteinase 2, 17K
C/Species: Porphyromonas gingivalis
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C/Accession: C53113
R/Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A/Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isc
A/Reference number: A53113; MUID:94103245; PMID:8276827
A/Accession: C53113
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <PIK>
A/Experimental source: H66
A/Note: sequence extracted from NCBI backbone (NCBIP:141693)

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          14 FTE 16
|||
Db          3 FTE 5

RESULT 46
S05671
hirudin Ia - medicinal leech (fragment)

```

N:Alternate names: thrombin inhibitor
 C:Species: Hirudo medicinalis (medicinal leech)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Jul-1998
 C:Accession: S05671
 R:Scharf, M.; Engels, J.; Tripiet, D.
 FEBS Lett. 255, 105-110, 1989

A:Title: Primary structures of new 'iso-hirudins'.
 A:Reference number: S05671; MUID:90005945; PMID:2792365
 A:Accession: S05671
 A:Molecule type: protein
 A:Residues: 1-17 <SCH>
 C:Superfamily: thrombin inhibitor
 C:Keywords: anticoagulant; serine proteinase inhibitor; sulfoprotein
 F:6-14/Disulfide bonds: #status predicted

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 7 TES 9

RESULT 47
 S05033
 photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)
 N:Alternate names: photosystem II 5K protein
 C:Species: Synechococcus sp.
 C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C:Accession: S05033
 R:Ikeuchi, M.; Koike, H.; Inoue, Y.
 FEBS Lett. 251, 155-160, 1989

A:Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
 A:Reference number: S05030
 A:Molecule type: protein
 A:Accession: S05033
 A:Residues: 1-17 <IKE>
 A>Note: the source is designated as Synechococcus vulcanus
 C:Genetics:
 A:Gene: psbL
 C:Keywords: photosynthesis; photosystem II; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
 ||||
 Db 9 PVE 11

RESULT 48
 B31769
 T-cell receptor delta-2 chain J region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Nov-1999
 C:Accession: B31769
 R:Loch, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988
 A:Title: Human T-cell-receptor delta chain: genomic organization, diversity, and expression
 A:Reference number: A94221; MUID:8901766; PMID:2974163
 A:Accession: B31769
 A:Molecule type: DNA
 A:Residues: 1-17 <LOH>
 A:Cross-references: GB:L36386; NID:g540455; PIDN:AAA61108.1; PID:g540456
 C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11-VEP 13

Db 15 VEP 17
 ||||

RESULT 49
 G85956
 hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain 1)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: G85956
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Ma'iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamocousis, K.; Apodis, Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: G85956
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-17 <STO>
 A:Cross-references: GB:AE005174; NID:gl2517539; PIDN:AGS8115.1; GSPDB:GN00145; UWGP
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z4331

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
 ||||
 Db 6 PFP 8

RESULT 50
 S29264
 ovohemerythrin - duck leech (fragment)
 N:Alternate names: 14K yolk protein
 C:Species: Theromyzon tessulatum (duck leech)
 C>Date: 19-Mar-1997 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: S29264
 R:Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.
 Eur. J. Biochem. 209, 563-569, 1992
 A:Title: Ovohemerythrin, a major 14-kDa yolk protein distinct from vitellogenin in 1
 A:Reference number: S29264; MUID:93049299; PMID:1425663
 A:Accession: S29264
 A:Molecule type: protein
 A:Residues: 1-18 <BAE>
 A:Cross-references: PIDN:AA23969.1; PID:g258980
 C:Superfamily: hemerythrin
 C:Keywords: egg yolk; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EFP 14
 ||||
 Db 5 EFP 7

RESULT 51
 H64711
 hypothetical protein HP1536 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: H64711
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McK son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: H64711
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <TOM>
A;Cross-references: GB:AE000651; GB:AE000511; NID:G2314708; PIDN:AA08578.1; PID:G2314711

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKY 9
Db 15 PKY 17

RESULT 52
S58277
insulin-like growth factor receptor type II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S58277
R;Smrzka, O.W.; Stoger, R.; Kurbauer, R.; Fae, I.; Fischer, G.F.; Barlow, D.P.
submitted to the EMBL Data Library, January 1995
A;Description: Conservation of a methylation imprint and a putative imprinting box at the
A;Reference number: S58277
A;Accession: S58277
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <SMR>
A;Cross-references: EMBL:X83702; NID:G929644; PIDN:CAA56675.1; PID:G929645
C;Keywords: growth factor receptor

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
Db 5 TES 7

RESULT 53
S71592
serine proteinase inhibitor, 31K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C;Accession: S71592
R;Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.
Arch. Biochem. Biophys. 317, 311-314, 1995
A;Title: Novel extracellular matrix-associated serine proteinase inhibitors from human s
A;Reference number: S71592; MUID:95177668; PMID:7872799
A;Accession: S71592
A;Molecule type: protein
A;Residues: 1-18 <RAO>
C;Function:
A;Description: involved in turnover of connective tissues
C;Keywords: serine proteinase inhibitor

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14
Db 5 EPF 7

RESULT 54
I46653
T-cell receptor delta-chain J-delta-2 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 30-May-1997
C;Accession: I46653

R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-c
A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I46653
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-18 <YAN>
A;Cross-references: GB:DA9561; NID:G1041174; PID:G1041175
C;Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13
Db 16 VEP 18

RESULT 55
A59137
protein Pil - golden needle mushroom (fragment)
C;Species: Flammulina velutipes (golden needle mushroom)
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: A59137
R;Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A;Description: Differences of proteins expressed in the fruiting dikaryon and the nor
A;Reference number: A59137
A;Accession: A59137
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <SAK>

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFT 15
Db 15 PFT 17

RESULT 56
BWSMCN
cinnamycin - Streptovorticillium cinnamoneum
N;Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C;Species: Streptovorticillium cinnamoneum
C;Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C;Accession: A45767
R;Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase,
J. Antibiot. 42, 837-845, 1989
A;Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and propertie
A;Reference number: A45767; MUID:89291558; PMID:2544544
A;Accession: A45767
A;Molecule type: protein
A;Residues: 1-19 <NAR>
R;Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A;Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structu
A;Reference number: A53359
A;Contents: annotation; strain L337-2
C;Superfamily: cinnamycin precursor
C;Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F;1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F;4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F;5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F;6-19/Cross-link: (2xi,9S)-lysinoalanine (Ser-Lys) #status experimental
F;15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
 ||||
 Db 9 PFT 11

RESULT 57

S59485
 A:Title: hyroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)
 C:Species: Phaseolus vulgaris (kidney bean)
 C:Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 05-Dec-1998
 C:Accession: S59485; S59484; S59483
 R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to different
 A:Reference number: S59481; MUID:96011753; PMID:7548825
 A:Accession: S59485
 A:Molecule type: protein
 A:Residues: 1-19 <WOJ>
 A:Note: hyroxyproline-rich cell wall glycoprotein, 42K
 A:Accession: S59484
 A:Molecule type: protein
 A:Residues: 1-15 <WOW>
 A:Note: hyroxyproline-rich cell wall glycoprotein, 84K
 A:Accession: S59483
 A:Molecule type: protein
 A:Residues: 1-14 <WOP>
 A:Note: hyroxyproline-rich cell wall glycoprotein, 136K, minor component
 C:Superfamily: proline-rich protein 3
 C:Keywords: glycoprotein; hydroxyproline
 F:6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
 ||||
 Db 6 PVE 8

RESULT 58

S43641
 A:Title: carboxylesterase (EC 3.1.1.1), thermostable - Alicyclobacillus acidocaldarius (fragment)
 C:Species: Alicyclobacillus acidocaldarius
 C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
 C:Accession: S43641
 R:Manco, G.; di Gennaro, S.; de Rosa, M.; Rossi, M.
 Eur. J. Biochem. 221, 965-972, 1994
 A:Title: Purification and characterization of a thermostable carboxylesterase from the
 A:Reference number: S43641; MUID:94237161; PMID:8181479
 A:Accession: S43641
 A:Molecule type: protein
 A:Residues: 1-19 <MAN>
 A:Experimental source: strain MT3
 A:Note: the source is designated as Bacillus acidocaldarius
 C:Keywords: carboxylic ester hydrolase; monomer

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
 ||||
 Db 4 PVE 6

RESULT 59

C56661
 A:Title: S-locus specific glycoprotein (allele S9) - wild cabbage (fragment)
 C:Species: Brassica oleracea (wild cabbage)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C:Accession: C56661
 R:Gaude, T.; Denoroy, L.; Dumas, C.
 Electrophoresis 12, 646-653, 1991
 A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal
 A:Reference number: A56661; MUID:92090397; PMID:1752245
 A:Accession: C56661
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <GAU>
 A:Experimental source: stigma extracts, var. acephala
 A:Note: sequence extracted from NCBI backbone (NCBIP:72301)
 C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in
 C:Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 7 TES 9

RESULT 60

PQ0492
 A:Title: self-incompatibility locus glycoprotein epsilon - wild cabbage (fragment)
 C:Species: Brassica oleracea (wild cabbage)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-1995
 C:Accession: PQ0492
 R:Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
 Plant Cell 5, 75-86, 1993
 A:Title: Expression of a self-incompatibility gene in a self-compatible line of Bras
 A:Reference number: JQ1733; MUID:93177215; PMID:8439745
 A:Accession: PQ0492
 A:Molecule type: protein
 A:Residues: 1-19 <GAU>
 A:Experimental source: stigma, var. acephala P57S1
 C:Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 7 TES 9

RESULT 61

A61144
 A:Title: probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi (fragment)
 C:Species: Trypanosoma cruzi
 C:Date: 10-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 24-Feb-1995
 C:Accession: A61144
 R:Bua, J.; Bontempi, E.J.; Levin, M.; Orn, A.; Velasco, D.; Moreno, M.; Levi-Yeyati,
 Exp. Parasitol. 72, 54-62, 1991
 A:Title: Trypanosoma cruzi: cellular and antibody response against the parasite in m
 A:Reference number: A61144; MUID:91130571; PMID:1993465
 A:Accession: A61144
 A:Molecule type: mRNA
 A:Residues: 1-19 <BUA>

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
 ||||
 Db 17 VEP 19

RESULT 62

C39305


```

neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997
C:Accession: C39305
R:Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
Toxicon 29, 1225-1233, 1991
A>Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria
A:Reference number: A39305; MUID:92196803; PMID:1801316
A:Accession: C39305
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <REZ>
C:Keywords: neurotoxin

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
   |||
Db 7 ESQ 9

RESULT 63
I46654
T-cell receptor delta-chain J-delta-3 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46654
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A>Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46654
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-19 <YAN>
A:Cross-references: GB:D49562; NID:gl041176; PIDN:BAA08506.1; PID:gl041177
C:Keywords: T-cell receptor

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
   |||
Db 17 VEP 19

RESULT 64
S69166
ferredoxin b - Japanese radish (fragments)
C:Species: Kaiware daikon (Japanese radish)
C>Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C:Accession: S69166
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A>Title: Four ferredoxins from Japanese radish leaves.
A:Reference number: S69164; MUID:95168867; PMID:7864635
A:Accession: S69166
A:Molecule type: protein
A:Residues: 1-19 <OBA>
C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
   |||
Db 13 HKE 15

neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997
C:Accession: C39305
R:Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
Toxicon 29, 1225-1233, 1991
A>Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria
A:Reference number: A39305; MUID:92196803; PMID:1801316
A:Accession: C39305
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <REZ>
C:Keywords: neurotoxin

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
   |||
Db 7 ESQ 9

RESULT 63
I46654
T-cell receptor delta-chain J-delta-3 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46654
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A>Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46654
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-19 <YAN>
A:Cross-references: GB:D49562; NID:gl041176; PIDN:BAA08506.1; PID:gl041177
C:Keywords: T-cell receptor

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
   |||
Db 17 VEP 19

RESULT 64
S69166
ferredoxin b - Japanese radish (fragments)
C:Species: Kaiware daikon (Japanese radish)
C>Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C:Accession: S69166
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A>Title: Four ferredoxins from Japanese radish leaves.
A:Reference number: S69164; MUID:95168867; PMID:7864635
A:Accession: S69166
A:Molecule type: protein
A:Residues: 1-19 <OBA>
C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
   |||
Db 13 HKE 15

```

```

RESULT 65
S11611
ribosomal protein S2 [validated] - Halobacterium salinarum (fragment)
N:Alternate names: ribosomal protein HS5A
C:Species: Halobacterium salinarum
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C:Accession: S11611
R:Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A>Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archa
A:Reference number: S11609
A:Accession: S11611
A:Molecule type: protein
A:Residues: 1-19 <YAG>
A>Note: the protein is designated as ribosomal protein HS5A
C:Keywords: protein biosynthesis; ribosome

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
   |||
Db 7 TES 9

RESULT 66
S06466
T-cell receptor alpha chain J segment (DO) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 06-Jun-1997
C:Accession: S06466
R:Rague, J.; Blackman, M.; Born, W.; Marrack, P.; Kappler, J.; Palmer, E.
Nucleic Acids Res. 16, 11355-11364, 1988
A>Title: The structure of V-alpha and J-alpha segments in the mouse.
A:Reference number: S06466; MUID:89083566; PMID:2849763
A:Accession: S06466
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 <YAG>
A:Experimental source: strain Balb/c
C:Genetics:
A:Map position: 14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; T-cell receptor
F:1-18/Domain: J segment <JSE>
F:19-20/Domain: C region (fragment) <CRE>

Query Match      16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
   |||
Db 16 VEP 18

RESULT 67
JP0059
ribosomal protein L30 - Thermoactinomyces intermedius (fragment)
C:Species: Thermoactinomyces intermedius
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03-May-1996
C:Accession: JP0059
R:Ochi, K.
submitted to JIPID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0059
A:Molecule type: protein
A:Residues: 1-20 <OCH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

```

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ESQ 18
Db 17 ESQ 19

RESULT 68
PL0145
Carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydoflava (fr
C/Species: Pseudomonas carboxydoflava
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C/Accession: PL0145
R/Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A/Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop
A/Reference number: PL0138; MUID:90055678; PMID:2818128
A/Accession: PL0145
A/Molecule type: protein
A/Residues: 1-20 <K2A>
C/Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C/Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 VEP 13
Db 18 VEP 20

RESULT 69
PQ0046
citrate (sl)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)
N/Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloaceta
C/Species: Streptomyces hygroscopicus
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-May-2000
C/Accession: PQ0046
R/Shimotomo, K.W.; Imai, S.; Murakami, T.; Seto, H.
Agric. Biol. Chem. 54, 463-470, 1990
A/Title: Purification and characterization of citrate synthase from Streptomyces hygrosc
A/Reference number: PS0106; MUID:90334852; PMID:1368511
A/Accession: PQ0046
A/Molecule type: protein
A/Residues: 1-20 <SHI>
A/Experimental source: strain SF-1293
C/Comment: This enzyme catalyzes the synthesis of citric acid.
C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 YPV 11
Db 16 YPV 18

RESULT 70
S29635
jacalin beta chain - Artocarpus tonkinensis
C/Species: Artocarpus tonkinensis
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C/Accession: S29635
R/Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
A/Reference number: S29635; MUID:93152601; PMID:8427879
A/Accession: S29635
A/Status: preliminary

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 YPV 11
Db 16 YPV 18

RESULT 70
S29635
jacalin beta chain - Artocarpus tonkinensis
C/Species: Artocarpus tonkinensis
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C/Accession: S29635
R/Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
A/Reference number: S29635; MUID:93152601; PMID:8427879
A/Accession: S29635
A/Status: preliminary

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ESQ 18
Db 6 ESQ 8

RESULT 71
B30208
hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C/Accession: B30208
R/Faluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988
A/Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a prote
A/Reference number: A30208; MUID:88234499; PMID:2967496
A/Accession: B30208
A/Molecule type: DNA
A/Residues: 1-20 <PAL>
A/Cross-references: GB:J03262

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PFP 7
Db 6 PFP 8

RESULT 72
S58382
hypothetical protein 1 - human
C/Species: Homo sapiens (man)
C/Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C/Accession: S58382
R/Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. 23, 2815-2822, 1995
A/Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis in
A/Reference number: S58382; MUID:95388493; PMID:7659502
A/Accession: S58382
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-20 <DIR>
A/Cross-references: EMBL:X83705; NID:g951023; PIDN:CAA58678.1; PID:g951024

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PFP 7
Db 12 PFP 14

RESULT 73
I46652
T-cell receptor delta-chain J-delta-1 segment - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C/Accession: I46652
R/Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A/Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-
A/Reference number: I46623; MUID:95363165; PMID:7636249
A/Accession: I46652
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-20 <YAN>
A:Cross-references: GB:D49560; NID:g1041172; PIDN:BAA08504.1; PID:g1041173
C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13
|||
Db 18 VEP 20

RESULT 74

A41439
acid ribonuclease (EC 3.1.1.-) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
C:Accession: A41439
R:Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A:Title: Purification of acid ribonucleases from bovine spleen.
A:Reference number: A41439; MUID:88227899; PMID:3131316
A:Accession: A41439
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-20 <OHG>
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPK 8
|||
Db 12 FPK 14

RESULT 75

GKHU
growth-modulating peptide - human
C:Species: Homo sapiens (man)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:858356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth of others.
C:Superfamily: unassigned animal peptides

Query Match 11.1%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HK 2
||
Db 2 HK 3

Search completed: November 25, 2003, 19:36:08
Job time : 12.3488 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-22
Perfect score: 18
Sequence: 1 HKEMPPFKYVPEPTESQ 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	16.7	7	1	IGAO_DACDE
2	3	16.7	7	1	WHA3_ACHFU
3	3	16.7	10	1	WHA3_HUMAN
4	3	16.7	11	1	EPG_GLOPA
5	3	16.7	13	1	LMT4_LOGMI
6	3	16.7	13	1	UHA3_CANFA
7	3	16.7	13	1	YPE2_LACLC
8	3	16.7	14	1	CAL1_CALGI
9	3	16.7	15	1	ESTJ_MANSE
10	3	16.7	15	1	UC08_MAIZE
11	3	16.7	15	1	UC16_MAIZE
12	3	16.7	15	1	UC25_MAIZE
13	3	16.7	16	1	H5_COTJA
14	3	16.7	16	1	ODEB_SOLTU
15	3	16.7	17	1	ITHB_HIRME
16	3	16.7	17	1	PSBL_SYNVU
17	3	16.7	18	1	D7AI_ACASC
18	3	16.7	18	1	HEMH_THETS
19	3	16.7	18	1	LCTN_LAMGL
20	3	16.7	19	1	DURA_STRGV
21	3	16.7	19	1	TX3_PHONI
22	3	16.7	20	1	CSYJ_STRHY
23	3	16.7	20	1	SB60_MAIZE
24	2	11.1	3	1	GRWM_HUMAN
25	2	11.1	5	1	PAP2_PARMA
26	2	11.1	5	1	RE31_LITRU
27	2	11.1	5	1	RE32_LITRU
28	2	11.1	5	1	SUGA_ACHDO
29	2	11.1	6	1	ASF2_LACSN
30	2	11.1	7	1	ALL3_CARMA
31	2	11.1	7	1	CARP_MYTED
32	2	11.1	7	1	E105_LITRU
33	2	11.1	7	1	FAR1_HELTI

RESULT 1

34	2	11.1	7	1	PAR5_HIRME	P42564	hirudo medi
35	2	11.1	7	1	UF04_MOUSE	P38642	mus musculus
36	2	11.1	7	1	UN06_PIPES	P81675	pinus pinas
37	2	11.1	7	1	WWA1_ACHFU	P35919	achatina fu
38	2	11.1	8	1	AKH_LIBAU	P25418	libellula a
39	2	11.1	8	1	AKH_TABAT	P14595	tabanus atr
40	2	11.1	8	1	ANG2_BOTJA	Q10582	bothrops ja
41	2	11.1	8	1	CLP_THICU	P80488	thiobacillu
42	2	11.1	8	1	HTF2_PERAM	P04549	periplaneta
43	2	11.1	8	1	LMT2_LOGMI	P22396	locusta mig
44	2	11.1	8	1	LPK_LEUMA	P13049	leucophaea
45	2	11.1	8	1	ORMY_ORCLI	P82455	orconectes
46	2	11.1	8	1	PEK2_PERAM	P82692	periplaneta
47	2	11.1	8	1	PK3_PERAM	P82618	periplaneta
48	2	11.1	8	1	RS7_MYCIT	P33564	mycobacteri
49	2	11.1	8	1	UC26_MAIZE	P80632	zea mays (m
50	2	11.1	8	1	UF06_MOUSE	P38644	mus musculus
51	2	11.1	8	1	UPA1_HUMAN	P30087	homo sapien
52	2	11.1	8	1	UPA2_HUMAN	P30096	homo sapien
53	2	11.1	9	1	CCAP_CARMA	P38556	carcinus ma
54	2	11.1	9	1	CONO_CONGE	P05486	conus geogr
55	2	11.1	9	1	COXE_THUOB	P80975	thunus obe
56	2	11.1	9	1	FAR2_CALVO	P41857	calliphora
57	2	11.1	9	1	FAR3_CALVO	P41858	calliphora
58	2	11.1	9	1	FAR4_PENMO	P83313	penaeus mon
59	2	11.1	9	1	FARS_PENMO	P83320	penaeus mon
60	2	11.1	9	1	FIBB_MACFU	P19345	macaca fusc
61	2	11.1	9	1	FRF1_SARBU	P83350	sarcophaga
62	2	11.1	9	1	HUTU_KLEAE	P12381	klebsiella
63	2	11.1	9	1	KNL3_BOMVA	P83058	bombina var
64	2	11.1	9	1	LMT3_LOGMI	P41489	locusta mig
65	2	11.1	9	1	OXYA_SCYCA	P42996	scyllorhinu
66	2	11.1	9	1	OXIF_SCYCA	P42997	scyllorhinu
67	2	11.1	9	1	OXIV_SQUAC	P43000	squalus aca
68	2	11.1	9	1	SAMP_MUSCA	P19095	mustelus ca
69	2	11.1	9	1	THYF_PIG	P01255	sus scrofa
70	2	11.1	9	1	UHA2_HUMAN	P40929	homo sapien
71	2	11.1	9	1	UN19_CLOPA	P81355	clostridium
72	2	11.1	9	1	UPA3_HUMAN	P30089	homo sapien
73	2	11.1	10	1	ANG1_BOTJA	Q10581	bothrops ja
74	2	11.1	10	1	ANGT_BOVIN	P10107	bos taurus
75	2	11.1	10	1	ANGT_CHICK	P10108	gallus gall
76	2	11.1	10	1	EPF_VIPAS	P1351	vipera aspi
77	2	11.1	10	1	COXA_ONCMY	P80328	oncorhynch
78	2	11.1	10	1	FAR6_PANRE	P82660	panagrellus
79	2	11.1	10	1	GAJU_HUMAN	P01358	homo sapien
80	2	11.1	10	1	GON2_CHICK	P37043	gallus gall
81	2	11.1	10	1	HTF1_ROMMI	P18110	romalea mic
82	2	11.1	10	1	HTF2_CARMO	P11385	carausius m
83	2	11.1	10	1	HTF_TABAT	P14596	tabanus atr
84	2	11.1	10	1	LPK2_LOGMI	P41488	locusta mig
85	2	11.1	10	1	ODP2_BOVIN	P11180	bos taurus
86	2	11.1	10	1	PNEU_HUMAN	P22103	homo sapien
87	2	11.1	10	1	PNEU_RAT	P21996	rattus norv
88	2	11.1	10	1	PPCK_PASHE	P80525	fasciola he
89	2	11.1	10	1	PKK_LOGMI	P83382	locusta mig
90	2	11.1	10	1	Q20B_COMTE	P80465	comamonas t
91	2	11.1	10	1	RL16_ACHLA	P29221	acholeplasm
92	2	11.1	10	1	RT02_BOVIN	P29221	acholeplasm
93	2	11.1	10	1	SLAP_BACTG	P49325	bacillus th
94	2	11.1	10	1	SYK_CAMUP	Q46464	campylobact
95	2	11.1	10	1	TKNB_CHICK	P19851	gallus gall
96	2	11.1	10	1	TKNB_ONCMY	P28500	oncorhynch
97	2	11.1	10	1	TKNB_RANRI	P29135	rana ridibu
98	2	11.1	10	1	TKU1_UREUN	P40751	urechis uni
99	2	11.1	10	1	UH05_RAT	P56573	rattus norv
100	2	11.1	10	1	UPA5_HUMAN	P30091	homo sapien

ALIGNMENTS

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ICAO_DACDE
ID IGAO_DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]_TaxID=5132;
RP SEQUENCE.
RA Avidad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides."
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC BINDING TO ITS PROSTHETIC COPPER GROUP.
DR PIR; A01341; XEYDGD.
KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
DB 5 TES 7

RESULT 2
WVA3_ACHFU
ID WVA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]_TaxID=6530;
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93365912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica."
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB 2 KEM 4

RESULT 3
UHA3_HUMAN
ID UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994."
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
DB 2 VEP 4

RESULT 4
EFG_CLOPA
ID EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]_TaxID=1501;
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
DR InterPro; IPR000795; EF_GTPbind.
KW PROSITE; PS00301; EFACOR_GTP; PARTIAL.
FT ELONGATION factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71FD9C33B17 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
DB 1 KYP 3

RESULT 5
LMT4_LOCMI
ID LMT4_LOCMI STANDARD; PRT; 13 AA.

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AC P41490;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytotropin 4 (LOW-MT-4).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytotropin peptide family.;
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY). LOW-MT IV SEEMS TO BE A MORE POTENT MUSCLE
CC STIMULATOR THAN LOW-MT I, II AND III.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; B61620; B61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 13 13
FT AMIDATION.
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6
DB 7 MPF 9

RESULT 6
UHA3 CANFA
ID UHA3 CANFA STANDARD; PRT; 13 AA.
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9. ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
DB 7 PVE 9
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RESULT 7
YPE2_LACLC
ID YPE2_LACLC STANDARD; PRT; 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5'region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; PubMed=8188586;
RA Mierau I., Haandrikman A.J., Veltrop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pept and construction of a chromosomal
RT deletion mutant";
RL J. Bacteriol. 176:2854-2861(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L27596; AAA20625.1; -
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 5 EPF 7

RESULT 8
CAL1 CALGI
ID CAL1 CALGI STANDARD; PRT; 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calotropin DI (EC 3.4.22.-) (Fragment).
OS Calotropis gigantea (Madar) (Bowstring hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Gentianales; Apocynaceae; Asclepiadoideae;
OC Asclepiadeae; Calotropis.
OX NCBI_TaxID=4066;
RN [1]
RP SEQUENCE.
RA Bhattacharya D., Sengupta A., Sinha N.K.;
RT "Chemical modification and amino terminal sequence of calotropin DI
RT from Calotropis gigantea.";
RL Phytochemistry 26:633-636(1987).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR PIR; PT0026; PT0026.
DR MEROPS; C01.011; -.
DR InterPro; IPR000169; SHprot_accsite.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOI_PROTEASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
PYRROLIDONE CARBOXYLIC ACID.
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FT  NON_TER  14  14
SQ  SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 YPV 11
DB  5 YPV 7

RESULT 9
ESTJ MANSE
ID  ESTJ MANSE STANDARD; PRT; 15 AA.
AC  P1985;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  01-FEB-1994 (Rel. 28, Last annotation update)
DE  Juvenile hormone esterase (EC 3.1.1.59) (JH esterase) (Fragment).
OS  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Spingioidea;
OC  Spingidae; Spinginae; Manduca.
OX  NCBI_TaxID=7130;
RN  [1]
RP  SEQUENCE.

RC  TISSUE=Larval plasma;
RX  MEDLINE=91072375; PubMed=2254326;
RA  Venkatesh K., Abdel-Aal Y.A.I., Armstrong F.B., Roe R.M.;
RT  Characterization of affinity-purified juvenile hormone esterase from
RT  the plasma of the tobacco hornworm, Manduca sexta.;
RL  J. Biol. Chem. 265:21727-21732(1990).
CC  -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF
CC  JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
CC  ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
CC  -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
CC  trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-
CC  epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
CC  -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC  PIR; A36527; A36527.
DR  InterPro; IPR02018; CarbesteraseB.
DR  PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR  PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW  Hydrolase; Serine esterase.
FT  NON_TER  15
SQ  SEQUENCE 15 AA; 1659 MW; D321EA432E58B848 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 TES 17
DB  12 TES 14

RESULT 10
UC08 MAIZE
ID  UC08 MAIZE STANDARD; PRT; 15 AA.
AC  P80614;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE  (Fragment).
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]
RP  SEQUENCE.

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RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
RT  genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC  -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC  family.
DR  Maize-2DPAGE; P80614; COLEOPTILE.
DR  MaizeDB; 123934; -.
FT  NON_TER  1
FT  NON_TER  15
SQ  SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

Query Match      16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 YPV 11
DB  8 YPV 10

RESULT 11
UC16 MAIZE
ID  UC16 MAIZE STANDARD; PRT; 15 AA.
AC  P80622;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 308)
DE  (Fragment).
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]
RP  SEQUENCE.

RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
RT  genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 5.9, ITS MW IS: 18.6 kDa.
DR  Maize-2DPAGE; P80622; COLEOPTILE.
DR  MaizeDB; 123948; -.
FT  NON_TER  1
FT  NON_TER  15
SQ  SEQUENCE 15 AA; 1796 MW; D331A518F7440BE7 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 VEP 13
DB  12 VEP 14

RESULT 12
UC25 MAIZE
ID  UC25 MAIZE STANDARD; PRT; 15 AA.
AC  P80631;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE  (Fragment).

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OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Ricciardi F., Morin C., Danerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.
 CC Maize-2DPAGE; P80631; COLEOPTILE.
 DR MaizeDB; 123957; -.
 FT NON TER 1 15
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CFOCE1614D0 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 PVE 12
 Db ||||
 10 PVE 12
 RESULT 13
 ID_H5_COTJA STANDARD; PRT; 16 AA.
 AC P8638;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Histone H5 (Fragment).
 OS Coturnix coturnix Japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277939; PubMed=962913;
 RA Seligy V., Roy C., Dove M., Yaguchi M.;
 RT "Species variability of N-terminal sequence of avian erythrocyte-
 RT specific histone H5.";
 RL Biochem. Biophys. Res. Commun. 71:196-202(1976).
 CC -1- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING
 CC NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER
 CC ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: ERYTHROID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
 KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.
 FT NON TER 16 16
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 TES 17
 Db ||||
 1 TES 3
 RESULT 14
 ID_ODPB_SOLTU STANDARD; PRT; 16 AA.
 AC P81419;

DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
 DE (EC 1.2.4.1) (PDHE1-B) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Romano; TISSUE=Tuber;
 RX MEDLINE=98399821; PubMed=9729464;
 RA Millar A.H., Knorr C., Leaver C.J., Hill S.A.;
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and
 RT identification of catalytic components in potato.";
 RL Biochem. J. 334:571-576(1998).
 CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
 CC multiple copies of three enzymatic components: pyruvate
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
 CC lipoamide dehydrogenase (E3).
 CC -1- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
 CC acetyldihydrolipoamide + CO(2).
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
 CC -1- SUBUNIT: Tetramer of two alpha and two beta subunits (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
 KW Phosphorylation; Mitochondrion.
 FT NON TER 16 16
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KEM 4
 Db ||||
 5 KEM 7
 RESULT 15
 ID_ITHB_HIRME STANDARD; PRT; 17 AA.
 AC P28502;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hirudin IA (Fragment).
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'.";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: Hirudin is a potent thrombin-specific protease
 CC inhibitor. It forms a stable non-covalent complex with alpha-
 CC thrombin, thereby abolishing its ability to cleave fibrinogen.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 CC PIR; S05671; S05671.
 DR HSP; P01050; IHC.
 DR InterPro; IPR000429; Hirudin.
 DR Pfam; PF00713; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT NON TER 17 17
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1877 MW; 8904C6786C301CE7 CRC64;


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Query Match          16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
DB 7 TES 9

RESULT 16
ID PSBL_SYNNU STANDARD; PRT; 17 AA.
AC P12241;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II reaction center L protein (PSII 5 kDa protein)
DE (Fragment).
GN PSBL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RA Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of psbI and psbL gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160(1989).
CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
CC B559.
CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
CC PIR; S05033; S05033.
DR InterPro: IPR003372; PSII_PsbL.
DR Pfam; PF02419; PSBL; 1.
KW Photosynthesis; Photosystem II.
FT NON TER 17
SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match          16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
DB 9 PVE 11

RESULT 17
D7A1_ACASC STANDARD; PRT; 18 AA.
AC PB3402;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)
DE (Fragment).
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.
RC TISSUE=Liver;
RX MEDLINE=21956475; PubMed=11959129;
RA Tang W.-K., Cheng C.H.K., Fong W.-P.;
RT "First purification of the antiquitin protein and demonstration of its
RT enzymatic activity.";
RL FEBS Lett. 516:183-186(2002).
CC -!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid +
CC NADH.

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CC -!- SUBUNIT: Homotetramer.
CC -!- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is
CC 2.0 mM and Vmax is 1.3 micromol/min x mg enzyme.
CC -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
DR GO; GO:0004029; F:aldehyde dehydrogenase (NAD+) activity; IDA.
DR GO; GO:0006081; P:aldehyde metabolism; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PARTIAL.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; PARTIAL.
KW Oxidoreductase; NAD.
FT NON TER 18
SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;

Query Match          16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
DB 8 PKY 10

RESULT 18
HEMH_THETS STANDARD; PRT; 18 AA.
ID PS0155;
AC P80155;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ovohemerythrin (vp14) (Fragment).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Oocyte;
RX MEDLINE=93049299; PubMed=1425663;
RA Baert J.-L., Britel M., Sautiere P., Malecha J.;
RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from
RT vitellogenin in leech.";
RL Eur. J. Biochem. 209:563-569(1992).
CC -!- FUNCTION: MAJOR YOLK PROTEIN. THIS IRON PROTEIN MAY PLAY A ROLE
CC IN THE DETOXIFICATION OF FREE IRON AFTER A BLOOD MEAL.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the hemerythrin family.
DR PIR; S29264; S29264.
DR HSP; P02247; 2MHR.
DR InterPro; IPR002063; Hemerythrin.
DR Pfam; PF01814; Hemerythrin; 1.
DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
KW Oxygen transport; Metal-binding; Iron; Yolk.
FT NON TER 18
SQ SEQUENCE 18 AA; 2368 MW; 33397EE587C81F1 CRC64;

Query Match          16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 5 EPF 7

RESULT 19
LCTN_LAMGL STANDARD; PRT; 18 AA.
ID P83315;
AC P83315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lactophorin (Whey protein) (Fragment).
OS Lama glama (Llama).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=20000588; PubMed=10531593;
 RA Kappeler S., Farah Z., Puhon Z.;
 RT "Alternative splicing of lactophorin mRNA from lactating mammary gland
 of the camel (Camelus dromedarius).";
 RL J. Dairy Sci. 82:1-10(1999).
 CC -!- SIMILARITY: BELONGS TO THE PP3 / GLYCAM-1 FAMILY.
 DR GO:0005576; C:extracellular; ISS.
 DR Pfam: PF05242; GLYCAM-1; 1.
 FT NON TER
 FT 18
 SQ SEQUENCE 18 AA; 2079 MW; CD59615E5B236AC6 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred.No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ESQ 18
 DB [1]
 DB 15 ESQ 17
 RESULT 20
 DURA_STRGV STANDARD; PRT; 19 AA.
 AC P36504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Lantibiotic duramycin (leucopeptin) (Antibiotic P448009).
 OS Streptovorticillium griseocephalum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=68215;
 RN [1]
 RP SEQUENCE, AND STRUCTURE BY NMR.
 RC STRAIN=PA-48009;
 RX MEDLINE=91107438; PubMed=2272918;
 RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
 RA Itazaki H.;
 RT "The structure of P448009: the revised structure of duramycin.";
 RL J. Antibiot. 43:1421-1430(1990).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=91107436; PubMed=2125590;
 RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycins B and C, two new lantionine containing antibiotics as
 inhibitors of phospholipase A2. Structural revision of duramycin and
 cinnamycin.";
 RL J. Antibiot. 43:1403-1412(1990).
 CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
 Thr, and Ser into dehydrated AA and the formation of thioether
 bonds with cysteine or the formation of dialkylamine bonds with
 lysine. This is followed by membrane translocation and cleavage of
 the modified precursor.
 CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
 FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
 FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
 FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
 FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred.No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PFT 15

Db [1]
 9 PFT 11
 RESULT 21
 TX3_PHONI STANDARD; PRT; 19 AA.
 AC P31010;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotoxin Tx3 (Fragment).
 OS Phoneutria nigriventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
 OX NCBI_TaxID=6918;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom; PubMed=1801316;
 RX MEDLINE=92196803; PubMed=1801316;
 RA Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;
 RT "Isolation of neurotoxic peptides from the venom of the 'armed'
 spider Phoneutria nigriventer.";
 RL Toxicon 29:1225-1233(1991).
 CC -!- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.
 DR PIR; C39305; C39305.
 KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor.
 FT NON TER
 FT 19
 SQ SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred.No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ESQ 18
 DB [1]
 DB 7 ESQ 9
 RESULT 22
 CISY_STRHY STANDARD; PRT; 20 AA.
 ID CISY_STRHY STANDARD; PRT; 20 AA.
 AC P20903;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Citrate synthase (EC 2.3.3.1) (Fragment).
 GN GUTA.
 OS Streptomyces hygroscopicus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1912;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=SF1293;
 RX MEDLINE=90334852; PubMed=1368511;
 RA Shimotohno K.W., Inai S., Murakami T., Seto H.;
 RT "Purification and characterization of citrate synthase from
 Streptomyces hygroscopicus SF-1293 and comparison of its properties
 with those of 2-phosphoenolpyruvate carboxykinase.";
 RL Agric. Biol. Chem. 54:463-470(1990).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
 CoA.
 CC -!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.
 CC -!- PATHWAY: Tricarboxylic acid cycle.
 CC -!- SUBUNIT: Homohexamer.
 CC -!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CAPABLE OF OXIDATIVE METABOLISM.
 CC -!- SIMILARITY: Belongs to the citrate synthase family.
 DR PIR; PQ0046; PQ0046.

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DR InterPro; IPR002020; Citrate_synt.
KW PROSITE; PS00480; CITRATE SYNTHASE; PARTIAL.
KW Transferase; Tricarboxylic acid cycle; Allosteric enzyme.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2234 MW; C527EC7A87119597 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11
   |||
Db 16 YPV 18

RESULT 23
SB60 MAIZE
ID _SB60 MAIZE STANDARD; PRT; 20 AA.
AC P82868;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative 60 kDa spermidine-binding protein (Fragment).
OS Zea mays (Maize)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION
RC STRAIN=cv. Cecillia; TISSUE=Coleoptile;
RX MEDLINE=21948208; PubMed=11950979;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;
RT "Spermidine-binding proteins. Purification and expression analysis in
   maize.";
RL Plant Physiol. 128:1303-1312(2002).
CC -!- FUNCTION: May have spermidine-binding activity.
CC -!- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -!- SUBCELLULAR LOCATION: Mitochondrial membrane.
CC -!- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
DR GO; GO:0005792; C:microsome; NAS.
KW Membrane; Microsome.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2093 MW; 7FD730C00391579A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YEP 13
   |||
Db 6 YEP 8

RESULT 24
GRWM HUMAN
ID GRWM HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
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CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR GO; GO:0001558; P:regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HK 2
   ||
Db 2 HK 3

RESULT 25
PAP2 PARMA
ID PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moose sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidei; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
   polypeptides from the secretion of the Red sea moose sole (Pardachirus
   marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
   properties. Forms voltage-dependent, ion-permeable channels
   in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
   ||
Db 4 PP 5

RESULT 26
RE31 LITRU
ID RE31 LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
   Tyler M.J., Wallace J.C.;
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RP "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=PEP.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
Db 4 FT 5

RESULT 27
RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
Db 4 FT 5

RESULT 28
SUGA_ACHDO STANDARD; PRT; 5 AA.
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Subesophageal ganglion pentapeptide.
OS Acheta domestica (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]

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RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT subesophageal ganglion of Acheta domestica (Orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
DR PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
Db 4 PF 5

RESULT 29
ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CB1;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -1- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
Db 2 KE 3

RESULT 30
ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).

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CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 KW -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EP 13
 ||
 Db 1 EP 2

RESULT 31
 CARP MYTED STANDARD; PRT; 7 AA.
 ID _CARP MYTED
 AC P10420;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE Catch-relaxing peptide (CARP).
 OS Mytilus edulis (Blue mussel).
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 CC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88052022; PubMed=3676797;
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
 RA Muneoka Y.,
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."
 RL Brain Res. 422:374-376(1987).
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
 AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
 CC RETRACTOR MUSCLE.
 DR PIR. A29342; ECMUCR.
 KW Hormone; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MP 5
 ||
 Db 2 MP 3

RESULT 32
 EI05 LITRU STANDARD; PRT; 7 AA.
 ID _EI05 LITRU
 AC P82101;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 5.
 OS Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 CC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella."
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EP 13
 ||
 Db 3 EP 4

RESULT 33
 FAR1 HELTI STANDARD; PRT; 7 AA.
 ID _FAR1 HELTI
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GDFPLRF-amide.
 OS Helisoma trivolvis (Snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 CC Lymnaeidae; Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RA "FMRFamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvis."
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PF 6
 ||
 Db 3 PF 4

RESULT 34
 FAR5 HIRME STANDARD; PRT; 7 AA.
 ID _FAR5 HIRME
 AC P42564;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GKGVMRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

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SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;
Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KY 9
   ||
Db 3 KY 4

RESULT 35
UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON_TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PK 8
   ||
Db 1 PK 2

RESULT 36
UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-W., Plomieu C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;
Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
   ||
Db 6 PF 7

RESULT 37
WWAL_ACHF STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DB WWamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion; PubMed=8495720;
RX MEDLINE=93265912;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, 2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
   ||
Db 3 EM 4

RESULT 38
AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
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KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
DB 4 FT 5

RESULT 39
AKH TABAT
ID AKH TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
RC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC PIR; A33995; A33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
DB 4 FT 5

RESULT 40
ANG2 BOTJA
ID ANG2 BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jarakara).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;

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[1]
RN SEQUENCE.
RP TISSUE=Plasma;
RC MEDLINE=96208932; PubMed=8829801;
RX Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RA "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
DB 7 PF 8

RESULT 41
CLP_THICU
ID CLP_THICU STANDARD; PRT; 8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolithotroph-specific protein (Fragment).
OS Thobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]_SEQUENCE.
RP STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOLITHOTROPHICALLY.
FT NON_TER 8
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PV 11
DB 2 PV 3

RESULT 42
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (PeA-CAH-II) (IleD-CC-II) (Hypertrehalosaemic cockroach),
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]_SEQUENCE.

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RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L.; Schaffer M.H.; O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RN
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioceleratory and hyperglycemic activity from the corpora
RT cardiaca of *Periplaneta americana*.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RN
RP SEQUENCE.
RC SPECIES=L.deceimlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RN
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
RT *Gromphadorhina portentosa*, *Blattella germanica* and *Blatia orientalis*
RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR IncerPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 FT 15
Db 4 FT 5

RESULT 43
LMT2_LOCM1
ID LMT2_LOCM1 STANDARD; PRT; 8 AA.
AC P22396;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamigratorin 2 (LOM-MT-2).
OS Locusta migratoria (Migratoria locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamigratorin II, an
RT additional neuropeptide of *Locusta migratoria*. Member of the
RT cephalomyotomic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 FT 15
Db 4 FT 5

RESULT 44
LPK_LEUMA
ID LPK_LEUMA STANDARD; PRT; 8 AA.
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucopyrokinin (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN
RN SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN [2]
RN
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RT neuropeptide isolated from the cockroach, *Leucophaea maderae*.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC
CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
CC PENTAPEPTIDE FRAGMENT FTPEL.
CC
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A23967; A23967.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY      14 FT 15
DB      4 FT 5

RESULT 45
ID _ORCL1 STANDARD; PRT; 8 AA.
AC P8245;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomyotropin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]

RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdick S., Sauter A., Keller R.;
RT "Two orokins and the novel octapeptide orcomyotropin in the hindgut
RT of the crayfish Orconectes limosus: identified myostimulatory
RT neuropeptides originating together in neurones of the terminal
RT abdominal ganglion."
RL J. Exp. Biol. 203:2807-2818(2000).
CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
CC BY ABDOMINAL GANGLIONIC NEURONS.
CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
KW Amidation; Neuropeptide.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 FT 15
DB      4 FT 5

RESULT 46
FPK2_PERAM
ID _PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Eckert M.;
RT "Isolation and structural elucidation of two pyrokinnins from the
RT retrocerebral complex of the American cockroach."
RL Peptides 18:473-478(1997).
RN [2]

RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RL the American cockroach."
RN [2]

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 FT 15
DB      4 FT 5

RESULT 47
PPK3_PERAM
ID _PPK3_PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinnin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach."
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]

RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RL the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKINNIN FAMILY.
KW Neuropeptide; Amidation; Pyrokinnin.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PF 6
DB      3 PF 4

RESULT 48
RS7_MYCIT
ID _RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE 30S ribosomal protein S7 (Fragment).
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]
RP SEQUENCE FROM N.A. PubMed=8451173;
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC tRNA (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L08171; AAA25376.1; -.
DR PIR: S35538; S35538.
DR HAMAP: MF_00480; -; 1.
DR InterPro: IPR000235; Ribosomal S7.
DR PROSITE: PS00052; RIBOSOMAL S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; tRNA-binding; tRNA-binding.
FT INIT MET 0 0 BY SIMILARITY.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PK 8
Db 7 PK 8

RESULT 49
UC26 MAIZE
ID UC26 MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RT Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.

DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EP 13
Db 2 EP 3

RESULT 50
UF06 MOUSE
ID UF06 MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EP 13
Db 3 EP 4

RESULT 51
UPAL HUMAN
ID UPAL HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RT Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1 1

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FT UNSURE      8      8
SQ NON_TER     8      8
SQ SEQUENCE    8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ES 17
   ||
DB 3 ES 4

RESULT 52
UPAA HUMAN
ID UPAA HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7. ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER     1      1
FT VARIANT      5      5 F -> P.
FT /FTID=VAR_000004.
FT NON_TER     8      8
SQ SEQUENCE    8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YP 10
   ||
DB 6 YP 7

RESULT 53
CCAP CARMA
ID CCAP CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Halbach C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the

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RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID     3      9
FT MOD_RES      9      9 AMIDATION.
FT SEQUENCE     9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
   ||
DB 1 PF 2

RESULT 54
CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RN J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID     1      6

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FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1037 MW; DAFC276EB4540059 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PK 8
Db 7 PK 8
RESULT 55
COXE THUOB
ID -COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103 (1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
PIR: S77984; S77984.
DR IncerPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 1 9
FT NON TER 1 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KE 3
Db 1 KE 2
RESULT 56
FAR2_CALVO
ID -FAR2_CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]

RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330 (1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 SQ 18
Db 3 SQ 4
RESULT 57
FAR3_CALVO
ID -FAR3_CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330 (1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: C41978; C41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 SQ 18
Db 3 SQ 4
RESULT 58
FAR4_PENMO
ID -FAR4_PENMO STANDARD; PRT; 9 AA.
AC P63319;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRPamide-like neuropeptide FLP4 (SQPSMLRF-amide).
OS Peneaus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasm C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRPamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Peneaus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SQ 18
DB 1 SQ 2

RESULT 59
FAR5_PENMO
ID FAR5_PENMO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRPamide-like neuropeptide FLP5 (SMPSLRFR-amide).
OS Peneaus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasm C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRPamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Peneaus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
DB 2 MP 3

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RESULT 60
FIBB_MACFU
ID FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons."
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ES 17
DB 3 ES 4

RESULT 61
FRFL_SARBU
ID FRFL_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRPamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRPamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.

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CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SQ 18
Db 3 SQ 4

RESULT 62
HUTU KLEAE
ID HUTU KLEAE STANDARD; PRT; 9 AA.
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
DE hydrolase) (Fragment).
GN HUTU.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88198018; PubMed=2834335;
RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
RT "Bidirectional promoter in the hut(P) region of the histidine
RT utilization (hut) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 170:2240-2246(1988).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=90368611; PubMed=2203754;
RA Schwacha A., Bender R.A.;
RT "Nucleotide sequence of the gene encoding the repressor for the
RT histidine utilization genes of Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5481(1990).
CC -|- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
CC -yl)propanoate = urocanate + H(2)O.
CC -|- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -|- PATHWAY: Histidine degradation; second step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
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DR EMBL; M19665; AAA25078.1; -.
DR EMBL; M34604; AAA25076.1; -.
DR HAMAP; MF 00577; -.
DR InterPro; IPR000193; Urocanase.
DR PROSITE; PS01233; UROCANASE; PARTIAL.
KW Histidine metabolism; Lyase; NAD.
FT NON TER 9
SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5335A6C5 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 8 KY 9
Db 5 KY 6

RESULT 63
KNL3 BOMVA
ID KNL3 BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
[1]
SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McLean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -|- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PF 6
Db 7 PF 8

RESULT 64
LMT3 LOCM1
ID LMT3 LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-WT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
[1]
SEQUENCE, AND SYNTHESIS.
RP TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -|- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

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Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PF 6
      ||
Db      4 PF 5

RESULT 65
OXYF SCYCA
ID OXYF SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994)
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PV 11
      ||
Db      7 PV 8

RESULT 66
OXYF SCYCA
ID OXYF SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994)
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.

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CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PV 11
      ||
Db      7 PV 8

RESULT 67
OXYV SQUAC
ID OXYV SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Vala-
RT oxytocin) and asparatocin (Aspa-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 9
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PV 11
      ||
Db      7 PV 8

RESULT 68
SAMP MUSCA
ID SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19035;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

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OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharthiniiformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]_TaxID=7812;
RP SEQUENCE
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC -!- ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC -!- IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN
FT NON TER 1 >9 PENTAXIN.
FT NON TER 2 9
SQ SEQUENCE 9 AA; 965 MW; D0SB5735B3386769 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 2 FP 3

RESULT 69
THYF_FIG
ID THYF_PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_TaxID=9823;
RP SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR; A01523; YFPG.
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 1 1
FT MOD RES 1 1
SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SQ 18
DB 4 SQ 5

RESULT 70
UPA2_HUMAN
ID UPA2_HUMAN STANDARD; PRT; 9 AA.
AC P40929;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
```

```
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
FT NON TER 9
SQ SEQUENCE 9 AA; 1104 MW; 8874B1BBSB01B2CA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TE 16
DB 4 TE 5

RESULT 71
UN19_CLOPA
ID UN19_CLOPA STANDARD; PRT; 9 AA.
AC P81355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]_TaxID=1501;
RP SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum WS.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC VARIANT 8 8 M -> D.
FT NON TER 9
SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 7 EM 8

RESULT 72
UPA3_HUMAN
ID UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
```


OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 FP 7
 Db 4 FP 5
 RESULT 73
 ANGL_BOTJA
 ID ANGL_BOTJA STANDARD; PRT; 10 AA.
 AC Q10581;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10
 FT PEPTIDE 1 8
 FT PEPTIDE 2 8
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1308 MW; CEP50DD761F2DB42 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PF 6
 Db 7 PF 8
 RESULT 74
 ANGL_BOVIN
 ID ANGL_BOVIN STANDARD; PRT; 10 AA.
 AC P01017;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SRP-2003 (Rel. 42, Last annotation update)

DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III)]
 DE (Fragment).
 DE AGT OR SERPINAS.
 GN AGT OR SERPINAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE.
 RA Elliott D.F., Peart W.S.;
 RT "The amino acid sequence in a hypertensin.";
 RL Biochem. J. 65:246-254(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACR (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A90345; A90345.
 DR PDB; 3ER5; 15-JUL-92.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10
 FT PEPTIDE 1 8
 FT PEPTIDE 2 8
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1382 MW; CEEFDD761F2DB42 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PF 6
 Db 7 PF 8
 RESULT 75
 ANGT_CHICK
 ID ANGT_CHICK STANDARD; PRT; 10 AA.
 AC P01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III)]
 DE (Fragment).
 DE AGT OR SERPINAS.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]
 RN SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RN SEQUENCE.
 RC SPECIES=C.G.japonica;
 RX MEDLINE=90284684; PubMed=2191893;

RA Takei Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A60624; A60624.
 DR PIR; A90917; A90917.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
 Db ||
 7 PF 8

Search completed: November 25, 2003, 19:28:22
 Job time : 7.45515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVPEFTESQ 18

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL.23.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp_mmc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertibrate.*
14: sp_unclassified.*
15: sp.rvirus.*
16: sp.bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4	22.2	8	11	P82598
2	4	22.2	13	5	Q9TWR4
3	4	22.2	15	2	Q9A5Z5
4	4	22.2	18	11	Q8CJPD4
5	3	16.7	8	2	Q934S4
6	3	16.7	10	4	Q8WXB5
7	3	16.7	10	6	Q9N1X1
8	3	16.7	10	10	Q9FS93
9	3	16.7	10	11	Q9GVJ5
10	3	16.7	10	11	Q9QVJ6
11	3	16.7	10	13	Q73588
12	3	16.7	11	3	Q9UR95
13	3	16.7	11	5	P82700
14	3	16.7	12	4	Q9HBU4
15	3	16.7	12	10	Q9FSA9
16	3	16.7	12	11	Q9WUX1

17	3	16.7	12	15	O12036
18	3	16.7	13	4	Q9H4C1
19	3	16.7	13	5	Q9W5Q6
20	3	16.7	13	10	Q9FSA8
21	3	16.7	13	10	Q9FSA9
22	3	16.7	13	10	Q8SAT3
23	3	16.7	13	10	Q9S922
24	3	16.7	13	10	Q8SAT4
25	3	16.7	14	2	P83159
26	3	16.7	14	10	Q9FSA9
27	3	16.7	14	10	Q9FSA9
28	3	16.7	14	10	Q9FSA9
29	3	16.7	15	2	Q9R4M8
30	3	16.7	15	2	Q9R4U7
31	3	16.7	15	4	Q9UBK0
32	3	16.7	15	4	Q9BXQ0
33	3	16.7	15	4	Q81ZK4
34	3	16.7	15	6	Q8HZ79
35	3	16.7	15	8	Q9T2G9
36	3	16.7	15	9	Q38574
37	3	16.7	15	10	Q9FSA5
38	3	16.7	15	10	Q9FSB2
39	3	16.7	15	10	Q9FS98
40	3	16.7	15	10	Q9FEI3
41	3	16.7	15	10	Q9FSA0
42	3	16.7	15	10	Q9FS99
43	3	16.7	15	10	Q9FEI5
44	3	16.7	15	10	Q3FEI4
45	3	16.7	15	10	Q9FS80
46	3	16.7	15	10	Q9FSB0
47	3	16.7	15	13	Q9PRM3
48	3	16.7	16	2	Q9R4J0
49	3	16.7	16	2	Q9R4J4
50	3	16.7	16	2	Q44610
51	3	16.7	16	2	Q9R514
52	3	16.7	16	2	P82597
53	3	16.7	16	2	P82597
54	3	16.7	16	4	Q9UBQ9
55	3	16.7	16	6	Q9SM73
56	3	16.7	16	6	Q9TRK9
57	3	16.7	16	8	Q8HU42
58	3	16.7	16	8	Q8HU29
59	3	16.7	16	10	P83511
60	3	16.7	16	11	Q8C182
61	3	16.7	17	4	Q9R9C3
62	3	16.7	17	4	Q9Y3F6
63	3	16.7	17	4	Q9UC43
64	3	16.7	17	6	Q9TRH5
65	3	16.7	17	6	Q9SM49
66	3	16.7	17	8	Q36741
67	3	16.7	17	10	Q9S8Y2
68	3	16.7	17	11	Q9QVS7
69	3	16.7	17	12	Q9IHG7
70	3	16.7	17	12	Q9IHG9
71	3	16.7	17	12	Q9IHG4
72	3	16.7	17	12	Q9IH17
73	3	16.7	17	12	Q9IH44
74	3	16.7	17	12	Q9IH19
75	3	16.7	17	12	Q9IH14
76	3	16.7	17	12	Q9IHG9
77	3	16.7	17	12	Q9IHG5
78	3	16.7	17	12	Q9IH11
79	3	16.7	17	12	Q9IHG8
80	3	16.7	17	12	Q9IHG5
81	3	16.7	17	12	Q9IH18
82	3	16.7	17	12	Q9IH10
83	3	16.7	17	12	Q9IH16
84	3	16.7	17	12	Q9IH18
85	3	16.7	17	12	Q9IH22
86	3	16.7	17	12	Q9IHG3
87	3	16.7	17	12	Q9IH30
88	3	16.7	17	12	Q9IHG6
89	3	16.7	17	12	Q9IH11

O12036 caprine art
Q9H4C1 homo sapien
Q9W5Q6 drosophila
Q9FSA8 silene bacc
Q9FSA9 silene pent
Q8SAT3 flaveria ro
Q9S922 brassica ol
Q8SAT4 flaveria an
P83159 anabaena sp
Q9FSA9 silene pent
Q9FSA9 silene aega
Q9FSA9 silene sedo
Q9R4M8 bacillus fi
Q9R4U7 acinetobact
Q9UBK0 homo sapien
Q9BXQ0 homo sapien
Q81ZK4 homo sapien
Q8HZ79 bos taurus
Q9T2G9 solanum tub
Q38574 bacterioph
Q9FSA5 silene cryp
Q9FSB2 silene aega
Q9FSB2 silene laco
Q9FEI3 silene aega
Q9FSA0 silene haus
Q9FS99 silene inte
Q9FEI5 silene sedo
Q9FEI4 silene pent
Q9FSB0 silene zawa
Q9FSB0 silene aega
Q9PRM3 gallus gall
Q9R4J0 arthrobracte
Q9R4J4 pseudomonas
Q44610 buchnera ap
Q9R514 porphyromon
Q82597 streptomyce
P82597 bacillus sp
Q9UBQ9 homo sapien
Q9SM73 pan troglod
Q9TRK9 canis famli
Q8HU42 passiflora
Q8HU29 passiflora
P83511 delonix reg
Q9R9C3 mus musculus
Q9Y3F6 borrelia bu
Q9UC43 homo sapien
Q9TRH5 bos taurus
Q9SM49 bos taurus
Q36741 homo sapien
Q9S8Y2 lupinus arb
Q9QVS7 mus sp. lac
Q9IHG7 human polio
Q9IHG9 human polio
Q9IHG4 human polio
Q9IH17 human polio
Q9IH44 human polio
Q9IH19 human polio
Q9IH14 human polio
Q9IHG9 human polio
Q9IHG5 human polio
Q9IH11 human polio
Q9IHG8 human polio
Q9IHG5 human polio
Q9IH18 human polio
Q9IH10 human polio
Q9IH16 human polio
Q9IH18 human polio
Q9IH22 human polio
Q9IHG3 human polio
Q9IH30 human polio
Q9IHG6 human polio
Q9IH11 human polio

90 Q9IHI3 human polio
 91 Q9IHH0 human polio
 92 Q9IHH6 human polio
 93 Q9IHH7 human polio
 94 Q9IHI5 human polio
 95 Q9IHI2 human polio
 96 Q9IHH3 human polio
 97 Q9IHH2 human polio
 98 Q8X4A4 escherichia
 99 Q9UC87 homo sapien
 100 Q98365 myosurus mi

ALIGNMENTS

RESULT 1
 P82598 ID P82598 PRELIMINARY; PRT; 8 AA.
 AC P82598, 2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE 38kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=20198203; PubMed=10731662;
 RA Kim K.-Y., Choi I., Kim S.-S.;
 RT "Purification and characterization of a novel inhibitor of the
 proliferation of hepatic stellate cells.";
 RL J. Biochem. 127:23-27(2000).
 CC -1- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
 HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
 ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
 CC -1- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
 PROTEIN.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 22.2%; Score 4; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
 |||||
 Db 3 PVEP 6

RESULT 2
 Q9TWR4 ID Q9TWR4 PRELIMINARY; PRT; 13 AA.
 AC Q9TWR4, 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Peptide T-BRADYKININ potentiator.
 OS Tityus serrulatus (Brazilian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butchoidea; Butidae; Tityus.
 OX NCBI_TaxID=6887;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94024945; PubMed=8212046;
 RA Ferreira L.A., Alves E.W., Henriques O.B.;
 RT "Peptide T, a novel bradykinin potentiator isolated from Tityus
 serrulatus scorpion venom.";
 RL Toxicon 31:941-947(1993).
 SQ SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;

Query Match 22.2%; Score 4; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
 |||||
 Db 5 YPVE 8

RESULT 3
 Q9R5Z5 ID Q9R5Z5 PRELIMINARY; PRT; 15 AA.
 AC Q9R5Z5, 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Streptolysin O (Fragment).
 OS Streptococcus equisimilis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=119602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93273535; PubMed=8500915;
 RA Gerlach D., Kohler W., Gunther E., Mann K.;
 RT "Purification and characterization of streptolysin O secreted by
 RT Streptococcus equisimilis (group C).";
 RL Infect. Immun. 61:2727-2731(1993).
 SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match 22.2%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5
 |||||
 Db 3 KEMP 6

RESULT 4
 Q8CJD4 ID Q8CJD4 PRELIMINARY; PRT; 18 AA.
 AC Q8CJD4, 2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Podocin (Fragment).
 GN NPHS2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morita H., Yoshimura A., Makino R., Inui K., Nakao N., Usami T.,
 RA Roselli S., Antignac C., Matsuyama M., Ideura T.;
 RT "Rat genome fragment containing a part of exons and all of the 3'UTR
 of Nphs2 as well as microsatellite sites.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB094124; BAC23094.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 18 AA; 2033 MW; D47829DCFF05F4B CRC64;

Query Match 22.2%; Score 4; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
 |||||
 Db 4 PVEP 7

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RESULT 5
Q934S4
ID Q934S4 PRELIMINARY; PRT; 8 AA.
AC Q934S4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MerD protein (Fragment).
GN MERD.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G66; TRANSPOSON=Tn5037;
RA Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
RA Nikiforov V.G.;
RT "Tn5037, a Tn21-like mercury resistance transposon from Thiobacillus
RT ferrooxidans.";
RL Russ. J. Genet. 37:972-975(2001).
DR EMBL; AJ251743; CAC69252.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 937 MW; ED15A2D77B5DD446 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
Db |||
4 YPV 6

RESULT 6
Q8WXB5
ID Q8WXB5 PRELIMINARY; PRT; 10 AA.
AC Q8WXB5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE EYA2B (Fragment).
GN EYA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fee B.E., Doyle C.A., Cleveland J.L.;
RT "A novel eyes absent protein is expressed in the human eye.";
RL Gene 0:0-0(2002)
DR EMBL; AF455148; AAL57875.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1298 MW; 18021202C69B132B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
Db |||
4 KEM 6

RESULT 7
Q9N1X1
ID Q9N1X1 PRELIMINARY; PRT; 10 AA.
AC Q9N1X1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Alcohol dehydrogenase 3 (Fragment).
GN ADH3.

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OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134056; AAF31299.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match 16.7%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db |||
5 VEP 7

RESULT 8
Q9FS93
ID Q9FS93 PRELIMINARY; PRT; 10 AA.
AC Q9FS93;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296133; CAC13025.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1108 MW; CF1AB6D1B2CAB1A9 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db |||
2 PFT 4

RESULT 9
Q9QVJ5
ID Q9QVJ5 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myo-inositol hexakisphosphate phosphohydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.

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RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 1075:75-82(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1096 MW; 37A8EA4B1B1B02D7 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
Db 3 PVE 5

RESULT 10
Q9QVJ6 PRELIMINARY; PRT; 10 AA.
ID Q9QVJ6 AC Q9QVJ6 PRELIMINARY; PRT; 11 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYO-inositol hexakisphosphate phosphohydrolase (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 1075:75-82(1991).
SQ SEQUENCE 10 AA; 1124 MW; 28B8EA4B1B1B02D7 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
Db 3 PVE 5

RESULT 11
O73588 PRELIMINARY; PRT; 10 AA.
ID O73588 AC O73588 PRELIMINARY; PRT; 10 AA.
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Engrailed-3 (fragment).
GN EN-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryo;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U26148; AAC06186.1; -.
FT NON_TER 1
FT NON_TER 10

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SQ SEQUENCE 10 AA; 1118 MW; 73C0BE144735B72B CRC64;

Query Match 16.7%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
Db 8 ESQ 10

RESULT 12
Q9UR95 PRELIMINARY; PRT; 11 AA.
ID Q9UR95 AC Q9UR95 PRELIMINARY; PRT; 11 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Heat shock protein 60 homolog (fragment).
OS Pichia angusta (yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE
RX MEDLINE=93223840; PubMed=8096822;
RA Evers M.E., Hulse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula
RT polymorpha using immobilized denatured alcohol oxidase.";
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 16.7%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
Db 2 HKE 4

RESULT 13
P82700 PRELIMINARY; PRT; 11 AA.
ID P82700 AC P82700 PRELIMINARY; PRT; 11 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Periviscerokinin-3 (LEM-FVK-3).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia (Argentinian wood cockroach), and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD_RES 11
FT AMIDATION.

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SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
 DB 7 PFP 9

RESULT 14

Q9HBU4 ID Q9HBU4 PRELIMINARY; PRT; 12 AA.
 AC Q9HBU4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Caspase 8 isoform i (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eckhart L., Fischer H., Bach J., Henry M., Ban J., Tschachler E.;
 RT "Identification and characterization of novel splice variants of human
 RT caspase-8";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF207672; AAG10682.1; -.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1343 MW; 80F055095B6B02D1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
 DB 6 VEP 8

RESULT 15

Q9FSA9 ID Q9FSA9 PRELIMINARY; PRT; 12 AA.
 AC Q9FSA9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene aegaea.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49732;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296130; CAC13014.1; -.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1304 MW; 83269695B441B2CA CRC64;

Query Match 16.7%; Score 3; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
 DB 11

Db 2 PFT 4

RESULT 16

Q9WUX1 ID Q9WUX1 PRELIMINARY; PRT; 12 AA.
 AC Q9WUX1;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE APOBEC-1 protein (Fragment).
 GN APOBEC-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98335789; PubMed=9672068;
 RA Greave J., Axelos D., Welker S., Schipper M., Greten H.;
 RT "Distinct promoters induce APOBEC-1 expression in rat liver and
 RT intestine.";
 RL Arterioscler. Thromb. Vasc. Biol. 18:1079-1092 (1998).
 DR EMBL; AJ006695; CAB44439.1; -.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1357 MW; 70FE1679699325BB CRC64;

Query Match 16.7%; Score 3; DB 11; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 DB 4 TES 6

RESULT 17

OL2036 ID OL2036 PRELIMINARY; PRT; 12 AA.
 AC OL2036;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Envelope glycoprotein (fragment).
 GN ENV.
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97296261; PubMed=9151845;
 RA Turelli P., Guiguen F., Mornex J.F., Vigne R., Querat G.;
 RT "dUTPase-minus caprine arthritis-encephalitis virus is attenuated for
 RT pathogenesis and accumulates G-to-A substitutions.";
 RL J. Virol. 71:4522-4530 (1997).
 DR EMBL; U81390; AAC57905.1; -.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
 DB 2 HKE 4

RESULT 18

Q9H4C1 ID Q9H4C1 PRELIMINARY; PRT; 13 AA.
 AC Q9H4C1;

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DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Angiopoietin-2B (Fragment).
GN ANGIOPOIETIN-2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2042311; PubMed=10964717;
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francese V.,
RA Vilgrasa X., Mezquita C.;
RT "Genomic structure and alternative splicing of chicken angiopoietin-
RT 2.";
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DR EMBL; AJ289780; CAC08179.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1548 MW; C3A19DA93EE95B02 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB |||
3 KEM 5

RESULT 19
Q9W5Q6 PRELIMINARY; PRT; 13 AA.
ID Q9W5Q6;
AC Q9W5Q6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Snap25 protein.
GN SNAP25 OR CG17676 OR CG17884.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agayani A., An H.-J., Andrews-Prannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF002931; AAF45394.2; -.
DR FlyBase; FBgn0011289; Snap25.
SQ SEQUENCE 13 AA; 1483 MW; 47FD7CC5C0AF9B13 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB |||
6 KEM 8

RESULT 20
Q9FSA8 PRELIMINARY; PRT; 13 AA.
ID Q9FSA8;
AC Q9FSA8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene baccifera (Berry catchfly) (Cucubalus baccifer).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=54818;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296139; CAC13015.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB |||
2 PFT 4

RESULT 21
Q9FS94 PRELIMINARY; PRT; 13 AA.
ID Q9FS94;
AC Q9FS94;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.

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OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296132; CAC13024.1; -.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 22
Q9S922 Q9S922 PRELIMINARY; PRT; 13 AA.
ID Q9S922
AC Q9S922
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Non-C4 chloroplastic NADP-malic enzyme (Fragment).
GN CHLME2-2.
OS Flaveria robusta.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=163089;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=21648948; PubMed=11788758;
RA Lai L.B., Wang L., Nelson T.M.;
RT "Distinct But Conserved Functions for Two Chloroplastic NADP-Malic
RT Enzyme Isoforms in C(3) and C(4) Flaveria Species.";
RL Plant Physiol. 128:125-139(2002).
DR EMBL; AF288914; AAL74058.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1697 MW; 95393F9D91422775 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
Db 7 PKY 9

RESULT 23
Q9S922 Q9S922 PRELIMINARY; PRT; 13 AA.
ID Q9S922
AC Q9S922
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE S3 SGP=S-locus specific glycoprotein (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN RP SEQUENCE.
RX MEDLINE=92090397; PubMed=1752245;
RA Gaude T., Denoroy L., Dumas C.;

"Use of a fast protein electrophoretic purification procedure for N-
terminal sequence analysis to identify S-locus related proteins in
stigma of Brassica oleracea.";
RL Electrophoresis 12:646-653(1991).
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1351 MW; 9C23EDFF999601B5 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 7 TES 9

RESULT 24
Q8SAT4 Q8SAT4 PRELIMINARY; PRT; 13 AA.
ID Q8SAT4
AC Q8SAT4
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Non-C4 chloroplastic NADP-malic enzyme (Fragment).
GN CHLME2.
OS Flaveria angustifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=163088;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=21648948; PubMed=11788758;
RA Lai L.B., Wang L., Nelson T.M.;
RT "Distinct But Conserved Functions for Two Chloroplastic NADP-Malic
RT Enzyme Isoforms in C(3) and C(4) Flaveria Species.";
RL Plant Physiol. 128:125-139(2002).
DR EMBL; AF288896; AAL74057.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1697 MW; 95393F9D91422775 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
Db 7 PKY 9

RESULT 25
P83159 P83159 PRELIMINARY; PRT; 14 AA.
ID P83159
AC P83159
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,
DE rod (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
CC DIRECTED AND OPTIMAL ENERGY TRANSFER.

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CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS
 CC ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
 KW Phycobilisome; Photosynthesis.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1405 MW; 96823B44F60A3115 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
 Db 12 EPF 14

RESULT 26
 Q9FS95 PRELIMINARY; PRT; 14 AA.
 AC Q9FS95;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene pentelica.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49735;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296131; CAC13023.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
 Db 2 PPT 4

RESULT 27
 Q9FSB1 PRELIMINARY; PRT; 14 AA.
 AC Q9FSB1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene aegaea.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49732;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296122; CAC13007.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;
 Query Match 16.7%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
 Db 2 PPT 4

RESULT 28
 Q9FS91 PRELIMINARY; PRT; 14 AA.
 AC Q9FS91;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene sedoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=39790;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296105; CAC13028.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
 Db 2 PPT 4

RESULT 29
 Q9R4M8 PRELIMINARY; PRT; 15 AA.
 AC Q9R4M8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Catalase isozyme I (Fragment).
 OS Bacillus firmus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1399;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95267795; PubMed=7748885;
 RA Hicks D.B.;
 RT "Purification of three catalase isozymes from facultatively
 alkaliphilic Bacillus firmus OF4.";
 RL Biochim. Biophys. Acta 1229:347-355(1995).
 SQ SEQUENCE 15 AA; 1677 MW; 12E47DC8F66876ED CRC64;

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
 Db 13 PPT 15

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RESULT 30
Q9R4U7 PRELIMINARY; PRT; 15 AA.
ID Q9R4U7
AC Q9R4U7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Malonate decarboxylase gamma subunit (Fragment).
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95050812; PubMed=7961952;
RA Kim Y.S., Byun H.S.;
RT "Purification and properties of a novel type of malonate decarboxylase
RT from Acinetobacter calcoaceticus".
RL J. Biol. Chem. 269:29636-29641(1994).
SQ SEQUENCE 15 AA; 1816 MW; 4E14F10E389F9FEA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPK 8
Db 11 FPK 13

RESULT 31
Q9UEK0 PRELIMINARY; PRT; 15 AA.
ID Q9UEK0
AC Q9UEK0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Renal tissue-nonspecific alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RL Clin. Chem. 38:2539-2542(1992).
SQ SEQUENCE 15 AA; 1931 MW; 9A28FDE13F01F716 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKY 9
Db 9 PKY 11

RESULT 32
Q9BXQ0 PRELIMINARY; PRT; 15 AA.
ID Q9BXQ0
AC Q9BXQ0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Tissue transglutaminase (BC 2.3.2.13) (Fragment).
GN TGM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Festoff B.W.;
RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF311286; AAK15272.1; -.
RW Acyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1641 MW; C340982AFEF851 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14
Db 2 EPF 4

RESULT 33
Q8IZK4 PRELIMINARY; PRT; 15 AA.
ID Q8IZK4
AC Q8IZK4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Breast and ovarian cancer susceptibility protein (Fragment).
GN BRCA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Valarmathi M.T., Agarwal A., Deo S.S.V., Shukla N.K., Das S.N.;
RT "BRCA1 germline mutations in Indian breast cancer families.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY093484; AAM18218.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1807 MW; D156E8F11AB530FB CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ESQ 18
Db 10 ESQ 12

RESULT 34
Q8HZ79 PRELIMINARY; PRT; 15 AA.
ID Q8HZ79
AC Q8HZ79;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Alpha-synuclein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE FROM N.A.
RA Tompkins M.M., Gai W.P., Douglas S., Bunn S.J.;
RT "Alpha-synuclein expression localizes to the Golgi apparatus in bovine
RT adrenal medullary chromaffin cells.";

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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY124580; AM94359.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1774 MW; 1715433C9115DADA CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5
DB 1 EMP 3

RESULT 35
Q9T2G9 ID Q9T2G9 PRELIMINARY; PRT; 15 AA.
AC Q9T2G9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Carbonic anhydrase (EC 4.2.1.1) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=96327808; PubMed=8680307;
RA Rumeau D., Cuine S., Fina L., Gault N., Nicole M., Peltier G.;
RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum
L. leaves: characterization of two compartment-specific isoforms.";
RL Planta 199;79-88(1996).
SQ SEQUENCE 15 AA; 1647 MW; CA5B7063CDD32976 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
DB 10 PVE 12

RESULT 36
Q38574 ID Q38574 PRELIMINARY; PRT; 15 AA.
AC Q38574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lysis protein (Fragment).
OS Bacteriophage Kuf.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=12021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96207403; PubMed=8615017;
RA Gronsveld H., Oudot F., van Duin J.V.;
RT "RNA phage Kuf has an insertion of 18 nucleotides in the start codon
of its lysis gene."
RL Virology 218;141-147(1996).
DR EMBL; S81763; AAD14372.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1736 MW; EA4430EAC749D708 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
DB 8 HKE 10

RESULT 37
Q9FSA5 ID Q9FSA5 PRELIMINARY; PRT; 15 AA.
AC Q9FSA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene cryptoneura.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39877;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data."
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296138; CAC13016.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
DB 2 PPT 4

RESULT 38
Q9FSB2 ID Q9FSB2 PRELIMINARY; PRT; 15 AA.
AC Q9FSB2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data."
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296115; CAC13000.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1633 MW; D3420931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
DB 2 PPT 4

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RESULT 39
Q9FS98
ID Q9FS98 PRELIMINARY; PRT; 15 AA.
AC Q9FS98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene laconica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49734;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296136; CAC13020.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1596 MW; 2C2EBDCD29DD87C CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 2 PFT 4

RESULT 40
Q9FE13
ID Q9FE13 PRELIMINARY; PRT; 15 AA.
AC Q9FE13;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296128; CAC13013.1; -.
DR EMBL; AJ296113; CAC12998.1; -.
DR EMBL; AJ296116; CAC13001.1; -.
DR EMBL; AJ296117; CAC13002.1; -.
DR EMBL; AJ296118; CAC13003.1; -.
DR EMBL; AJ296119; CAC13004.1; -.
DR EMBL; AJ296120; CAC13005.1; -.
DR EMBL; AJ296121; CAC13006.1; -.
DR EMBL; AJ296123; CAC13008.1; -.
DR EMBL; AJ296125; CAC13010.1; -.
DR EMBL; AJ296126; CAC13011.1; -.
DR EMBL; AJ296127; CAC13012.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 2 PFT 4

RESULT 41
Q9FSA0
ID Q9FSA0 PRELIMINARY; PRT; 15 AA.
AC Q9FSA0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene haussknechtii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49733;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296137; CAC13018.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 2 PFT 4

RESULT 42
Q9FS99
ID Q9FS99 PRELIMINARY; PRT; 15 AA.
AC Q9FS99;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene integrifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39889;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296135; CAC13019.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 2 PFT 4

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RESULT 43
Q9FE15          PRELIMINARY;      PRT;      15 AA.
AC Q9FE15;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene sedoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39790;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296112; CAC13035.1; -
DR EMBL; AJ296104; CAC13027.1; -
DR EMBL; AJ296106; CAC13029.1; -
DR EMBL; AJ296107; CAC13030.1; -
DR EMBL; AJ296108; CAC13031.1; -
DR EMBL; AJ296109; CAC13032.1; -
DR EMBL; AJ296110; CAC13033.1; -
DR EMBL; AJ296111; CAC13034.1; -
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 44
Q9FE14          PRELIMINARY;      PRT;      15 AA.
AC Q9FE14;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296134; CAC13026.1; -
DR EMBL; AJ296129; CAC13022.1; -
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 45
Q9FS80          PRELIMINARY;      PRT;      15 AA.
AC Q9FS80;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene zawadskii (Zawadskii's campion).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39923;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296141; CAC13039.1; -
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 46
Q9FSB0          PRELIMINARY;      PRT;      15 AA.
AC Q9FSB0;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296124; CAC13009.1; -
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1616 MW; C96B0931E2CF0AF6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 47
QY 13 PFT 15
Db 2 PFT 4

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Q9PRM3
ID Q9PRM3 PRELIMINARY; PRT; 15 AA.
AC Q9PRM3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 17 kDa major immunophilin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE.
RX MEDLINE=94072550; PubMed=7504525;
RA Yem A.W., Reardon I.M., Leone J.W., Reinrikson R.L., Deibel M.R.Jr.;
RT "An active FK506-binding domain of 17,000 daltons is isolated
RT following limited proteolysis of chicken thymus hsp56.";
RL Biochemistry 32:12571-12576(1993)
SQ SEQUENCE 15 AA; 1606 MW; 6269732398D1B71C CRC64;

Query Match 16.7%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 7 TES 9

RESULT 48
Q9RAJ0
ID Q9RAJ0 PRELIMINARY; PRT; 16 AA.
AC Q9RAJ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE LIMONATE dehydrogenase (Fragment).
OS Arthrobacter globiformis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=1665;
RN [1]
RP SEQUENCE.
RX MEDLINE=96045380; PubMed=7546548;
RA Subayda C.G., Omura M., Hasegawa S.;
RT "Limonate dehydrogenase from Arthrobacter globiformis: the native
RT enzyme and its N-terminal sequence.";
RL Phytochemistry 40:17-20(1995).
SQ SEQUENCE 16 AA; 1759 MW; 514B2DE906FD5984 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6
Db 1 MPF 3

RESULT 49
Q9RAJ4
ID Q9RAJ4 PRELIMINARY; PRT; 16 AA.
AC Q9RAJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Peptidyl-ASP metalloendopeptidase (Fragment).
OS Pseudomonas fragi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=296;
RN [1]

Q9PRM3
ID Q9PRM3 PRELIMINARY; PRT; 15 AA.
AC Q9PRM3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 17 kDa major immunophilin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE.
RX MEDLINE=95405303; PubMed=7674963;
RA Hagmann M.L., Geuss U., Fischer S., Kresse G.B.;
RT "Peptidyl-ASP metalloendopeptidase.";
RL Meth. Enzymol. 248:782-787(1995).
SQ SEQUENCE 16 AA; 1868 MW; 0521B93A81CBE07D CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 11 TES 13

RESULT 50
Q44610
ID Q44610 PRELIMINARY; PRT; 16 AA.
AC Q44610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Shikimate dehydrogenase (Fragment).
GN ARCE.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95212914; PubMed=7535281;
RA Roubbakhsh D., Baumann P.;
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
RT gene.";
RL Gene 155:107-112(1995).
DR ENBL: U10499; AAA79128.1; --
FT NON_TER 1
SQ SEQUENCE 16 AA; 1891 MW; 72A8175598D30DF1 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8
Db 9 FPK 11

RESULT 51
Q9R514
ID Q9R514 PRELIMINARY; PRT; 16 AA.
AC Q9R514;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 17 kDa lysine-specific cysteine proteinase (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RX MEDLINE=94103245; PubMed=8276827;
RA Pike R., McGraw W., Potempa J., Travis J.;
RT "Lysine- and arginine-specific proteinases from Porphyromonas
RT gingivalis. Isolation, characterization, and evidence for the existence
RT of complexes with hemagglutinins.";
RL J. Biol. Chem. 269:406-411(1994).
SQ SEQUENCE 16 AA; 1819 MW; D864F9BF367828C6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0

QY 14 FTE 16
Db 3 FTE 5

RESULT 52

Q8KLP7 PRELIMINARY; PRT; 16 AA.
AC Q8KLP7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Adenosine phosphotransferase (Fragment).
GN APT.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OX Streptomycineae; Streptomycetaceae; Streptomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RA Wehmeier U.F.;
RT "Analysis of the secDF genes from Streptomyces griseus N2-3-11.";
RL Submitted (AUG-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF505986; CAD44524.1; -;
KW Transferase.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1838 MW; 5B369FE66365B45F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0

QY 15 TES 17
Db 5 TES 7

RESULT 53

P82597 PRELIMINARY; PRT; 16 AA.
AC P82597;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE The most stable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23) (Fragment).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE.
RC STRAIN=H-257;
RA Imamura S.; Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from the moderately thermophilic Bacillus sp. H-257.";
RL J. Biochem. 127:419-425(2000).
CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY OCCURRING WITH 1-MONOLAURYLGLYCEROL.
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0

QY 9 YPV 11
Db 4 YPV 6

RESULT 54

Q9UBQ9 PRELIMINARY; PRT; 16 AA.
AC Q9UBQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Apolipoprotein (A) (Fragment).
GN APOA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93163698; PubMed=7679504;
RA Wade D.P., Clarke J.G., Lindahl G.E., Liu A.C., Zysow B.R., Meer K., Schwartz K., Lawn R.M.;
RT "5' control regions of the apolipoprotein(a) gene and members of the related plasminogen gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1369-1373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93087573; PubMed=1454851;
RA Magaretti N., Acquati P., Magnaghi P., Bruno L., Pontoglio M., Rocchi M., Saccone S., Della Valle G., D'Urso M., LePaslier D., Ottolenghi S., Taramelli R.;
RT "Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) and plasminogen genes and identification of the apolipoprotein(a) 5' flanking region.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11584-11588(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91097523; PubMed=2268308;
RA Magaretti N., Bruno L., Pontoglio M., Candiani G., Meroni G., Ottolenghi S., Taramelli R.;
RT "Definition of the transcription initiation site of human plasminogen gene in liver and non hepatic cell lines.";
RL Biochem. Biophys. Res. Commun. 173:1013-1018(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92207924; PubMed=1554698;
RA Ichinose A.;
RT "Multiple members of the plasminogen-apolipoprotein(a) gene family associated with thrombosis.";
RL Biochemistry 31:3113-3118(1992).
DR EMBL; L07899; AAB66587.2; -;
DR EMBL; M90079; AAA35546.1; -;
DR EMBL; M90078; AAA35547.1; -;
DR EMBL; M62890; AAA36454.1; -;
DR EMBL; M86878; AAA51749.1; -;
DR EMBL; M86877; AAB49909.1; -;
KW Lipoprotein.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1912 MW; 66BDFBF28EDB1A69 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0

QY 1 HKE 3
Db 3 HKE 5


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RESULT 55
Q95M73
ID Q95M73 PRELIMINARY; PRT; 16 AA.
AC Q95M73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Apolipoprotein (Fragment).
GN A.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=211303645; PubMed=11301336;
RA Ruby T., Dachtel C., Lawn R.W., Wickings J., Chapman M.J., Thillet J.;
RT "Functional analysis of the chimpanzee and human apo(a) promoter
RT sequences. Identification of sequence variations responsible for
RT elevated transcriptional activity in chimpanzee."
RL J. Biol. Chem. 276:22209-22214(2001).
DR EMBL; AY028467; AAK38764.1; -.
KW Lipoprotein.
FT NON_TER
SQ SEQUENCE 16 AA; 1912 MW; 68BDFEF28EDB1A69 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db 3 HKE 5

RESULT 56
Q9TRK9
ID Q9TRK9 PRELIMINARY; PRT; 16 AA.
AC Q9TRK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Casein kinase II=24 kDa polypeptide (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054738; PubMed=1331100;
RA Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT "Casein kinase II phosphorylation of signal sequence receptor alpha
RT and the associated membrane chaperone calnexin."
RL J. Biol. Chem. 267:23789-23796(1992).
FT NON_TER
SQ SEQUENCE 16 AA; 2053 MW; F31011034124F59B CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14
Db 6 EPF 8

RESULT 57
Q8HU42
ID Q8HU42 PRELIMINARY; PRT; 16 AA.
AC Q8HU42;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

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OS Delonix regia (Royal poinciana).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Caesalpinioideae; Caesalpinieae;
 OC Delonix.
 NCBI_TaxID=72433;
 RN [1]
 RN SEQUENCE AND CHARACTERIZATION.
 RP TISSUE=Seed;
 RC PubMed=12168698;
 RX Pando S.C., Macedo M.L.R., Freire M.G.M., Toyama M.H., Novello J.C.,
 RA Marangoni S.;
 RA "Biochemical characterization of a lectin from Delonix regia seeds.";
 RT J. Protein Chem. 21:279-285(2002).
 RL J. Protein Chem. 21:279-285(2002).
 CC -!- FUNCTION: GLUCOSE-SPECIFIC LECTIN.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: OPTIMAL PH IS 8.0-9.0. ACTIVE UP TO 60 DEGREES
 CC CELSIUS.
 CC -!- MISCELLANEOUS: REQUIRES MANGANESE BUT NOT CALCIUM IONS FOR CELL-
 CC AGGLUTINATING ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
 DR InterPro: IPR001220; Lectin_legB.
 DR PROSITE: PS00307; LECTIN_LEGUME_BETA; PARTIAL.
 KW Lectin; Glycoprotein; Manganese.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1816 MW; D3DA3A36D1C308BE CRC64;
 Query Match 16.7%; Score 3; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 FPK 8
 DB ||||
 DB 5 FPK 7

RESULT 60
 Q8CIS2 PRELIMINARY; PRT; 16 AA.
 ID Q8CIS2;
 AC Q8CIS2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plasminogen (Fragment).
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Liver;
 RX PubMed=12149246;
 RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
 RA Farmer R.J., Miles L.A.;
 RT "Localization of Regulatory Elements Mediating Constitutive and
 RT Cytokine-stimulated plasminogen Gene Expression.";
 RL J. Biol. Chem. 277:38579-38588(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Liver;
 RA Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,
 RA Farmer R.J., Miles L.A.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY134430; AAN15805.1; -.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;
 Query Match 16.7%; Score 3; DB 11; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKE 3
 DB ||||

Db 3 HKE 5
 RESULT 61
 Q9R9C3 PRELIMINARY; PRT; 17 AA.
 ID Q9R9C3;
 AC Q9R9C3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Plasmid cp32-3, possible partition proteins (Fragment).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG plasmid cp32.3.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 NCBI_TaxID=139;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=B31;
 RC MEDLINE=98361033; PubMed=9695920;
 RX Stevenson B., Casjens S., Rosa P.;
 RT "Evidence of past recombination events among the genes encoding the
 RT Rsp antigens of Borrelia burgdorferi.";
 RL Microbiology 144:1869-1879(1998).
 DR EMBL, AF022480; AAC35442.1; -.
 DR InterPro: IPR004180; DUF2226.
 DR Pfam: PF02890; DUF226; 1.
 KW Plasmid.
 FT NON TER 1 1
 SQ SEQUENCE 17 AA; 2069 MW; 7FDE0D04EF50172D CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KYP 10
 DB ||||
 DB 1 KYP 3

RESULT 62
 Q9Y3F6 PRELIMINARY; PRT; 17 AA.
 ID Q9Y3F6;
 AC Q9Y3F6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EST00098 protein (Fragment).
 GN EST00098.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=99299247; PubMed=10369878;
 RX Gilley J., Fried M.;
 RT "Extensive gene order differences within regions of conserved synteny
 RT between the Fugu and human genomes: implications for chromosomal
 RT evolution and the cloning of disease genes.";
 RL Hum. Mol. Genet. 8:1313-1320(1999).
 DR EMBL, Y17449; CAB44366.1; -.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1695 MW; 1EA4692B032AF8D0 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PVE 12
 DB ||||
 DB 2 PVE 4

```
RESULT 63
Q9UC43
ID Q9UC43 PRELIMINARY; PRT; 17 AA.
AC Q9UC43;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interferon-alpha-induced protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96132854; PubMed=8557639;
RA Rich S.A., Bose M., Tempest P., Rudofsky U.H.;
RT "Purification, microsequencing, and immunolocalization of p36, a new
RT interferon-alpha-induced protein that is associated with human lupus
RT inclusions.";
RL J. Biol. Chem. 271:1118-1126(1996).
SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACBC CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
DB 15 KYP 17

RESULT 64
Q9TRH5
ID Q9TRH5 PRELIMINARY; PRT; 17 AA.
AC Q9TRH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-S1-casein homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93231344; PubMed=1299613;
RA Neuteboom B., Gluffrida M.G., Conti A.;
RT "Isolation of a new ligand-carrying casein fragment from bovine
RT mammary gland microsomes.";
RL FEBS Lett. 305:189-191(1992).
SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
DB 4 PFP 6

RESULT 65
Q9SM49
ID Q9SM49 PRELIMINARY; PRT; 17 AA.
AC Q9SM49;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Acetyl-CoA-carboxylase alpha (EC 6.4.1.2) (Fragment).
GN ACC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao J., Molenaar A., Wheeler T.T., Seyfert H.M.;
RT "STAT5-binding is mandatory for lactational stimulation of the bovine
RT promoter PIII of the Acetyl-Coenzyme A-Carboxylase alpha-encoding gene
RT in the mammary gland but not in other tissues.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mao J.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Rostock, Rostock, Germany.
DR EMBL; AJ312201; CAC59690.1; -.
KW Ligase.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 2082 MW; 0B379CCF0A078E55 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB 9 KEM 11

RESULT 66
Q36741
ID Q36741 PRELIMINARY; PRT; 17 AA.
AC Q36741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Glutaryl CoA dehydrogenase (Fragment).
GN GCDH.
OS Homo sapiens (Human).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95315953; PubMed=7795610;
RA Greenberg C.R., Reimer D., Singal R., Triggs-Raine B., Chudley A.E.,
RA Dilling L.A., Phillips S., Haworth J.C., Seargeant L.E., Goodman S.I.;
RT "A G-to-T transversion at the +5 position of intron 1 in the glutaryl
RT CoA dehydrogenase gene is associated with the Island Lake variant of
RT glutaric acidemia type I.";
RL Hum. Mol. Genet. 4:493-495(1995).
DR EMBL; S77773; AAB34724.2; -.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 17 AA; 1896 MW; 4D77B628C59A9E32 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
DB 7 TES 9

RESULT 67
Q9S8Y2
ID Q9S8Y2 PRELIMINARY; PRT; 17 AA.
AC Q9S8Y2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (Tree lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]
RP SEQUENCE
RX MEDLINE=92344803; PubMed=1368361;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RL Phytochemistry 31:1519-1527(1992).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1877 MW; DB7925924D5F46AF CRC64;

Query Match 16.7%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPF 6
Db 3 MPF 5

RESULT 68
Q9QVS7 PRELIMINARY; PRT; 17 AA.
ID Q9QVS7;
AC Q9QVS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lactate dehydrogenase-A (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95201434; PubMed=7534515;
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,
RA FAVOR J.;
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the
RT mouse.";
RL Mamm. Genome 5:777-780(1994).
SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db 11 HKE 13

RESULT 69
Q9IHG7 PRELIMINARY; PRT; 17 AA.
ID Q9IHG7;
AC Q9IHG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6013TAJ94;
RL MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;

L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (Tree lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]
RP SEQUENCE
RX MEDLINE=92344803; PubMed=1368361;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RL Phytochemistry 31:1519-1527(1992).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1877 MW; DB7925924D5F46AF CRC64;

Query Match 16.7%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPF 6
Db 3 MPF 5

RESULT 68
Q9QVS7 PRELIMINARY; PRT; 17 AA.
ID Q9QVS7;
AC Q9QVS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lactate dehydrogenase-A (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95201434; PubMed=7534515;
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,
RA FAVOR J.;
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the
RT mouse.";
RL Mamm. Genome 5:777-780(1994).
SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db 11 HKE 13

RESULT 69
Q9IHG7 PRELIMINARY; PRT; 17 AA.
ID Q9IHG7;
AC Q9IHG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6013TAJ94;
RL MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;

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RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233188; AAF35092.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1840 MW; 004DEB22D713051 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16
Db 8 FTE 10

RESULT 70
Q9IHH9 PRELIMINARY; PRT; 17 AA.
ID Q9IHH9;
AC Q9IHH9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6427ING95;
RL MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233176; AAF35080.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB22D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16
Db 8 FTE 10

RESULT 71
Q9IHG4 PRELIMINARY; PRT; 17 AA.
ID Q9IHG4;
AC Q9IHG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6433PAK95;
RL MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233191; AAF35095.1; -.
FT NON_TER 1

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FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 72
Q9IHI7 PRELIMINARY; PRT; 17 AA.
AC Q9IHI7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3038USA82DI58;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233168; AAF35072.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 73
Q9IHH4 PRELIMINARY; PRT; 17 AA.
AC Q9IHH4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7TAJ91;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233181; AAF35085.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 74
Q9IHI9 PRELIMINARY; PRT; 17 AA.
AC Q9IHI9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D48;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233166; AAF35070.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 75
Q9IHI4 PRELIMINARY; PRT; 17 AA.
AC Q9IHI4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=422RUS91;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233171; AAF35075.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10
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Search completed: November 25, 2003, 19:34:00
Job time : 34.8023 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
(without alignments)
62.189 Million cell updates/sec

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Title: US-09-641-801-22
Perfect score: 18
Sequence: 1 HKMPFFKYPVEPTES 18

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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq	length: 3
Maximum DB seq	length: 20

Post-processing: Listing first 100 summaries

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19:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Ewe colostrinin pe
5	18	100.0	18	23	Colostrinin consti
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Neural cell regula
8	11	61.1	14	15	Hypotensive polype
9	10	55.6	11	17	CNS-inhibiting pep

83 4 22.2 14 22 AAM98010 Human peptide #128
 84 4 22.2 14 22 AAU28525 DPI tryptic digest
 85 4 22.2 14 22 AAU26171 Depression-Asocia
 86 4 22.2 14 23 ABG96070 Cysteine-contains
 87 4 22.2 14 24 ABP57207 Breast cancer asso
 88 4 22.2 15 16 AAR70027 Hydroxylamin pepti
 89 4 22.2 15 16 AAR79630 Endocarditis speci
 90 4 22.2 15 16 AAR79631 Endocarditis speci
 91 4 22.2 15 21 AAY93322 Antigenic peptide
 92 4 22.2 15 21 AAY93322 Antigenic peptide
 93 4 22.2 15 21 AAY76361 Fragment of human
 94 4 22.2 15 22 ABP24630 HIV DR super motif
 95 4 22.2 15 22 AAB72253 Colostrinin derive
 96 4 22.2 15 22 AAB72507 Colostrinin peptid
 97 4 22.2 15 22 AAB72539 Colostrinin peptid
 98 4 22.2 15 22 AAB59313 Ewe colostrinin pe
 99 4 22.2 15 23 ABP58951 Human macroprotein
 100 4 22.2 15 23 AAO26556 Human macroprotein

ALIGNMENTS

RESULT 1
 AAB72267
 ID AAB72267 standard; peptide; 18 AA.
 XX
 AC AAB72267;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 22.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO20011937-A2.
 XX
 XX 22-FEB-2001.
 PD
 XX
 PF 17-AUG-2000; 2000WO-US22818.
 XX
 PR 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGG-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2001-202804/20.
 DR
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX
 XX Claim 1; Page 34; 50pp; English.
 PS
 XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKMPFPKYPVPFPTESQ 18
 ||||||||||||||||
 DB 1 HKMPFPKYPVPFPTESQ 18
 ||||||||||||||||
 RESULT 2
 AAB72520
 ID AAB72520 standard; Peptide; 18 AA.
 XX
 AC AAB72520;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #21.
 XX
 KW Dermatological; oxidative stress regulator; colostrinin.
 XX
 OS Unidentified.
 XX
 PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 XX
 PR 17-AUG-1999; 99US-0149310.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2001-218342/22.
 DR
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 XX Claim 6; Page 26; 48pp; English.
 PS
 XX The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKMPFPKYPVPFPTESQ 18
 ||||||||||||||||
 DB 1 HKMPFPKYPVPFPTESQ 18
 ||||||||||||||||
 RESULT 3
 AAB72552
 ID AAB72552 standard; Peptide; 18 AA.
 XX
 AC AAB72552;
 XX
 DT 09-MAY-2001 (first entry)
 XX

DE Colostrinin peptide #21.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW Colostrum.
 XX Unidentified.
 XX OS
 XX PN WO200112651-A2.
 XX PD 22-FEB-2001.
 XX PF 17-AUG-2000; 2000WO-US22774.
 XX PR 17-AUG-1999; 99US-0149633.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Boldogh I;
 XX WI; 2001-226545/23.
 XX DE
 XX PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 XX PS Claim 6; Page 21; 35pp; English.
 XX CC
 XX CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 XX SQ Sequence 18 AA;
 DE Query Match 100.0%; Score 18; DB 22; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKEMPPFKYPVEPTESQ 18
 DB 1 HKEMPPFKYPVEPTESQ 18
 DE
 DE RESULT 4
 DE AAB59330
 ID AAB59330 standard; Peptide; 18 AA.
 XX AC
 XX AC AAB59330;
 XX DT 21-MAR-2001 (first entry)
 XX DE Ewe colostrinin peptide fragment C-5.
 XX DE
 XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX OS
 XX OS Ovis sp.
 XX PN WO200075173-A2.
 XX PD 14-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-GB02128.
 XX PR 02-JUN-1999; 99GB-0012852.
 XX PA (RBGE-) REGEN THERAPEUTICS PLC.
 XX PI Georgiades JA;
 XX WI; 2001-071058/08.
 XX PT Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 XX PS Claim 7; Page 27; 63pp; English.
 XX CC
 XX CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX SQ Sequence 18 AA;
 DE Query Match 100.0%; Score 18; DB 22; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKEMPPFKYPVEPTESQ 18
 DB 1 HKEMPPFKYPVEPTESQ 18
 DE
 DE RESULT 5
 DE AAE20249
 ID AAE20249 standard; peptide; 18 AA.
 XX AC
 XX AC AAE20249;
 XX DT 18-JUN-2002 (first entry)
 XX DE Colostrinin constituent peptide #21.
 XX DE
 XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 XX OS Unidentified.
 XX PH
 XX FT Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optionally C-terminal amide"
 XX
 XX PN WO200213850-A1.
 XX PD 21-FEB-2002.
 XX PF 17-AUG-2000; 2000WO-US22776.
 XX PR 17-AUG-2000; 2000WO-US22776.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Stanton GJ, Hughes TK, Boldogh I;
 XX WI; 2002-269151/31.
 XX DE
 XX PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX PS Claim 6; Page 26; 51pp; English.
 XX CC
 XX CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.
 XX
 XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKEMPPPKYPVEPFTESQ 18
 Db 1 HKEMPPPKYPVEPFTESQ 18
 RESULT 6
 AAM51056
 ID AAM51056 standard; Peptide; 18 AA.
 AC AAM51056;
 XX
 XX 30-MAY-2002 (first entry)
 DT Colostrinin constituent peptide (casein amino acids 121-138).
 DE Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 18
 FT /note= "optional C-terminal amidation"
 FT
 XX WO200213849-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22775.
 PF
 XX 17-AUG-2000; 2000WO-US22775.
 PR (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2002-269150/31.
 DR
 XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX Claim 1; Page 34; 54pp; English.
 PS
 XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor, and
 CC corresponds to casein amino acids 121-138. Methods are claimed
 CC for: inducing a cytokine in a cell by contact with an immunological
 CC regulator, where the cell is present in a cell culture, a tissue,
 CC an organ or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide. Cytokines
 CC induced by this peptide in human leucocyte cultures include
 CC interferon-gamma, tumour necrosis factor-alpha and interleukin-10.
 XX
 XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKEMPPPKYPVEPFTESQ 18
 Db 1 HKEMPPPKYPVEPFTESQ 18
 RESULT 7
 AAO14598
 ID AAO14598 standard; peptide; 18 AA.
 AC AAO14598;
 XX
 XX 27-MAY-2002 (first entry)
 DT Neural cell regulatory colostrinin peptide 21.
 DE Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 18
 FT /note= "Optional C-terminal amide"
 FT
 XX WO200213851-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22777.
 PF
 XX 17-AUG-2000; 2000WO-US22777.
 PR (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I, Stanton JG, Hughes TK;
 XX WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -
 XX Claim 7; Page 21; 37pp; English.
 PS
 XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrin peptide used in
 CC the method of the invention.

XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKEMFFPKYPVEPTESQ 18
 |||||
 Db 1 HKEMFFPKYPVEPTESQ 18

RESULT 8
 AAR58339
 ID AAR58339 standard; peptide; 14 AA.

AC AAR58339;
 XX
 DT 22-SEP-1994 (first entry)
 XX
 DE Hypotensive polypeptide.
 XX
 KW Hypotensive; antioxidative; calcium absorption; salt; food;
 KW pharmaceuticals; physiologically active agents.

OS Lactobacillus helveticus.

XX JP06041191-A.

XX 15-FEB-1994.

XX 03-MAR-1993; 93JP-0043047.

XX 04-MAR-1992; 92JP-0047340.

XX (CALV) CALPIS SHOKUJIN KOGYO KK.

XX WPI; 1994-089332/11.

XX New polypeptide - used in physiologically active agents having
 PT e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity

XX Claim 1-2; Page 10; 10pp; Japanese.

XX Sequences (AAR58319-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.

XX SQ Sequence 14 AA;
 Query Match 61.1%; Score 11; DB 15; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.3e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKEMFFPKYPV 11
 |||||
 Db 1 HKEMFFPKYPV 11

RESULT 9
 AAR03290
 ID AAR03290 standard; peptide; 11 AA.

XX AC AAR03290;

XX 23-MAR-1997 (first entry)

XX

DE CNS-inhibiting peptide from casein.
 XX
 KW casein; central nervous system; CNS inhibiting; antitussive;
 KW analgesic; sedative.
 XX
 OS Synthetic.

XX JP08269090-A.

XX 15-OCT-1996.

XX 28-MAR-1995; 95JP-0094516.

XX 28-MAR-1995; 95JP-0094516.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX WPI; 1996-515013/51.

XX New peptide(s) obtd. by digestion of casein - useful as drugs
 PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
 PT activities

XX Claim 1; Page 2; 11pp; Japanese.

XX Acid casein was prepared from raw milk by acid precipitation, and
 CC beta casein was formed by the product by the method of Hipp et al.
 CC This material was digested with porcine pepsin. The digested protein
 CC was neutralised with NaOH, then heated to inactivate the enzyme. The
 CC product was further digested with bovine pancreatin, trypsin and porcine
 CC kidney-derived LAP and then subjected to reverse phase chromatography
 CC to provide the present peptide.
 CC The peptide is useful as a drug having CNS inhibiting, antitussive,
 CC analgesic and sedative activities

XX SQ Sequence 11 AA;

Query Match 55.6%; Score 10; DB 17; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.9e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVEPFTESQ 18
 |||||

Db 1 YPVEPFTESQ 10

RESULT 10
 AAR03291
 ID AAR03291 standard; peptide; 13 AA.

XX AC AAR03291;

XX 23-MAR-1997 (first entry)

XX CNS-inhibiting peptide from casein.

XX casein; central nervous system; CNS inhibiting; antitussive;
 KW analgesic; sedative.

XX Synthetic.

XX JP08269090-A.

XX 15-OCT-1996.

XX 28-MAR-1995; 95JP-0094516.

XX 28-MAR-1995; 95JP-0094516.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX WPI; 1996-515013/51.

XX

PT New peptide(s) obtd. by digestion of casein - useful as drugs
PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
PT activities
XX Claim 1; Page 2; 1lpp; Japanese.
XX Acid casein was prepared from raw milk by acid precipitation, and
CC beta casein was formed by the product by the method of Hipp et al.
CC This material was digested with porcine pepsin. The digested protein
CC was neutralised with NaOH, then heated to inactivate the enzyme. The
CC product was further digested with bovine pancreatin, trypsin and porcine
CC kidney-derived LAP and then subjected to reverse phase chromatography
CC to provide the present peptide.
CC The peptide is useful as a drug having CNS inhibiting, antitussive,
CC analgesic and sedative activities
XX Sequence 13 AA;
SQ Query Match 55.6%; Score 10; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 YPVEPFTSQ 18
Db 1 YPVEPFTSQ 10
RESULT 11
ABG32211
ID ABG32211 standard; peptide; 7 AA.
XX AC ABG32211;
XX DT 05-NOV-2002 (first entry)
XX DE Sheep colostrinin derived peptide #5.
XX Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;
KW central nervous system disorder; neurological disorder; neurosis;
KW mental disorder; psychosis; neurodegenerative disorder;
KW Alzheimer's disease; motor neuron disease; immune system disorder;
KW acquired immunological deficiency; bacterial infection; viral infection;
KW amyloid plaque; dietary supplement; cachexia; weight loss;
KW senile dementia; Parkinson's disease; emotional disturbance; depression;
KW drug addiction; drug withdrawal.
XX Ovis aries.
XX WO200246211-A2.
XX 13-JUN-2002.
XX 05-DEC-2001; 2001WO-GB05376.
XX 06-DEC-2000; 2000GB-0029777.
XX (REG-) REGEN THERAPEUTICS PLC.
XX Georgiades JA;
XX WPI; 2002-619016/66.
XX Novel peptides isolated from colostrinin polypeptide, useful for
PT treating viral and bacterial infections, disorders of immune system and
PT central nervous system e.g., Alzheimer's disease, dementia, and as food
PT additive -
XX Claim 1; Page 8; 16pp; English.
XX The invention relates to a peptide derived from colostrinin (a colostrum
CC protein known to be a cytokine inducer) substantially entirely consists
CC of the peptide sequences appearing as ABG32207-ABG32223. Also included
CC are a composition comprising two or more of the peptides in combination

CC with a carrier, a dietary supplement comprising an orally ingestible
CC combination of the peptide in combination with a carrier and an antibody
CC which binds to the peptide, and which is obtainable by using peptide as
CC an antigen. The peptide is useful as a medicament for treating chronic
CC disorders of central nervous system e.g., neurological disorders and/or
CC mental disorders such as psychosis and/or neurosis, dementia,
CC neurodegenerative disorders such as Alzheimer's disease, motor
CC neuron disease, chronic disorders of immune system, diseases
CC with bacterial and viral infections, acquired immunological deficiencies,
CC chronic bacterial, viral infections. The peptide is also useful for
CC treating diseases characterised by presence of amyloid plaque. The
CC peptide is also useful as a dietary supplement for babies, small
CC children, adults who have been subjected to chemotherapy and/or
CC adults who have suffered from cachexia or weight loss due to chronic
CC disease. The peptide is also useful for treating senile dementia,
CC Parkinson's disease, emotional disturbances and depression. The peptides
CC may also be used as an auxiliary withdrawal treatment for drug addicts,
CC after a period of detoxification, and in persons dependent on stimulants.
CC The present sequence is a colostrinin derived peptide of the invention.
XX Sequence 7 AA;
SQ Query Match 38.9%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 EMPFPKY 9
Db 1 EMPFPKY 7
RESULT 12
AAW03289
ID AAW03289 standard; peptide; 6 AA.
XX AC AAW03289;
XX DT 23-MAR-1997 (first entry)
XX CNS-inhibiting peptide from casein.
DE casein; central nervous system; CNS inhibiting; antitussive;
KW analgesic; sedative.
XX Synthetic.
XX JP08269090-A.
XX 15-OCT-1996.
XX 28-MAR-1995; 95JP-0094516.
XX 28-MAR-1995; 95JP-0094516.
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX WPI; 1996-515013/51.
XX New peptide(s) obtd. by digestion of casein - useful as drugs
PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
PT activities
XX Claim 1; Page 2; 1lpp; Japanese.
XX Acid casein was prepared from raw milk by acid precipitation, and
CC beta casein was formed by the product by the method of Hipp et al.
CC This material was digested with porcine pepsin. The digested protein
CC was neutralised with NaOH, then heated to inactivate the enzyme. The
CC product was further digested with bovine pancreatin, trypsin and porcine
CC kidney-derived LAP and then subjected to reverse phase chromatography
CC to provide the present peptide.
CC The peptide is useful as a drug having CNS inhibiting, antitussive,
CC analgesic and sedative activities

XX Sequence 6 AA;
 SQ Query Match 33.3%; Score 6; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVEPF 14
 |||||
 Db 1 YPVEPF 6

RESULT 13
 ABG32212
 ID ABG32212 standard; peptide; 6 AA.
 XX AC ABG32212;
 XX DT 05-NOV-2002 (first entry)
 XX DE Sheep colostrinin derived peptide #6.
 XX KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;
 KW central nervous system disorder; neurological disorder; neurosis;
 KW mental disorder; psychosis; neurodegenerative disorder;
 KW Alzheimer's disease; motor neuron disease; immune system disorder;
 KW acquired immunological deficiency; bacterial infection; viral infection;
 KW amyloid plaque; dietary supplement; cachexia; weight loss;
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;
 KW drug addiction; drug withdrawal.
 XX OS Ovis aries.
 XX FN WO200246211-A2.
 XX PD 13-JUN-2002.
 XX PF 05-DEC-2001; 2001WO-GB053376.
 XX PR 06-DEC-2000; 2000GB-0029777.
 XX PA (REGG-) REGEN THERAPEUTICS PLC.
 XX PI Georgiades JA;
 XX DR WPI; 2002-619016/66.
 XX PT Novel peptides isolated from colostrinin polypeptide, useful for
 PT treating viral and bacterial infections, disorders of immune system and
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food
 PT additive -
 XX PS Claim 1; Page 8; 16pp; English.
 XX CC The invention relates to a peptide derived from colostrinin (a colostrum
 CC protein known to be a cytokine inducer) substantially entirely consists
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included
 CC are a composition comprising two or more of the peptides in combination
 CC with a carrier, a dietary supplement comprising an orally ingestible
 CC combination of the peptide in combination with a carrier and an antibody
 CC which binds to the peptide, and which is obtainable by using peptide as
 CC an antigen. The peptide is useful as a medicament for treating chronic
 CC disorders of central nervous system e.g., neurological disorders and/or
 CC mental disorders such as psychosis and/or neurosis, dementia,
 CC neurodegenerative disorders such as Alzheimer's disease, motor
 CC neuron disease, chronic disorders of immune system, diseases
 CC with bacterial and viral etiology, acquired immunological deficiencies,
 CC chronic bacterial, viral infections. The peptide is also useful for
 CC treating diseases characterised by presence of amyloid plaque. The
 CC peptide is also useful as a dietary supplement for babies, small
 CC children, adults who have been subjected to chemotherapy and/or
 CC adults who have suffered from cachexia or weight loss due to chronic
 CC disease. The peptide is also useful for treating senile dementia,

CC Parkinson's disease, emotional disturbances and depression. The peptides
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,
 CC after a period of detoxification, and in persons dependent on stimulants.
 CC The present sequence is a colostrinin derived peptide of the invention.
 XX SQ Sequence 6 AA;
 Query Match 33.3%; Score 6; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPFT 15
 |||||
 Db 1 PVEPFT 6

RESULT 14
 AAR58330
 ID AAR58330 standard; peptide; 15 AA.
 XX AC AAR58330;
 XX DT 22-SEP-1994 (first entry)
 XX DE Hypotensive polypeptide.
 XX KW Hypotensive; antioxidative; calcium absorption; salt; food;
 KW pharmaceuticals; physiologically active agents.
 XX OS Lactobacillus helveticus.
 XX FN JP06041191-A.
 XX PD 15-FEB-1994.
 XX PF 03-MAR-1993; 93JP-0043047.
 XX PR 04-MAR-1992; 92JP-0047340.
 XX PA (CALV) CALPIS SHOKUHIN KOGYO KK.
 XX DR WPI; 1994-089332/11.
 XX PT New polypeptide - used in physiologically active agents having
 PT e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity
 XX PS Claim 1-2; Page 8; 10pp; Japanese.
 XX CC Sequences (AAR58319-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.
 XX SQ Sequence 15 AA;
 Query Match 33.3%; Score 6; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFTESQ 18
 |||||
 Db 6 PFTESQ 11

RESULT 15
 AAE07187
 ID AAE07187 standard; peptide; 10 AA.
 XX AC AAE07187;
 XX DT 06-NOV-2001 (first entry)

XX DE Colostrinin peptide 3.

XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;

XX KW central nervous system disorder; neurodegenerative disorder; weight loss;

XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

XX KW acquired immunological deficiency; neurological disorder; dementia;

XX KW antiviral.

XX OS Unidentified.

XX FT WO200155199-A1.

XX PN 02-AUG-2001.

XX PD 26-JAN-2001; 2001WO-GB00329.

XX PF 26-JAN-2000; 2000GB-0001825.

XX PR (REG-) REGEN THERAPEUTICS PLC.

XX PA Georgiades JA;

XX PI WPI; 2001-488775/53.

XX DR Peptide useful as an inter alia in the treatment of e.g. disorders of

XX PT the immune system and the central nervous system comprises ten

XX PT amino-terminal amino acid sequence derived from peptides present in

XX PT colostrinin -

XX PS Claim 1; Page 15; 40pp; English.

XX CC The invention relates to colostrinin peptide fragments which are useful,

XX CC inter alia, in the treatment of chronic disorders of the immune system

XX CC and the central nervous system. Colostrinin peptides are used as a

XX CC medicament in the treatment of neurological disorders e.g., dementia,

XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron

XX CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and

XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and

XX CC viral infections and diseases characterised by the presence of beta-

XX CC amyloid plaques and as a dietary supplement for babies, small children,

XX CC adults and senile persons, who have been subjected to chemotherapy or

XX CC have suffered from cachexia or weight loss due to the chronic disease.

XX CC Colostrinin peptides are also used as food additives and as an auxiliary

XX CC withdrawal treatment for drug addicts, after a period of detoxification

XX CC and in persons dependent on stimulants. Colostrinin peptides are used to

XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional

XX CC disturbances of psychiatric patients in a state of depression. These

XX CC colostrinin peptides improves the development of immune system in a new

XX CC born child and to correct the immunological deficiencies in a child.

XX CC The present sequence is colostrinin peptide 3 related to the invention.

XX SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPF 14

Db 4 PVEPF 8

RESULT 16

AAE07197

ID AAE07197 standard; peptide; 10 AA.

XX AC AAE07197;

XX CC

DT 06-NOV-2001 (first entry)

XX DE Modified colostrinin cyclic peptide #3.

XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;

XX KW central nervous system disorder; neurodegenerative disorder; weight loss;

XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

XX KW acquired immunological deficiency; neurological disorder; dementia;

XX KW antiviral; cyclic.

XX OS Synthetic.

XX FT Unidentified.

XX PN WO200155199-A1.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-GB00329.

XX PR 26-JAN-2000; 2000GB-0001825.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-488775/53.

XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of

XX PT the immune system and the central nervous system comprises ten

XX PT amino-terminal amino acid sequence derived from peptides present in

XX PT colostrinin -

XX PS Example 2; Page 8; 40pp; English.

XX CC The invention relates to colostrinin peptide fragments which are useful,

XX CC inter alia, in the treatment of chronic disorders of the immune system

XX CC and the central nervous system. Colostrinin peptides are used as a

XX CC medicament in the treatment of neurological disorders e.g., dementia,

XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron

XX CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and

XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and

XX CC viral infections and diseases characterised by the presence of beta-

XX CC amyloid plaques and as a dietary supplement for babies, small children,

XX CC adults and senile persons, who have been subjected to chemotherapy or

XX CC have suffered from cachexia or weight loss due to the chronic disease.

XX CC Colostrinin peptides are also used as food additives and as an auxiliary

XX CC withdrawal treatment for drug addicts, after a period of detoxification

XX CC and in persons dependent on stimulants. Colostrinin peptides are used to

XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional

XX CC disturbances of psychiatric patients in a state of depression. These

XX CC colostrinin peptides improves the development of immune system in a new

XX CC born child and to correct the immunological deficiencies in a child.

XX CC The present sequence is modified colostrinin cyclic peptide #3 related to

XX CC the invention.

XX SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPF 14

Db 5 PVEPF 9

RESULT 17

AAG98055

ID AAG98055 standard; Peptide; 14 AA.

XX AC AAG98055;

```
XX 19-SEP-2001 (first entry)
XX AC AAB72250;
XX DT 14-MAY-2001 (first entry)
XX DE Colostrin derived cytokine inducing peptide SEQ ID 5.
XX DE Colostrin derived cytokine inducing peptide SEQ ID 5.
XX KW Colostrin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.
XX OS Synthetic.
XX PN W020011937-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22818.
XX PR 17-AUG-1999; 99US-0149311.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX PT Inducing a cytokine and modulating an immune response, useful for
XX PT treating central nervous system diseases and bacterial and viral
XX PT infections, comprises administering colostrin as an immunological
XX PT regulator -
XX PS Claim 1; Page 34; 50pp; English.
XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
XX CC a proline rich polypeptide aggregate contained in colostrum. The
XX CC peptides have immune response modulatory activity, and are capable of
XX CC inducing cytokines. Colostrin and its derived peptides are useful for
XX CC inducing cytokine production, for modulating an immunological response
XX CC and for inducing blood cell proliferation. The peptides are useful in the
XX CC treatment of disorders of the central nervous system, neurological
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,
XX CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
XX CC disorders of the immune system, bacterial and viral infections and
XX CC acquired immunological deficiencies.
XX SQ Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 10 PVEPF 14
XX DB 8 PVEPF 12
XX RESULT 19
XX AAB72504
XX ID AAB72504 standard; Peptide; 15 AA.
XX XX
XX AC AAB72504;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrin peptide #5.
XX KW Dermatological; oxidative stress regulator; colostrin.
XX OS Unidentified.
XX XX
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```
XX 19-SEP-2001 (first entry)
XX AC AAB72250;
XX DT 14-MAY-2001 (first entry)
XX DE Colostrin derived cytokine inducing peptide SEQ ID NO. 697.
XX DE Colostrin derived cytokine inducing peptide SEQ ID NO. 697.
XX KW Human; single nucleotide polymorphism; SNP; angiopoietin;
XX KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
XX KW adenosine triphosphate-dependent RNA helicase;
XX KW major histocompatibility complex Class I histocompatibility antigen; MHC;
XX KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
XX KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
XX KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN W0200148245-A2.
XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-US35346.
XX PR 27-DEC-1999; 99US-0472688.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX WPI; 2001-418297/44.
XX PT Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase,
XX PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
XX PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
XX PT diseases and infections -
XX PS Disclosure; Page 444; 484pp; English.
XX CC The invention relates to nucleic acids (AAH79386-AAH80036) encoding
XX CC polymorphic variants of proteins (AAG98010-AAG98038) related to
XX CC angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
XX CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
XX CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
XX CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
XX CC proteins have potential immunosuppressive, immunostimulatory,
XX CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
XX CC antileukemic, neuroprotective and antimicrobial activity and may be
XX CC useful in gene/protein therapy, vaccines, modulation of the expression
XX CC and activity of proteins related to angiopoietin, 4-hydroxybutyrate,
XX CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
XX CC major histocompatibility complex (MHC) Class I histocompatibility antigen
XX CC and/or phosphoglycerate kinase. Disorders that may be prevented,
XX CC diagnosed and/or treated by the above methods include multifactorial
XX CC diseases with a genetic component, such as autoimmune diseases (e.g.
XX CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
XX CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers
XX CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of
XX CC the nervous system, an infection of pathogenic organisms. They may also
XX CC be used to alter phenotypic traits such as longevity, appearance,
XX CC strength, speed and endurance.
XX SQ Sequence 14 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 13 PFTES 17
XX DB 9 PFTES 13
XX RESULT 18
XX AAB72250
XX ID AAB72250 standard; peptide; 15 AA.
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PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 XX
 PR 17-AUG-1999; 99US-0149310.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred.No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PVEPF 14
 Db 8 PVEPF 12
 |||||
 RESULT 20
 ID AAB72536 standard; Peptide; 15 AA.
 XX
 AC AAB72536;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #5.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22774.
 XX
 PR 17-AUG-1999; 99US-0149633.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 PS Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred.No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PVEPF 14
 Db 8 PVEPF 12
 |||||
 RESULT 21
 ID AAB59322 standard; Peptide; 15 AA.
 XX
 AC AAB59322;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment B-7.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB02128.
 XX
 PR 02-JUN-1999; 99GB-0012852.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred.No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PVEPF 14
 Db 8 PVEPF 12
 |||||

RESULT 22	
AAE20232	
ID	AAE20232 standard; peptide; 15 AA.
XX	AAE20232;
AC	AAE20232;
XX	18-JUN-2002 (first entry)
DE	Colostrinin constituent peptide #5.
XX	Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW	therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW	tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW	transplantation; implantation; dermatological; vulnary.
XX	Unidentified.
OS	Unidentified.
XX	Key
XX	Modified-site
FT	15
FT	/note= "Optionally C-terminal amide"
XX	WO200213850-A1.
PN	21-FEB-2002.
XX	17-AUG-2000; 2000WO-US22776.
XX	(TEXA) UNIV TEXAS SYSTEM.
PA	Stanton GJ, Hughes TK, Boldogh I;
PI	WPI; 2002-269151/31.
XX	Composition useful for the modulation of blood cell proliferation in a
XX	patient comprises a blood cell regulator selected from colostrinin, its
PT	constituent peptide and/or analog
PT	Claim 6; Page 25; 5lpp; English.
PS	The invention relates to a composition which comprises a blood cell
XX	regulator selected from colostrinin, its constituent peptide and/or
CC	analogue. The invention is used for modulating the oxidative stress
CC	level in a cell e.g. mammalian or human cell present in a cell culture,
CC	tissue, organ, or organism; or for treating oxidative damage to the skin
CC	of a patient e.g. animal or human; to modulate oxidative stress during/
CC	after a premature birth or normal birth, preventing/delaying aging in a
CC	patient, enhancing wound healing, and the reduction of side effects of
CC	cosmetic procedures. The method changes the level of an oxidising species
CC	in the cell, such as decreases or prevents increase in the level of
CC	damage to a biomolecule of the patient selected from DNA, protein and/or
CC	lipid, compared to the same conditions when the oxidative stress
CC	regulator is not present. The modulation of oxidative stress results in
CC	enhanced repair, regeneration, and replacement of cells, tissues and
CC	organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC	external organs), as well as enhanced preservation of such organs for
CC	transplantation, implantation, or scientific research. The present
CC	sequence is a colostrinin constituent peptide.
XX	Sequence 15 AA;
SQ	Query Match 27.8%; Score 5; DB 23; Length 15;
	Best Local Similarity 100.0%; Pred. No. 45;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 PVEPFF 14
DB	8 PVEPFF 12
RESULT 23	
AAM51040	
ID	AAM51040 standard; Peptide; 15 AA.
XX	AAM51040;
AC	30-MAY-2002 (first entry)
XX	Colostrinin constituent peptide.
DE	Colostrinin; colostrum; immunomodulator; cardiovascular;
XX	Blood cell regulator; cytokine inducer; beta-casein; human.
KW	Homo sapiens.
OS	Key
XX	Modified-site
FT	15
FT	/note= "optional C-terminal amidation"
XX	WO200213849-A1.
PN	21-FEB-2002.
XX	17-AUG-2000; 2000WO-US22775.
XX	17-AUG-2000; 2000WO-US22775.
XX	(TEXA) UNIV TEXAS SYSTEM.
PA	(REGE-) REGEN THERAPEUTICS PLC.
XX	Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI	WPI; 2002-269150/31.
XX	Modulation of blood cell proliferation in a patient involves use of
XX	blood cell regulator selected from colostrinin, its constituent peptide
PT	and/or analogue
PT	Claim 1; Page 34; 54pp; English.
PS	The present sequence is that of a colostrinin constituent peptide
XX	that is preferred for use as an immunological regulator and as a
CC	blood cell regulator in claimed methods of the invention. It is
CC	classified as having a beta-casein homologue precursor. Methods
CC	are claimed for: inducing a cytokine in a cell by contact with an
CC	immunological regulator, where the cell is present in a cell
CC	culture, a tissue, an organ or an organism, and the cell is
CC	by contact with the immunological regulator an immune response in a cell
CC	effective to induce a cytokine; modulating an immune response in a
CC	patient by administering an immunological regulator under conditions
CC	effective to induce a cytokine, where the immunological regulator
CC	is administered topically or as part of a dietary supplement, and
CC	where the immune response is specific or non specific, an interferon
CC	response or an antibody response; modulating blood cell proliferation
CC	by contacting blood cells with a blood cell regulator, where the
CC	blood cells are present in a cell culture or an organism, are
CC	mammalian or human, and where the blood cells are increased in
CC	number or differentiated; and a method for modulating blood cell
CC	proliferation in a patent. A claimed cytokine-inducing composition
CC	comprises a pharmaceutical carrier and an active agent such as the
CC	present peptide. Cytokines induced by this peptide in human
CC	leucocyte cultures include interferon-gamma, tumour necrosis
CC	factor-alpha, interleukin-6 and interleukin-10.
XX	Sequence 15 AA;
SQ	Query Match 27.8%; Score 5; DB 23; Length 15;
	Best Local Similarity 100.0%; Pred. No. 45;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 PVEPFF 14
DB	8 PVEPFF 12

RESULT 24
AAO14581
ID AAO14581 standard; peptide; 15 AA.
XX
XX
AC AAO14581;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 5.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
XX Unidentified.
OS
FH Key Location/Qualifiers
FT Modified-site 15 /note= "Optional C-terminal amide"
XX
XX WO200213851-A1.
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US22777.
PF
XX
XX 17-AUG-2000; 2000WO-US22777.
PR
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX
XX Boldogh I, Stanton JG, Hughes TK;
PI
XX
XX WPI; 2002-269152/31.
DR
XX
XX Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog -
XX
XX Claim 7; Page 21; 37pp; English.
PS
XX
XX The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 10 PVEPF 14
Db 8 PVEPF 12
|||||
RESULT 25
AAB59352
ID AAB59352 standard; Peptide; 16 AA.
XX
XX
AC AAB59352;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment derived sequence #12.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
XX
PD 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
PF
XX
XX 02-JUN-1999; 99GB-0012852.
PR
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
PA
XX
XX Georgiades JA;
PI
XX
XX WPI; 2001-071058/08.
DR
XX
XX Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
FT and immune system, viral and bacterial infections, and diseases
FT characterized by amyloid plaques -
XX
XX Claim 8; Page 27; 63pp; English.
PS
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 16 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 10 PVEPF 14
Db 9 PVEPF 13
|||||
RESULT 26
AAW65794
ID AAW65794 standard; peptide; 5 AA.
XX
XX AAW65794;
AC
XX
XX 19-OCT-1998 (first entry)
DT
XX
XX Polypyrrol inhibitor of cyclophilin.
DE
XX
XX polypyrrol; cyclophilin; inhibitor; neurotrophic compound; PPI;
KW ptiptydyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;
KW neuronal damage.
XX
XX
XX Synthetic.
OS
XX
XX WO9825950-A1.
PN
XX
XX 18-JUN-1998.
PD
XX
XX 08-DEC-1997; 97WO-US23102.
PF
XX
XX 09-DEC-1996; 96US-0761902.
PR
XX
XX (GUIL-) GUILFORD PHARM INC.
PA
XX
XX Hamilton GS, Steiner JP, Wei L;
PI
XX

DR WPI; 1998-348444/30.

XX Effecting neuronal activity in mammals - by administering tetra-

PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,

PT useful in treatment of neuronal damage or degeneration disorders

XX

PS Claim 11; Page 41; 70pp; English.

XX The invention relates to a method of effecting a neuronal activity. It

CC comprises administering a neurotrophic compound with an affinity for a

CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl

CC isomerase (rotamase) activity. The neurotrophic compound achieves the

CC stimulation of damaged neurons, promotion of neuronal regeneration or

CC prevention of neurodegeneration, and treatment of neurological disorder.

CC The neurotrophic compounds are potent peptidyl-proline isomerase

CC (rotamase) inhibitors. They are of use in disorders which include

CC peripheral neuropathy caused by physical injury or disease state, i.e.

CC physical injury to the brain or spinal cord, stroke, or neurological

CC disorder leading to neurodegeneration, notably Alzheimer's and

CC Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic

CC compounds avoid the side effects of immunosuppressant drugs, including

CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,

CC involuntary tremors, headaches, and hypertension. They are also free from

CC the difficulties in delivery and bioavailability of large molecular

CC weight proteins. The present sequence represents a specifically claimed

CC neurotrophic compound.

XX

SQ Sequence 5 AA;

Query Match 22.2%; Score 4; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Length 5;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8

Db 2 PFPK 5

|||||

RESULT 27

AAAY06327

ID AAY06327 standard; Peptide; 6 AA.

XX

AC AAY06327;

XX

XX 06-SEP-1999 (first entry)

DT

DE Cellulase EGIII-like enzyme conserved motif.

XX

KW Cellulase; endoglucanase; EGIII; textile; feed additive; baking;

KW food processing; grain wet milling; pulp; paper.

XX

OS Synthetic.

XX

PN WO9931255-A2.

XX

PD 24-JUN-1999.

XX

XX 14-DEC-1998; 98WO-US26552.

XX

PR 16-DEC-1997; 97US-0991720.

XX

PA (GEMV) GENENCOR INT INC.

XX

XX Bower BS, Fowler T, Phillips JI;

PT

DR WPI; 1999-395187/33.

XX

PT EGIII like cellulase

XX

PS Claim 1c; Page 34; 47pp; English.

XX

CC The invention relates to novel enzymes which share certain

CC conserved sequences (see AAY06325-29), including the present

CC sequence, with EGIII cellulase from *Trichoderma reesei* (see

CC AAY06330). These novel EGIII-like enzymes contain one or more of

CC the conserved motifs. PCR primers (see AAX59180-91) based on the

CC conserved motifs can be used to detect novel EGIII-like enzymes

CC (see AAY06331-70) in fungal and bacterial sources. The invention

CC also provides a vector comprising DNA encoding an EGIII-like

CC enzyme, host cells and a method of producing a cellulase by

CC culturing the host cell. The EGIII-like cellulases can be used in

CC the treatment of a cellulose-containing textile, as a feed

CC additive, in the treatment of wood pulp, in the reduction of

CC biomass to glucose, in the stone washing of indigo dyed denim, or

CC as a laundry detergent component (all claimed).

XX

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPPT 15

Db 3 EPPT 6

|||||

RESULT 28

AAAB14886

ID AAB14886 standard; peptide; 6 AA.

XX

AC AAB14886;

XX

DT 21-NOV-2000 (first entry)

XX

DE EGIII-like cellulase amino acid string #3.

XX

KW Endoglucanase III; EGIII; cellulase; mutant; *Trichoderma reesei*;

KW enzyme stability; textile treatment; wood pulp treatment; feed additive;

KW detergent.

XX

OS *Acremonium brachyphenium*.

OS *Chaetomium brasiliense*.

OS *Chaetomium vitellium*.

OS *Emericella desertoru*.

OS *Fusarium equiseti*.

OS *Gliocladium roseum*.

OS *Humicola grisea*.

OS *Myceliophthora thermophila*.

OS *Penicillium notatum*.

OS *Phanerochaete chrysosporium*.

OS *Trichoderma reesei*.

XX

PN WO200037614-A2.

XX

XX 29-JUN-2000.

XX

PD 12-NOV-1999; 99WO-US26704.

XX

PR 18-DEC-1998; 98US-0216295.

XX

PA (GEMV) GENENCOR INT INC.

XX

XX Mitchinson C, Wendt DJ;

PI

XX WPI; 2000-482483/42.

DR

XX

XX Novel endoglucanase III or endoglucanase III-like cellulase useful for

PT treating textiles and wood pulp comprises a substitution or deletion at

PT specified positions in the wild form of endoglucanase III -

XX

PS Disclosure; Page 8; 52pp; English.

XX

CC The present sequence is an amino acid string found in all cellulases

CC related to endoglucanase III (EGIII) from *Trichoderma reesei*. The

CC sequence was used to design primers to amplify EGIII-like genes from

CC genomic DNA libraries constructed from various microorganisms. The
 CC isolated genes were found to share significant homology with EGIII from
 CC Trichoderma reesei. Certain substitution and deletion mutations have
 CC been incorporated into EGIII and EGIII-like cellulases to produce
 CC variant enzymes with improved stability, e.g. increased resistance to
 CC temperature stress. The mutants may be used in textile and wood pulp
 CC treatment, as a feed additive, and for reducing biomass to glucose.
 CC They are also useful for stonewashing or indigo dyed denim and as an
 CC agent in laundry and dish detergents.

SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
 ||||
 Db 3 EPFT 6

RESULT 29
 AAU77071
 ID AAU77071 standard; peptide; 6 AA.
 XX
 AC AAU77071;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Endoglucanase EGIII-like cellulase BOX3 motif #1.
 XX
 KW EGIII; cellulase; BOX3; endoglucanase III; detergent;
 KW cellulose treatment; stonewashing; indigo dyed denim; feed additive;
 KW wood pulp treatment; biomass reduction; laundry; dish detergent;
 KW milling; depilling; softening; surface fibre removal; anti-greying.
 XX
 OS Acromonium chrysogenum.
 OS Chaetomium brasiliense.
 OS Chaetomium vitellium.
 OS Emericella desertoru.
 OS Fusarium equiseti.
 OS Gliocladium roseum.
 OS Humicola grisea var thermoida.
 OS Myceliophthora thermophila.
 OS Penicillium notatum.
 OS Phanerochaete chrysosporium.
 XX
 PN WO200212466-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 31-JUL-2001; 2001WO-US23991.
 XX
 PR 04-AUG-2000; 2000US-0633085.
 XX
 PA (GEMV) GENENCOR INT INC.
 XX
 PI Day AG, Gualfetti P, Mitchinson C, Shaw A;
 XX
 DR WPI; 2002-241752/29.
 XX
 PT Novel variant of endoglucanase III or endoglucanase III-like cellulase
 PT for treating cellulose containing textile, has performance sensitive
 PT residues replaced to residue having modified stability -
 XX
 PS Disclosure; Page 6; 47pp; English.
 XX
 CC The invention relates to a variant of endoglucanase III (EGIII) or
 CC EGIII-like cellulase comprising a substitution or deletion at a position
 CC corresponding to one or more of residues W7, G31, A35, T145, Y147, Q162
 CC and/or Y168 in EGIII from Trichoderma reesei. Also included are a
 CC DNA encoding the variant, a vector comprising the DNA, a host cell
 CC transformed with the vector and a detergent composition comprising a

CC surfactant and the variant. The variant is useful in the treatment of a
 CC cellulose containing textile, stonewashing or indigo dyed denim or as a
 CC feed additive or in the treatment of wood pulp, in reduction of biomass
 CC to glucose. The detergent composition is useful as the main component of
 CC a laundry or dish detergent and is further useful as pre-wash
 CC composition, pre-soak composition or for cleaning during the regular wash
 CC or clean cycle. The variant increases value of animal feed, improves the
 CC drainability of food pulp, enhances food products and reduces fibre in
 CC grain during grain wet (or dry) milling process. Further cellulase
 CC improves the feel e.g. smoothness and/or appearance e.g. removing pills
 CC and fibrils which tend to reduce the sharpness in appearance of a
 CC fabric, of cellulose containing fabric, and imparts desirable effects
 CC such as depilling, softening, anti-pilling, surface fiber removal,
 CC anti-greying and cleaning. The present sequence is a BOX motif found
 CC in the EGIII-like cellulases, used to construct degenerate primers
 CC for isolation of the genes encoding the EGIII-like cellulases.

XX
 XX SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
 ||||
 Db 3 EPFT 6

RESULT 30
 AAU77438
 ID AAU77438 standard; peptide; 6 AA.
 XX
 AC AAU77438;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE EGIII-like cellulase consensus peptide #3.
 XX
 KW Endoglucanase III-like cellulase; EGIII-like; fungus;
 KW cellulose containing textile.
 XX
 OS Synthetic.
 XX
 PN WO200212464-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 31-JUL-2001; 2001WO-US23989.
 XX
 PR 04-AUG-2000; 2000US-0632426.
 XX
 PA (GEMV) GENENCOR INT INC.
 XX
 PI Mitchinson C, Ropp TH, Swanson BA;
 XX
 DR WPI; 2002-241750/29.
 XX
 PT Novel endoglucanase III (EGIII)-like cellulase variant comprising
 PT substitution/deletion at positions corresponding to specific residues
 PT in EGIII from Trichoderma reesei, useful for treating cellulose
 PT containing textile -
 XX
 PS Disclosure; Page 5; 41pp; English.
 XX
 CC The present invention relates to novel endoglucanase III (EGIII)-like
 CC cellulase variants which comprise a substitution or deletion at a
 CC position corresponding to one or more of residues M79, M154 and/or
 CC M118 in mature EGIII from the fungus, Trichoderma reesei. The variants
 CC are useful in the treatment of a cellulose containing textile. By
 CC substituting other amino acids for the native methionines at
 CC positions 79, 118 and 154 (sites where oxidation of the enzyme takes
 CC place) in EGIII from T. reesei, oxidatively more stable enzymes are
 CC obtained. The present sequence represents an EGIII-like cellulase

CC consensus peptide used to construct degenerate primers for the
 CC isolation of EGIII-like cellulases from different organisms.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Length 6;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPFT 15
 Db 3 EPFT 6

RESULT 31

ID AAU87807 standard; Peptide; 6 AA.

XX AC AAU87807;

DT 05-JUN-2002 (first entry)

XX Endoglucanase III (EGIII)-like cellulase peptide #3.

XX Endoglucanase III cellulase; EGIII; textile; stonewash;

KW indigo dyed denim; wood pulp; feed additive; grain wet milling;

KW grain dry milling; detergent; pre-wash composition;

KW pre-soak composition; paper processing; surfactant mediated stress;

XX thermal mediated stress.

XX Synthetic.

XX WO200212462-A2.

XX 14-FEB-2002.

XX 31-JUL-2001; 2001WO-US23946.

XX 04-AUG-2000; 2000US-0632570.

XX (GEMV) GENENCOR INT INC.

XX Mitchinson C, Gualfetti P, Phillips JI;

XX WPI; 2002-241748/29.

XX Variant endoglucanase-III, useful in treatment of cellulose containing
 PT textile and wood pulp, in treatment of biomass to glucose and as a feed
 PT additive, is a variant of EGIII from *Trichoderma reesei* -

PS Disclosure; Page 6; 44pp; English.

XX The invention describes a variant endoglucanase (EG)-III or EGIII-like
 CC cellulase (I), comprising a substitution or deletion at a position
 CC corresponding to residues P201, G170 and/or V210 in EGIII from
 CC *Trichoderma reesei*. (I) is useful in the treatment of a cellulose
 CC containing textile such as stonewashing or indigo dyed denim, in the
 CC treatment of wood pulp, in the reduction of biomass to glucose and as a
 CC feed additive. (I) is also useful in the treatment of starch during grain
 CC wet milling or dry milling to facilitate the production of glucose, high
 CC fructose corn syrup and/or alcohol. A detergent composition containing
 CC (I) is useful as pre-wash compositions, pre-soak compositions, and for
 CC cleaning during the regular wash or rinse cycle. (I) is useful in the
 CC processing of pulp and paper. (I) confers improved performance, including
 CC stability in the presence of thermal and/or surfactant mediated stress.
 CC This sequence represents a peptide encoded by a degenerate primer that
 CC can be used as a probe to identify EGIII-like cellulases in fungal
 CC genomic DNA.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 EPFT 15
 Db 3 EPFT 6

RESULT 32

AAW21388 standard; peptide; 7 AA.

XX AC AAW21388;

DT 29-JUL-1997 (first entry)

DE Plasminogen activator inhibitor 1 derived signal oligopeptide #16.

XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prerenin;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
 KW Treponema pallidum membrane protein; TWPA; islet amyloid polypeptide;
 KW fibroblast MMP; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX Homo sapiens.

OS WO9519568-A1.

PN 20-JUL-1995.

XX 12-JAN-1995; 95WO-US000575.

XX 14-JAN-1994; 94US-0182248.

XX (RATH/) RATH M.

XX Rath M;

XX WPI; 1995-263953/34.

XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication
 PT between protein(s)

PS Claim 5; Page 54; 88pp; English.

XX The sequences given in AAW21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface
 CC of the protein and are represented by the hydrophilicity maxima of
 CC the protein. These peptides are enriched in charged amino acids
 CC arranged with neutral spacer amino acids. The specific signal
 CC character of these oligopeptides is determined by a characteristic
 CC combination of conformation and charge within the signal sequence.
 CC These oligopeptides may be used as vaccines in the treatment of
 CC human disease, as competitive inhibitors to prevent or reduce the
 CC metabolic action or interaction of a selected protein by blocking
 CC its specific signal sequences, or as therapeutic agents to function
 CC as feedback regulators to reduce synthesis rate of a selected protein.
 CC These peptides may be modified by omitting one or more amino acids at
 CC the N- and/or C-terminal, by substituting one or more amino acids
 CC without consideration of charge and polarity, by substituting one or
 CC more amino acids with amino acid residues with similar charge and/or
 CC polarity, by omitting one or more amino acids or a combination of these.

XX Sequence 7 AA;

Query Match 22.2%; Score 4; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPFP 7
|
|
|
|
Db 2 MPFP 5

RESULT 33
AAY96209
ID AAY96209 standard; Peptide; 7 AA.

XX AC AAY96209;

XX DT 11-AUG-2000 (first entry)

XX DE Arabidopsis AHAS small subunit F3 gene fragment N-terminal sequence.

XX KW Herbicide-resistance; acetohydroxy-acid synthase; AHAS;

XX KW acetolactate synthase; imidazolinone; sulfonyleurea;

XX KW triazolopyrimidine sulfonamide; sulfamoylurea; enzyme;

XX KW pyrimidyl-oxy-benzoic acid; sulfonyleurea; transgenic plant;

XX KW branched-chain amino acid synthesis.

XX OS Arabidopsis.

XX PN WO200026390-A2.

XX PD 11-MAY-2000.

XX PF 28-OCT-1999; 99WO-US25452.

XX PR 29-OCT-1998; 98US-0106239.

XX PF (AMCY) AMERICAN CYANAMID CO.

XX PI Kakefuda G, Costello C, Sun M, Hu W;

XX DR WPI; 2000-365633/31.

XX PT New polynucleotide encoding eukaryotic acetohydroxy-acid synthetase
PT small subunit protein for producing transgenic herbicide resistant
PT plants and identifying mutations affecting enzymatic activity of the
PT synthetase -

XX PS Disclosure; Page 25; 57pp; English.

XX CC Arabidopsis acetohydroxy-acid synthase (AHAS) small subunit is needed
CC for branched-chain amino acid synthesis and so is essential for life.

XX CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme

CC in plants would lead to plant death and therefore inhibitors would be

CC potential herbicides. Certain herbicides are known to inhibit AHASs:

CC imidazolinones, sulfonyleureas, triazolopyrimidine sulfonamides,

CC pyrimidyl-oxy-benzoic acids, sulfamoylureas and sulfonyleureas.

CC Mutant AHAS may be resistant to these herbicides and may be used to

CC create herbicide resistant transgenic plants e.g. dicot and monocot crop

CC plants. A thrombin cleavage site was incorporated into an AHAS small

CC subunit gene. The AHAS small subunit gene fragments were cloned into

CC plasmid expression vectors, and were expressed as glutathione

CC transferase/AHAS small subunit fusion proteins. The glutathione

CC transferase was then cleaved via the thrombin cleavage site. Cleavage

CC however modifies the N-terminal sequence of the AHAS small subunit gene

CC fragments, in that the glycine and serine residues of the cleavage site

CC are maintained on the AHAS protein. The present sequence details the

CC N-terminal sequence of one such AHAS small subunit gene fragment,

CC F3, which is a near full length AHAS small subunit gene, with the

XX modification due to cleavage.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
|
|
|
|
Db 3 VEPF 6

RESULT 34

AAR61422
ID AAR61422 standard; peptide; 8 AA.

XX AC AAR61422;

XX DT 25-MAR-2003 (updated)

XX DT 25-AUG-1995 (first entry)

XX DE PF4-related octapeptide.

XX KW antiinflammatory; platelet factor 4; PF-4 autoimmune disease;

XX KW graft-versus-host; reperfusion injury; atherosclerosis; asthma.

XX OS Synthetic.

XX PN WO9500543-A1.

XX PD 05-JAN-1995.

XX PF 17-JUN-1994; 94WO-US06888.

XX PR 18-JUN-1993; 93US-0080371.

XX PA (COUN/) COUNTS D F.

XX PA (DUFF/) DUFF R G.

XX PI Counts DF, Duff RG;

XX DR WPI; 1995-052005/07.

XX PT New peptide(s) and derivs. based on platelet factor 4 - used for
PT inhibiting an immune response, including an inflammatory response
PT in e.g. autoimmune diseases.

XX PS Disclosure; Page 44; 99pp; English.

XX CC New peptides are disclosed which include any peptide, peptide
CC derivative or peptide analogue which comprises either (i) at least a
CC 4 amino acid portion of PF-4 (see AAR61401) or a functionally equivalent
CC sequence, or (ii) at least a 6 amino acid sequence which is at least

CC 66% homologous to a portion of the PF-4 sequence, or a functionally

CC equivalent sequence. Pref. the peptide contains the sequence

CC Thr-Ser-Gln and/or Val-Arg-Pro, and more preferably Thr-Thr-Ser-Gln

CC and/or Val-Arg-Pro-Arg. The most preferred peptide is

CC Thr-Thr-Ser-Gln-Val-Arg-Pro-Arg (see AAR61493), designated CT-112.

CC The peptide may be derivatised at the N- and/or C-terminal, or may be

CC cyclised, substituted, truncated or contain D-amino acid residues.

CC The present sequence is an analogue CT-112 containing Glu substitution.

CC The peptides exhibit antiinflammatory activity and may be used to treat

CC autoimmune diseases (such as insulin-dependent diabetes, ulcerative

CC colitis, rheumatoid arthritis, scleroderma, mixed connective tissue

CC disease and SLE), reperfusion tissue damage, inflammatory lung disease,

CC graft-versus-host disease, atherosclerosis and asthma.

CC When tested for antiinflammatory activity by a single 6 mg/kg

CC subcutaneous dose using the mouse ear acute inflammation model,

CC peptide CT-112 gave an inhibition value of 64.9%. In comparison,

CC the present sequence gave a value of 43.2%.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
|
|
|
|

Db	1 TESQ 4	
DE	Platelet factor 4 derived peptide SEQ ID NO:30.	
XX		
KW	Platelet factor 4; PF4; anti-inflammatory; inhibition; inflammation;	
KW	autoimmune disease; graft versus host disease; reperfusion injury;	
XX	atherosclerosis; asthma.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	US5776892-A.	
XX		
PD	07-JUL-1998.	
XX		
PF	16-JUN-1994; 94US-0259550.	
XX		
PR	16-JUN-1994; 94US-0259550.	
PR	21-DEC-1990; 90US-0631823.	
PR	24-MAR-1993; 93US-0037486.	
PR	18-JUN-1993; 93US-0080371.	
XX		
PA	(CURA-) CURATIVE HEALTH SERVICES INC.	
XX		
PI	Counts DF, Duff RG;	
XX		
DR	WPI; 1998-398086/34.	
XX		
PT	New antiinflammatory peptide(s) based on platelet factor 4 sequences	
PT	- used for treating e.g. auto:immune diseases, graft versus host	
PT	disease, reperfusion injury, atherosclerosis or asthma	
XX		
PS	Claim 2; Column 75; 55pp; English.	
XX		
CC	The present sequence represents a peptide which is related to platelet	
CC	factor 4 (PF4) and can be used to inhibit an inflammatory response.	
CC	Peptides, peptide analogues and peptide derivatives of PF4 can be used	
CC	for treating e.g. autoimmune diseases such as insulin dependent	
CC	diabetes, Goodpasture's syndrome, pemphigus and pemphigoid, primary	
CC	biliary cirrhosis, ulcerative colitis, rheumatoid arthritis,	
CC	scleroderma, mixed connective tissue disease and lupus erythematosus,	
CC	graft versus host disease, septic shock, reperfusion injury (including	
CC	injury subsequent to myocardial or cerebral infarction),	
CC	atherosclerosis, asthma and inflammatory lung disease. The peptides	
CC	give a new and effective method of inhibiting the inflammatory response	
CC	by acting on cytokines rather than the prior art arachidonic acid.	
CC	(Updated on 25-MAR-2003 to correct PF field.)	
XX		
SQ	Sequence 8 AA;	
	Query Match 22.2%; Score 4; DB 19; Length 8;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	15 TESQ 18	
Db	1 TESQ 4	
RESULT 37		
AAB45558	ID AAB45558 standard; Protein; 9 AA.	
XX		
AC	AAB45558;	
XX		
DT	02-MAR-2001 (first entry)	
XX		
DE	Human B99-1 HLA B*4403 immunogenic peptide SEQ ID NO 95.	
XX		
KW	Tumor-associated antigen; B99; immunogenic; humoral immune response;	
KW	cellular immune response; immunotherapy; cancer; kidney; lung; colon;	
KW	pancreas; breast; stomach; vaccine; diagnosis; treatment.	
XX		
OS	Homo sapiens.	
XX		

Db	1 TESQ 4	
RESULT 35		
AAW05539	ID AAW05539 standard; peptide; 8 AA.	
XX		
AC	AAW05539;	
XX		
DT	17-JUN-1997 (first entry)	
XX		
DE	Peptide fragment #1 of aminopeptidase of the invention.	
XX		
KW	Aminopeptidase; aspergillus oryzae; enzyme; protein hydrolysate; gluten;	
KW	protease; N-terminus.	
XX		
OS	Aspergillus oryzae.	
XX		
PN	WO9628542-A1.	
XX		
PD	19-SEP-1996.	
XX		
PF	15-MAR-1996; 96WO-DK00104.	
XX		
PR	16-MAR-1995; 95DK-0000262.	
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
PI	Dambmann C, Halkier T, Kauppinen S, Ostergaard PR;	
PI	Si JQ, Spendler T;	
XX		
DR	WPI; 1996-464617/46.	
XX		
PT	Enzyme with aminopeptidase activity - used in bread or	
PT	dough-improving compsns., and to reduce the bitter taste of proteins	
PT	or protein hydrolysates for foodstuffs, partic. cheese or cocoa	
XX		
PS	Claim 7; Page 56; 75pp; English.	
XX		
CC	AAW05538-W05543 represent fragments of the Aspergillus oryzae	
CC	aminopeptidase (see AAW05589) of the invention. Aminopeptidases are	
CC	capable of removing one or more amino terminal residues from	
CC	polypeptides. The enzyme is used in a preparation to reduce the bitter	
CC	taste of proteins or protein hydrolysates for foodstuffs, particularly	
CC	cheese or cocoa, so improving their flavour. It is also useful in a bread	
CC	or dough-improving composition, and in the preparation of baked products	
CC	from a flour dough or frozen dough. The enzyme is also useful to improve	
CC	dough stickiness, crumb structure or crust colour of a baked product. The	
CC	enzyme preparation can also be used to clean contact lenses and in	
CC	brewing. The enzyme does not degrade the network of the gluten normally	
CC	seen when proteases are used in the preparation of baked products. Thus,	
CC	the dough characteristics and crumb structure are unaffected.	
XX		
SQ	Sequence 8 AA;	
	Query Match 22.2%; Score 4; DB 17; Length 8;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	11 VEPF 14	
Db	4 VEPF 7	
RESULT 36		
AAW58608	ID AAW58608 standard; peptide; 8 AA.	
XX		
AC	AAW58608;	
XX		
DT	25-MAR-2003 (updated)	
DT	08-SEP-1998 (first entry)	
XX		

```

PN WO200066727-A1.
XX
PD 09-NOV-2000.
XX
PF 19-APR-2000; 2000WO-EP03552.
XX
PR 28-APR-1999; 99DE-1019225.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Heider K, Sommergruber W;
XX
DR WPI; 2000-679759/66.
XX
XX New tumor-associated antigen B99, useful in immunotherapy of cancer,
PT and related nucleic acid and antibodies -
XX
PS Example 7; Page 46; 75pp; German.
XX
CC This invention describes a novel tumor-associated antigen, designated
CC B99 which has anticancer activity. B99, or its immunogenic fragments or
CC peptides, induces a humoral and/or cellular immune response against
CC tumor cells that express B99. B99 (or its immunogenic fragments or
CC peptides) and also the nucleic acid that encodes them, are useful for
CC immunotherapy of cancer, in vivo or in vitro, especially cancers of
CC kidney, lung, colon, pancreas, breast or stomach. Cells that express B99
CC are useful in cancer vaccines and antibodies (Ab) directed against B99
CC are used for diagnosis and treatment of cancers that express B99,
CC optionally when coupled to a cytotoxin or radioisotope. Peptides from
CC B99 can also be used diagnostically to monitor a patient's response to
CC treatment and B99, or its DNA, are used to identify specific modulators,
CC particularly inhibitors, of B99 activity.
XX
SQ Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 EPFT 15
Db ||||
1 EPFT 4
RESULT 39
AAAY73039
ID AAY73039 standard; Peptide; 9 AA.
XX
AC AAY73039;
XX
DT 28-FEB-2000 (first entry)
XX
DE Hepatitis B virus (HBV)-derived MHC class I (CTL) epitope, #197.
XX
KW Chimeric; pan DR epitope; expression vector;
KW promoter; major histocompatibility complex; MHC; targeting; peptide;
KW epitope; antigen; presentation; class I; cytosolic pathway;
KW endoplasmic reticulum; class II; extracellular antigen;
KW endocytic pathway; helper T lymphocyte; HTL; universal epitope;
KW cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;
KW vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;
KW autoimmune disease; activation; antiviral; antimalarial;
XX immunoprotective.
XX
OS Synthetic.
OS Hepatitis b virus.
XX
PN WO9958658-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US10646.
XX
PR 13-MAY-1998; 98US-0078904.
PR 15-MAY-1998; 98US-0085751.
XX
XX (EPTM-) EPIMUNE INC.
XX
XX Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
PI Chesnut RW;
XX
DR WPI; 2000-039103/03.
XX
XX Expression vectors encoding major histocompatibility targeting
PT sequence, used as, e.g. tumor vaccines -

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PN WO200066727-A1.
XX
PD 09-NOV-2000.
XX
PF 19-APR-2000; 2000WO-EP03552.
XX
PR 28-APR-1999; 99DE-1019225.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Heider K, Sommergruber W;
XX
DR WPI; 2000-679759/66.
XX
XX New tumor-associated antigen B99, useful in immunotherapy of cancer,
PT and related nucleic acid and antibodies -
XX
PS Example 7; Page 46; 75pp; German.
XX
CC This invention describes a novel tumor-associated antigen, designated
CC B99 which has anticancer activity. B99, or its immunogenic fragments or
CC peptides, induces a humoral and/or cellular immune response against
CC tumor cells that express B99. B99 (or its immunogenic fragments or
CC peptides) and also the nucleic acid that encodes them, are useful for
CC immunotherapy of cancer, in vivo or in vitro, especially cancers of
CC kidney, lung, colon, pancreas, breast or stomach. Cells that express B99
CC are useful in cancer vaccines and antibodies (Ab) directed against B99
CC are used for diagnosis and treatment of cancers that express B99,
CC optionally when coupled to a cytotoxin or radioisotope. Peptides from
CC B99 can also be used diagnostically to monitor a patient's response to
CC treatment and B99, or its DNA, are used to identify specific modulators,
CC particularly inhibitors, of B99 activity.
XX
SQ Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 EPFT 15
Db ||||
2 EPFT 5
RESULT 38
AAB45559
ID AAB45559 standard; Protein; 9 AA.
XX
AC AAB45559;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human B99-1 HLA B7 immunogenic peptide SEQ ID NO 96.
XX
KW Tumor-associated antigen; B99; immunogenic; humoral immune response;
KW cellular immune response; immunotherapy; cancer; kidney; lung; colon;
KW pancreas; breast; stomach; vaccine; diagnosis; treatment.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200066727-A1.
XX
PD 09-NOV-2000.
XX
PF 19-APR-2000; 2000WO-EP03552.
XX
PR 28-APR-1999; 99DE-1019225.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Heider K, Sommergruber W;
XX
DR WPI; 2000-679759/66.

```


XX Claim 11; Page 65; 130pp; English.

PS Sequences AY72998-Y73086 represent hepatitis B virus (HBV)-derived MHC

XX class I (CTL) epitopes which are claimed for use in the present

CC invention. The invention relates to a novel expression vector comprising

CC a promoter operably linked to a fusion gene encoding a major

CC histocompatibility complex (MHC) targeting sequence, and two or more

CC heterologous peptide epitopes. The MHC targeting sequence may be a

CC class I targeting sequence, which directs an MHC class I epitope to

CC a cytosolic pathway or to the endoplasmic reticulum, or an MHC class

CC II targeting sequence, which directs extracellular antigens to

CC enter the endocytic pathway to be processed into antigen peptides

CC for presentation on MHC class II molecules. The heterologous

CC epitopes may comprise either helper T lymphocyte (HTL) epitopes,

CC or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL

CC epitope such as a pan DR epitope (PADRE). The vectors are useful

CC for stimulating an immune response in vivo, as well as for use in

CC assaying the human immunogenicity of a human T cell peptide epitope

CC vivo in a non-human mammal. They provide a nucleic acid vaccine for

CC enhancing immunity against infectious pathogens, such as viruses (e.g.,

CC HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g.,

CC Plasmodium falciparum, the cause of malaria) and also tumour cells and

CC autoimmune diseases. Universal MHC class II epitopes are advantageously

CC combined with other MHC class I and class II epitopes to increase the

CC number of cells that are activated in response to a given antigen and

CC provide a broader population coverage of MHC-reactive alleles.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTES 17

Db 2 FTES 5

RESULT 40

AAM24524

ID AAM24524 standard; Peptide; 9 AA.

XX AAM24524;

AC AAM24524;

XX 04-DEC-2001 (first entry)

DT Human MHC class I molecule HLA-A1 binding 83P5G4 peptide #1.

DE

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;

XW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;

KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;

KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;

KW chromosome 1q31-q32.

XX Homo sapiens.

OS

XX W0200159115-A2.

PN 16-AUG-2001.

PD

XX 09-FEB-2001; 2001WO-US04426.

PF

XX (UROC-) UROGENESYS INC.

PR

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

PI Mitchell SC, Jakobovits A;

PI WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or

XX therapeutic agent in multiple cancers such as prostate, bladder and

XX bone cancer -

XX Example 15; Page 79; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and

CC peptide fragments of the protein. 83P5G4 exhibits prostate specific

CC expression in normal adult tissue, but it is also aberrantly expressed in

CC many cancers including tumours of the prostate, testis, bladder, kidney,

CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,

CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and

CC peptide fragments and specific PCR primers are therefore useful for

CC diagnosing and treating cancer. A vector comprising a polynucleotide

CC which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a

CC polynucleotide having the 83P5G4 coding sequence, are both useful in the

CC preparation of a composition for treating a patient with a cancer that

CC expresses 83P5G4. The sequences can be used in diagnostic methods to

CC monitor the level of 83P5G4 gene products in serum, blood, urine and

CC tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18

Db 2 TESQ 5

RESULT 41

AAM24745

ID AAM24745 standard; Peptide; 9 AA.

XX AAM24745;

AC AAM24745;

XX 04-DEC-2001 (first entry)

DT Human MHC class I molecule HLA-A3 binding 83P5G4 peptide #22.

DE

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;

XW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;

KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;

KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;

KW chromosome 1q31-q32.

XX Homo sapiens.

OS

XX W0200159115-A2.

PN 16-AUG-2001.

PD

XX 09-FEB-2001; 2001WO-US04426.

PF

XX (UROC-) UROGENESYS INC.

PR

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

PI Mitchell SC, Jakobovits A;

PI WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or

XX therapeutic agent in multiple cancers such as prostate, bladder and

XX bone cancer -

XX Example 15; Page 79; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and

CC peptide fragments of the protein. 83P5G4 exhibits prostate specific

CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX
 XX
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 TESQ 18
 |||||
 Db 2 TESQ 5

RESULT 42
 AAM24826
 ID AAM24826 standard; Peptide; 9 AA.
 XX
 AC AAM24826;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #3.
 XX
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytotatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.
 XX
 OS Homo sapiens.
 XX
 PN WO200159115-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04426.
 XX
 PR 09-FEB-2000; 2000US-0181261.
 XX
 PA (UROG-) UROGENESYS INC.
 XX
 PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
 PI Mitchell SC, Jakobovits A;
 XX
 WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or
 XX therapeutic agent in multiple cancers such as prostate, bladder and
 XX bone cancer -
 XX
 XX Example 15; Page 81; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and
 XX peptide fragments of the protein. 83P5G4 exhibits prostate specific
 XX expression in normal adult tissue, but it is also aberrantly expressed in
 XX many cancers including tumours of the prostate, testis, bladder, kidney,
 XX brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 XX liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 XX peptide fragments and specific PCR primers are therefore useful for
 XX diagnosing and treating cancer. A vector comprising a polynucleotide
 XX which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX
 XX
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 TESQ 18
 |||||
 Db 2 TESQ 5

RESULT 43
 AAM24925
 ID AAM24925 standard; Peptide; 9 AA.
 XX
 AC AAM24925;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #2.
 XX
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytotatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.
 XX
 OS Homo sapiens.
 XX
 PN WO200159115-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04426.
 XX
 PR 09-FEB-2000; 2000US-0181261.
 XX
 PA (UROG-) UROGENESYS INC.
 XX
 PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
 PI Mitchell SC, Jakobovits A;
 XX
 WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or
 XX therapeutic agent in multiple cancers such as prostate, bladder and
 XX bone cancer -
 XX
 XX Example 15; Page 84; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and
 XX peptide fragments of the protein. 83P5G4 exhibits prostate specific
 XX expression in normal adult tissue, but it is also aberrantly expressed in
 XX many cancers including tumours of the prostate, testis, bladder, kidney,
 XX brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 XX liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 XX peptide fragments and specific PCR primers are therefore useful for
 XX diagnosing and treating cancer. A vector comprising a polynucleotide
 XX which encodes a single chain monoclonal antibody, that immunospecifically
 XX binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 XX polynucleotide having the 83P5G4 coding sequence, are both useful in the
 XX preparation of a composition for treating a patient with a cancer that
 XX expresses 83P5G4. The sequences can be used in diagnostic methods to
 XX monitor the level of 83P5G4 gene products in serum, blood, urine and
 XX tissue and to thereby detect the presence of cancerous cells.

CC	treating cancer and the vector is useful for treating a patient with a
CC	cancer that expresses 83P2H3.The immunological methods are useful for
CC	generating an immune response against 83P2H3, and for detecting the
CC	presence of 83P2H3-related protein or polynucleotide in a biological
CC	sample from a patient who has or who is suspected of having cancer. The
CC	antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC	methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC	83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC	isolating 83P2H3 homologues/related molecules, and for generating anti-
CC	idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
CC	is an HLA binding peptide motif from 83P2H3 or its related protein
CC	CatRfP2E11.
XX	
SQ	Sequence 9 AA;
	Query Match 22.2%; Score 4; DB 23; Length 9;
	Best Local Similarity 100.0%; Pred.No. 9.3e+05;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	8 KYPV 11
Dd	6 KYPV 9
RESULT 45	
AAU94868	ID ID AAU94868 standard; Peptide; 9 AA.
XX	
XX	AAU94868;
XX	
DT	02-JUL-2002 (first entry)
XX	
DE	Human novel protein CatRfP2E11 HLA binding peptide #401.
XX	
KW	Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatRfP2E11;
XW	calcium transport protein; cancer; prostate cancer; cycostatic;
XW	chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX	
OS	Homo sapiens.
XX	
PN	W0200214361-A2.
XX	
PD	21-FEB-2002.
XX	
XX	17-AUG-2001; 2001WO-US25782.
PX	
PF	
PR	17-AUG-2000; 2000US-226329P.
XX	
PA	(AGEN-) AGENSYS INC.
PI	Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
PI	Levin E, Hubert RS, Ge W, Jakobovits A;
XX	
DR	WFI; 2002-269179/31.
XX	
PT	Monitoring 83P2H3 gene products for monitoring the presence of cancer
PT	in a subject, comprises determining the status of 83P2H3 gene products
PT	in a tissue sample from the subject and comparing it to a normal sample
PT	-
XX	
PS	Example 11; Page 193; 270pp; English.
XX	
CC	The invention relates to monitoring 83P2H3 (a calcium transport
CC	protein whose gene is located on chromosome 7q34) gene products in a
CC	biological sample from a patient who has or is suspected of having
CC	cancer (especially prostate cancer), comprises: (a) determining the
CC	status of 83P2H3 gene products expressed by cells in a tissue sample from
CC	an individual and (b) comparing the status to the status of 83P2H3 gene
CC	products in a normal sample. Also included are modulators of 83P2H3
CC	function or status, generating antibodies/immune response against
CC	83P2H3 (or related protein CatRfP2E11 whose gene is located on chromosome
CC	12q24.1) using identified HLA (human leukocyte antigen) binding
CC	peptides derived from the protein, delivering a cytotoxic agent to

CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 KYPV 11
 ||||
 Db 1 KYPV 4

RESULT 46
 AAU95255
 ID AAU95255 standard; Peptide; 9 AA.

XX AC AAU95255;
 XX AC

DT 02-JUL-2002 (first entry)

XX Human novel protein CaTrF2E11 HLA binding peptide #588.

DE Human; human leukocyte antigen; HLA; immunogen: 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DBH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX WPI; 2002-269179/31.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer
 PT in a subject, comprises determining the status of 83P2H3 gene products
 PT in a tissue sample from the subject and comparing it to a normal sample

PS Example 11; Page 208; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 KYPV 11
 ||||
 Db 4 KYPV 7

RESULT 47
 ABU20159
 ID ABU20159 standard; Peptide; 9 AA.

XX AC ABU20159;
 XX AC

DT 10-APR-2003 (first entry)

XX MHC binding peptide SEQ ID No 324.

DE Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
 XX antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 XX inflammation; gene therapy; MHC binding peptide.

OS Synthetic.

XX WO200294981-A2.

PN 28-NOV-2002.

XX 16-MAY-2002; 2002WO-IL00383.

XX 16-MAY-2001; 2001US-290958P.
 PR 29-MAY-2001; 2001US-0855548.
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
 XX WPI; 2003-210043/20.
 DR Identifying peptides that are capable of binding to major
 PT histocompatibility complex (MHC) molecules of a particular haplotype by
 PT analyzing peptides bound to the soluble and secreted form of the MHC
 PT molecules of the particular haplotype -
 XX Claim 58; Page 226; 238pp; English.
 XX The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention.
 XX Sequence 9 AA;
 SQ
 Query Match 22.2%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 EPFT 15
 Db 5 EPFT 8
 ||||
 ||||
 RESULT 48
 AAY94204
 ID AAY94204 standard; peptide; 10 AA.
 XX AC AAY94204;
 XX 28-JUL-2000 (first entry)
 DT Human cytotoxic T lymphocyte-recognised gata-1 peptide hug 378-87.
 DE Hug 378-87; peptide; epitope; gata-1 gene; leukaemia; immunotherapy;
 XX transcription factor.
 KW Homo sapiens.
 XX OS
 XX W0200026249-Al.
 XX 11-MAY-2000.
 XX 02-NOV-1999; 99WO-GB03572.
 XX 02-NOV-1998; 98GB-0023897.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA Stauss HJ, Gao L;
 PI WPI; 2000-376123/32.
 XX Novel peptides comprising WT-1 and GATA-1 epitopes, their fragments or
 PT variants, useful as vaccines for cancer immunotherapy -
 XX

PS Claim 3; Page 74; 93pp; English.
 XX The present sequence is peptide epitope hug 378-87, produced by gata-1
 CC expressing cells and found at residues 378-387 of the gata-1 protein,
 CC which is recognised by cytotoxic T lymphocytes. Gata-1 is aberrantly
 CC expressed in leukaemias. The peptide can be used as a vaccine to
 CC stimulate the elimination, by cytotoxic T lymphocytes, of cancer cells
 CC aberrantly expressing gata-1. In addition, the nucleic acid encoding the
 CC peptide may also be used in the same manner. Alternatively, the peptide
 CC may be used in vitro to produce activated cytotoxic T lymphocytes.
 XX Sequence 10 AA;
 SQ
 Query Match 22.2%; Score 4; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 MPFP 7
 Db 3 MPFP 6
 ||||
 ||||
 RESULT 49
 AAG68075
 ID AAG68075 standard; peptide; 10 AA.
 XX AC AAG68075;
 XX 17-DEC-2001 (first entry)
 DT Antitumour cancer cell recognition peptide PI9-9.
 DE Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 XX tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.
 XX Homo sapiens.
 XX OS
 XX JP2001245675-A.
 XX 11-SEP-2001.
 XX 25-DEC-2000; 2000JP-0393047.
 XX 28-DEC-1999; 99JP-0374322.
 XX (ITOY/) ITO Y.
 XX WPI; 2001-610076/70.
 XX New peptides for recognizing cancer cells with tumor specific cytotoxic
 PT T lymphocytes and for treating cancer -
 XX Example 1; Page 10; 14pp; Japanese.
 XX The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides
 CC of sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity
 CC with the above mentioned sequences; and (4) peptides with one or more
 CC deleted, substituted, added or inserted amino acid(s) of the above
 CC mentioned sequences, particularly those having recognising property due
 CC to HLA-A2402 binding CTL, especially having at least 5 amino acids,
 CC used for medicine, particularly anticancer agents, derived from
 CC antitumour antigenic peptides of lck, src family, SART-1, SART-3 or
 CC cyclophilin B genes. The antitumour peptides have cytostatic activities.
 CC The peptides are used for the treatment of cancer. The peptides cause
 CC activation of CTL in cancer patients. The present sequence represents
 CC a peptide used in an example from the present invention.
 XX Sequence 10 AA;
 SQ

Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6
 ||||
Db 5 EMPF 8

RESULT 50
AAB75678
ID AAB75678 standard; Peptide; 10 AA.
XX AC
XX AAB75678;
DT 10-APR-2001 (first entry)
XX DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:81.
XX XX
XX Human; cancer associated antigen precursor; cancer associated antigen;
KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
KW vaccine; cancer.
XX OS Homo sapiens.
XX WO200100874-A2.
PN 04-JAN-2001.
PD
XX 23-JUN-2000; 2000WO-US17207.
PF 30-JUN-1999; 99US-0346498.
PR (LUDW-) LUDWIG INST CANCER RES.
XX PA
XX Sahin U, Tureci O, Pfreundschuh M;
PI WPI; 2001-112465/12.
XX DR
XX Diagnosing a disorder characterized by expression of a human cancer
PT associated antigen precursor, comprises detecting interaction of an
PT agent with a nucleic acid molecule encoding the antigen precursor -
XX
XX Example 10; Page 63; 126pp; English.
PS
CC The present invention describes a method for diagnosing a disorder
CC characterised by expression of a human cancer associated antigen (CAA)
CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1)
CC comprising contacting the biological sample with an agent (A) that
CC specifically binds to N1, (I) or its fragment, complexed with an human
CC leukocyte antigen (HLA) molecule and determining the interaction between
CC the agent and N1 or (I). (I) has cytostatic activity and can be used in
CC gene therapy and vaccine production. The method can be used for treating
CC a subject with a condition characterised by expression of (I) in cells
CC of a subject. AAB75607 and AAB75608 represent proteins from human cancer
CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA
CC class I binding motifs in human cancer associated antigen precursors
CC given in the exemplification of the present invention.
XX
XX SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
 ||||
Db 5 PVEP 8

RESULT 51
AAB49971
ID AAB49971 standard; peptide; 10 AA.

XX AAB49971;
AC 08-MAR-2001 (first entry)
DT Human melanoma associated antigen MAGE-12 peptide.
XX Human; melanoma associated antigen; vaccine; cancer; immunogen.
XX Homo sapiens.
OS
XX WO200071573-A2.
PN 30-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-EP04465.
PF 21-MAY-1999; 99IT-MI01121.
PR (GENE-) GENERA SPA.
XX PA
XX Traversari C, Tanzarella S, Bordignon C;
PI WPI; 2001-032020/04.
XX DR
XX Novel peptides that bind to allele HLA-B (asterisk)3701, useful for
PT preparing anti-tumour medicament, and as a cancer vaccine -
PT
XX Claim 1; Page 23; 33pp; English.
PS
XX The present invention provides novel peptides based on the melanoma
CC associated antigens MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-6 and MAGE-12.
CC These peptides can be used in vaccines to treat cancer, particularly
CC melanoma.
XX
XX SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
 ||||
Db 2 EPFT 5

RESULT 52
AAM24575
ID AAM24575 standard; Peptide; 10 AA.
XX AC AAM24575;
XX 04-DEC-2001 (first entry)
DT
XX Human MHC class I molecule HLA-A1 binding 83P5G4 peptide #52.
DE
XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
XX Homo sapiens.
OS
XX WO200159115-A2.
PN 16-AUG-2001.
PD
XX 09-FEB-2001; 2001WO-US04426.
PF 09-FEB-2000; 2000US-0181261.
PR
XX (UOOG-) UROGENESYS INC.
PA

XX Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX WPI; 2001-514669/56.
DR
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX Example 15; Page 75; 112pp; English.
XX The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TESQ 18
Db 2 TESQ 5
RESULT 53
AAM24783
ID AAM24783 standard; Peptide; 10 AA.
XX
AC AAM24783;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A3 binding 83P5G4 peptide #60.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN W0200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX WPI; 2001-514669/56.
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and/or

PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX Example 15; Page 80; 112pp; English.
XX The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TESQ 18
Db 5 TESQ 8
RESULT 54
AAM24905
ID AAM24905 standard; Peptide; 10 AA.
XX
AC AAM24905;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #82.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN W0200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX WPI; 2001-514669/56.
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX Example 15; Page 83; 112pp; English.
XX The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific

CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, and
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
 ||||
 Db 3 TESQ 6

RESULT 55
 AAM24911
 ID AAM24911 standard; Peptide; 10 AA.

XX AC AAM24911;

XX DT 04-DEC-2001 (first entry)

XX DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #88.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome lq31-q32.

XX OS Homo sapiens.

XX PN WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UROG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PI Mitchell SC, Jakobovits A;

XX PS WPI; 2001-514669/56.

XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -

XX PS Example 15; Page 84; 112pp; English.

XX CC The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
 ||||
 Db 2 TESQ 5

RESULT 56

AAM24914

ID AAM24914 standard; Peptide; 10 AA.

XX AC AAM24914;

XX DT 04-DEC-2001 (first entry)

XX DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #91.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome lq31-q32.

XX OS Homo sapiens.

XX PN WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UROG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PI Mitchell SC, Jakobovits A;

XX PS WPI; 2001-514669/56.

XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -

XX PS Example 15; Page 84; 112pp; English.

XX CC The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX


```

SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db ||||
4 TESQ 7

RESULT 57
AAM25003
ID AAM25003 standard; Peptide; 10 AA.
XX
AC AAM25003;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #80.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
XX Homo sapiens.
XX
XX WO200159115-A2.
XX
PD 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04426.
XX
XX 09-FEB-2000; 2000US-0181261.
XX
XX (UROC-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
XX WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
XX therapeutic agent in multiple cancers such as prostate, bladder and
XX bone cancer -
XX
XX Example 15; Page 86; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db ||||
4 TESQ 7

RESULT 58
AAM25222
ID AAM25222 standard; Peptide; 10 AA.
XX
AC AAM25222;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC molecule HLA-B35 binding 83P5G4 peptide #99.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
XX Homo sapiens.
XX
XX WO200159115-A2.
XX
PD 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04426.
XX
XX 09-FEB-2000; 2000US-0181261.
XX
XX (UROC-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
XX WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
XX therapeutic agent in multiple cancers such as prostate, bladder and
XX bone cancer -
XX
XX Example 15; Page 92; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db ||||
5 TESQ 8

RESULT 59
AAO17822
ID AAO17822 standard; peptide; 10 AA.

```

XX AAO17822;
AC
XX
DT 15-AUG-2002 (first entry)
XX
XX Sponge okadaic acid combining protein related peptide #3.
DE
XX
KW Sponge; okadaic acid combining protein; protein dephosphorylase 1;
KW protein dephosphorylase 2A; okadaic acid; cytotoxicity inactivation.
XX
XX Unidentified.
OS
XX
XX JP2002101886-A.
PN
XX
XX 09-APR-2002.
PD
XX
XX 28-SEP-2000; 2000JP-0297436.
PF
XX
XX 28-SEP-2000; 2000JP-0297436.
PR
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX
XX WPI; 2002-440456/47.
DR
XX
XX A new protein combining with Okadaic acid and its gene, has no
PT enzymatic activity of protein dephosphorylase 1 and 2A -
PT
XX
XX Example 3; Page 5; 12pp; Japanese.
PS
XX
XX The present invention relates to a protein having combinability to
CC Okadaic acid and having substantially no enzymatic activity of protein
CC dephosphorylase 1 and 2A. The protein is useful as a drug for
CC inactivating cytotoxicity of a substance enzymatic activity-inhibiting
CC activity such as Okadaic acid. The present sequence is a peptide
CC described in the exemplification of the invention.
CC
XX
SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||
Db 2 TESQ 5

RESULT 60
AAU94390
ID AAU94390 standard; Peptide; 10 AA.
XX
XX
AC AAU94390;
XX
XX
DT 02-JUL-2002 (first entry)
XX
XX Human novel protein CaTrF2E11 HLA binding peptide #173.
DE
XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX
XX Homo sapiens.
OS
XX WO200214361-A2.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US25782.
PF
XX
XX 17-AUG-2000; 2000US-226329P.
PR
XX
XX (AGEN-) AGENSYS INC.
PA
XX

PI Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX
XX WPI; 2002-269179/31.
DR
XX
XX Monitoring 83p2h3 gene products for monitoring the presence of cancer
PT in a subject, comprises determining the status of 83p2h3 gene products
PT in a tissue sample from the subject and comparing it to a normal sample
PT -
XX
XX Example 11; Page 176; 270pp; English.
PS
XX
XX The invention relates to monitoring 83p2h3 (a calcium transport
CC protein whose gene is located on chromosome 7q34) gene products in a
CC biological sample from a patient who has or is suspected of having
CC cancer (especially prostate cancer), comprises: (a) determining the
CC status of 83p2h3 gene products expressed by cells in a tissue sample from
CC an individual and (b) comparing the status to the status of 83p2h3 gene
CC products in a normal sample. Also included are modulators of 83p2h3
CC function or status, generating antibodies/immune response against
CC 83p2h3 (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding
CC peptides derived from the protein, delivering a cytotoxic agent to
CC a cell expressing 83p2h3 by conjugating the agent to an anti-83p2h3
CC antibody, a recombinant protein comprising an antigen-binding region of
CC the antibody, a non-human transgenic animal that produces the recombinant
CC protein, a hybridoma that produces the recombinant protein, a single-
CC chain monoclonal antibody that comprises the variable domains of the
CC heavy and light chains of the anti-83p2h3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83p2h3 protein, by providing a 83p2h3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83p2h3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83p2h3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83p2h3. The immunological methods are useful for
CC generating an immune response against 83p2h3, and for detecting the
CC presence of 83p2h3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83p2h3 and mutant
CC 83p2h3-related proteins, for purifying a 83p2h3-related protein, for
CC isolating 83p2h3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83p2h3 protein. The present sequence
CC is an HLA binding peptide motif from 83p2h3 or its related protein
CC CaTrF2E11.
XX
XX
SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11
|||
Db 6 KYPV 9

RESULT 61
AAU94412
ID AAU94412 standard; Peptide; 10 AA.
XX
XX
AC AAU94412;
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Human novel protein CaTrF2E11 HLA binding peptide #195.
DE
XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX

XX OS Homo sapiens.
XX PN WO200214361-A2.
XX PD 21-FEB-2002.
XX XX 17-AUG-2001; 2001WO-US25782.
XX PF 17-AUG-2000; 2000US-226329P.
XX PR (AGEN-) AGENSYS INC.
XX PA Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
XX PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX DR WPI; 2002-269179/31.
XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer
XX PT in a subject, comprises determining the status of 83P2H3 gene products
XX PT in a tissue sample from the subject and comparing it to a normal sample
XX -
XX PS Example 11; Page 177; 270pp; English.
XX CC The invention relates to monitoring 83P2H3 (a calcium transport
CC protein whose gene is located on chromosome 7q34) gene products in a
CC biological sample from a patient who has or is suspected of having
CC cancer (especially prostate cancer), comprises: (a) determining the
CC status of 83P2H3 gene products expressed by cells in a tissue sample from
CC an individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against
CC 83P2H3 (or related protein CatrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding
CC peptides derived from the protein, delivering a cytotoxic agent to
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
CC antibody, a recombinant protein comprising an antigen-binding region of
CC the antibody, a non-human transgenic animal that produces the recombinant
CC protein, a hybridoma that produces the recombinant protein, a single-
CC chain monoclonal antibody that comprises the variable domains of the
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC epitope that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CatrF2E11.
XX SQ Sequence 10 AA;
XX
XX Query Match 22.2%; Score 4; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4.2e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 KYPV 11
XX ||||
XX Db 7 KYPV 10

RESULT 62
AAU95356
ID AAU95356 standard; Peptide; 10 AA.
XX AC AAU95356;
XX DT 02-JUL-2002 (first entry)
XX DE Human novel protein CatrF2E11 HLA binding peptide #639.
XX KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatrF2E11;
XX KW calcium transport protein; cancer; prostate cancer; cytostatic;
XX KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX OS Homo sapiens.
XX PN WO200214361-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US25782.
XX PR 17-AUG-2000; 2000US-226329P.
XX PA (AGEN-) AGENSYS INC.
XX PI Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
XX PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX DR WPI; 2002-269179/31.
XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer
XX PT in a subject, comprises determining the status of 83P2H3 gene products
XX PT in a tissue sample from the subject and comparing it to a normal sample
XX -
XX PS Example 11; Page 212; 270pp; English.
XX CC The invention relates to monitoring 83P2H3 (a calcium transport
CC protein whose gene is located on chromosome 7q34) gene products in a
CC biological sample from a patient who has or is suspected of having
CC cancer (especially prostate cancer), comprises: (a) determining the
CC status of 83P2H3 gene products expressed by cells in a tissue sample from
CC an individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against
CC 83P2H3 (or related protein CatrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding
CC peptides derived from the protein, delivering a cytotoxic agent to
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
CC antibody, a recombinant protein comprising an antigen-binding region of
CC the antibody, a non-human transgenic animal that produces the recombinant
CC protein, a hybridoma that produces the recombinant protein, a single-
CC chain monoclonal antibody that produces the recombinant protein, a single-
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC epitope that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CatrF2E11.

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CC  CaTrF2E11.
XX  Sequence 10 AA;
SQ  Query Match 22.2%; Score 4; DB 23; Length 10;
    Best Local Similarity 100.0%; Pred. No. 4.2e+02;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8 KYPV 11
Db  5 KYPV 8
    ||||
    ||||

RESULT 63
AAU95384
ID  AAU95384 standard; Peptide; 10 AA.
XX
AC  AAU95384;
XX
DT  02-JUL-2002 (first entry)
XX
DE  Human novel protein CaTrF2E11 HLA binding peptide #651.
XX
KW  Human; human leukocyte antigen; HLA; immunogen; 83p2H3; CaTrF2E11;
KW  calcium transport protein; cancer; prostate cancer; cytostatic;
KW  chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX
OS  Homo sapiens.
XX
PN  WO200214361-A2.
XX
PD  21-FEB-2002.
XX
PF  17-AUG-2001; 2001WO-US25782.
XX
PR  17-AUG-2000; 2000US-226329P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI  Levin E, Hubert RS, Ge W, Jakobovits A;
XX
XX  WPI; 2002-269179/31.
XX
XX  Monitoring 83p2H3 gene products for monitoring the presence of cancer
PT  in a subject, comprises determining the status of 83p2H3 gene products
PT  in a tissue sample from the subject and comparing it to a normal sample
PT
XX
PS  Example 11; Page 196; 270pp; English.
XX
XX  The invention relates to monitoring 83p2H3 (a calcium transport
CC  protein whose gene is located on chromosome 7q34) gene products in a
CC  biological sample from a patient who has or is suspected of having
CC  cancer (especially prostate cancer), comprises: (a) determining the
CC  status of 83p2H3 gene products expressed by cells in a tissue sample from
CC  an individual and (b) comparing the status to the status of 83p2H3 gene
CC  products in a normal sample. Also included are modulators of 83p2H3
CC  function or status, generating antibodies/immune response against
CC  83p2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
CC  12q24.1) using identified HLA (human leukocyte antigen) binding
CC  peptides derived from the protein, delivering a cytotoxic agent to
CC  a cell expressing 83p2H3 by conjugating the agent to an anti-83p2H3
CC  antibody, a recombinant protein comprising an antigen-binding region of
CC  the antibody, a non-human transgenic animal that produces the recombinant
CC  protein, a hybridoma that produces the recombinant protein, a single-
CC  chain monoclonal antibody that comprises the variable domains of the
CC  heavy and light chains of the anti-83p2H3 antibody, a vector comprising a
CC  polynucleotide that encodes the monoclonal antibody and inducing an
CC  immune response to a 83p2H3 protein, by providing a 83p2H3-related
CC  protein that comprises a T cell or B cell epitope, and contacting the
CC  epitope with an immune system T cell or B cell, respectively. The method
CC  is useful for monitoring 83p2H3 gene products in a biological sample for
XX

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CC  monitoring the presence of cancer in an individual. The modulator is
CC  useful for inhibiting the growth of cancer cells that express 83p2H3, for
CC  treating cancer and the vector is useful for treating a patient with a
CC  cancer that expresses 83p2H3. The immunological methods are useful for
CC  generating an immune response against 83p2H3, and for detecting the
CC  presence of 83p2H3-related protein or polynucleotide in a biological
CC  sample from a patient who has or who is suspected of having cancer. The
CC  antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC  methodologies and treatment, to detect and quantify 83p2H3 and mutant
CC  83p2H3-related proteins, for purifying a 83p2H3-related protein, for
CC  isolating 83p2H3 homologues/related molecules, and for generating anti-
CC  idiotypic antibodies that mimic the 83p2H3 protein. The present sequence
CC  is an HLA binding peptide motif from 83p2H3 or its related protein
CC  CaTrF2E11.
XX
SQ  Sequence 10 AA;
    Query Match 22.2%; Score 4; DB 23; Length 10;
    Best Local Similarity 100.0%; Pred. No. 4.2e+02;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8 KYPV 11
Db  1 KYPV 4
    ||||
    ||||

RESULT 64
ABR47212
ID  ABR47212 standard; Peptide; 10 AA.
XX
AC  ABR47212;
XX
DT  10-JUN-2003 (first entry)
XX
DE  Staphylococcus aureus CHIPS-related peptide #2401.
XX
KW  CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5ar;
KW  formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW  inflammation; cardiovascular disease; central nervous system disease;
KW  gastrointestinal disease; skin disease; genitourinary disease;
KW  joint disease; respiratory disease; HIV infection; antiinflammatory;
KW  cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
KW  gynecological; immunosuppressive; anti-HIV.
XX
OS  Staphylococcus aureus.
OS  Synthetic.
XX
PN  WO2003006048-A1.
XX
XX  23-JAN-2003.
XX
PF  11-JUL-2001; 2001WO-EP080004.
XX
PR  11-JUL-2001; 2001WO-EP080004.
XX
PA  (JARI-) JARI PHARM BV.
XX
PI  Van Kessel CPM, Gosselaar-de Haas CUC, Kruijtzer JAW;
PI  Van Strijp JAG;
XX
XX  WPI; 2003-247783/25.
XX
XX  Combination of peptides derived from chemotaxis inhibiting protein from
PT  Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT  prophylaxis and treatment of inflammation, cardiovascular, skin and
PT  kidney diseases
XX
PS  Example 1; Page 55; 89pp; English.
XX
XX  The present invention relates to peptides (ABR44811-ABR47162 and
CC  ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC  from Staphylococcus aureus. The peptide fragments are useful in the
CC  prophylaxis or treatment of diseases or disorders involving the
XX

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CC C5a-receptor (C5aR) and/or formulated peptide receptor (FPR) or
 CC neutrophils, monocytes and endothelial cells or involving acute or
 CC chronic inflammation reactions. The diseases or disorders include
 CC cardiovascular diseases, disease of the central nervous system,
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
 CC diseases, respiratory diseases and HIV infection.
 CC
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFPK 8
 ||||
 Db 5 PFPK 8

RESULT 65
 ABR47239
 ID ABR47239 standard; Peptide; 10 AA.
 XX
 AC ABR47239;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #2428.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP08004.
 XX
 PR 11-JUL-2001; 2001WO-EP08004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-247783/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 CC Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 CC prophylaxis and treatment of inflammation, cardiovascular, skin and
 CC kidney diseases -
 XX
 PS Example 1; Page 55; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and
 CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
 CC from Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the
 CC C5a-receptor (C5aR) and/or formulated peptide receptor (FPR) or
 CC neutrophils, monocytes and endothelial cells or involving acute or
 CC chronic inflammation reactions. The diseases or disorders include
 CC cardiovascular diseases, disease of the central nervous system,
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
 CC diseases, respiratory diseases and HIV infection.
 CC
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPFT 15
 ||||
 Db 4 EPFT 7

RESULT 66
 ABR47292
 ID ABR47292 standard; Peptide; 10 AA.
 XX
 AC ABR47292;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #2481.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP08004.
 XX
 PR 11-JUL-2001; 2001WO-EP08004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-247783/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 CC Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 CC prophylaxis and treatment of inflammation, cardiovascular, skin and
 CC kidney diseases -
 XX
 PS Example 1; Page 56; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and
 CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
 CC from Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the
 CC C5a-receptor (C5aR) and/or formulated peptide receptor (FPR) or
 CC neutrophils, monocytes and endothelial cells or involving acute or
 CC chronic inflammation reactions. The diseases or disorders include
 CC cardiovascular diseases, disease of the central nervous system,
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
 CC diseases, respiratory diseases and HIV infection.
 CC
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPFP 7
 ||||
 Db 4 MPFP 7

XX EP600326-A2.
XX 08-JUN-1994.
XX 20-NOV-1993; 93EP-0118697.
XX 28-NOV-1992; 92DE-4240056.
XX (BOFF) BOEHRINGER MANNHEIM GMBH.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX Burns G, Engel W, Seidel C;
XX WPI; 1994-177677/22.
XX New streptolysin O-peptide antigen - for detecting specific
XX antibodies and is immunogens e.g. in vaccines, for diagnosis of,
XX and protection against, streptococcal infections
XX Claim 1; Page 10; 11pp; German.
XX Synthetic peptides having this sequence or at least a 4 (pref. less
XX than 7) amino acid fragment of it are streptolysin O peptide
XX antigens. The antigens are useful in immunoassays to determine
XX specific antibodies, e.g. to differentiate between rheumatism and
XX rheumatoid arthritis.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 11 AA;
XX
XX Query Match 22.2%; Score 4; DB 15; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 KEMP 5
XX DB 6 KEMP 9
XX
XX RESULT 70
XX AAB23183
XX ID AAB23183 standard; peptide; 12 AA.
XX AC
XX XX
XX DT 29-JAN-2001 (first entry)
XX DE Hsp47-binding hydrophobic phage display dodecapeptide, SEQ ID NO:5.
XX
XX KW Hsp47-binding hydrophobic dodecapeptide; phage display library;
XX KW Hsp47 external domain; carcinoma; cancer; targeting molecule;
XX KW therapy; diagnosis; detection; imaging; drug delivery; invasion;
XX KW migration; metastasis; modulation; tumour; skin; basal cells; colon;
XX KW large intestine; lung; breast; bladder; oral cancer;
XX KW head and neck cancer; larynx; nasopharynx; adrenal cortex;
XX KW apocrine gland; kidney; liver; pancreas; prostate.
XX OS Synthetic.
XX
XX XX WO200054805-A1.
XX PN
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000WO-US06588.
XX XX
XX PR 15-MAR-1999; 99US-0124481.
XX XX
XX PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX XX
XX PI Sauk JJ;
XX XX

DR WPI; 2000-655997/63.
XX Treating, diagnosing or modulating a carcinoma cell, which expresses
XX Heat shock protein 47 on its surface, involves administering an agent
XX comprising targeting moiety which binds to Hsp47 external domain -
XX Claim 6; Page 8; 87pp; English.
XX
XX The invention relates to methods of treating and diagnosing carcinomas
XX in which heat shock protein 47 (Hsp47) is expressed on the surface
XX of the carcinoma cells, involving administering an agent comprising a
XX targeting moiety which specifically binds to the external domain of
XX Hsp47. The invention also relates to peptides (AAB23181-B23203) which
XX specifically bind to external domains of such surface-localised Hsp47
XX molecules and have sequences encompassed by the generic sequences
XX XHYYXXHYYXXHYY or HYYXXHYYXXHYYXX where X, independently, can be
XX any amino acid and HY, independently, can be any hydrophobic amino acid.
XX The invention also encompasses methods of screening for agents which
XX bind Hsp47 external domains. Hsp47-binding agents can be used to
XX treat Hsp47-expressing carcinomas, and for modulating the activity of a
XX tumour cell with respect to invasion, migration, motility or metastasis,
XX or to its interaction with the extracellular matrix. The targeting
XX moiety (such as an Hsp47-binding peptide, a toxin or an antibody) may be
XX coupled with a therapeutic moiety (such as a cytotoxic agent or a
XX therapeutic gene) for cancer treatment, or with a detectable moiety for
XX imaging. Carcinomas which may be treated or diagnosed according to
XX methods of the invention include those of the skin, basal cells, large
XX intestine, lung, colon, breast, bladder, oral, head and neck, larynx,
XX nasopharynx, adrenal cortex, apocrine glands, kidney, liver, pancreas, or
XX prostate. Targeting carcinoma cells with Hsp47-binding agents results in
XX efficient delivery of therapeutic agents, reduced doses, reduced side
XX effects and sensitive detection or imaging of carcinoma cells. Sequences
XX AAB23181-B23191 represent predominantly hydrophobic phage display library
XX dodecapeptides identified as being able to bind Hsp47 in an
XX exemplification of the invention.
XX Sequence 12 AA;
XX
XX Query Match 22.2%; Score 4; DB 21; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 KYPV 11
XX DB 7 KYPV 10
XX
XX RESULT 71
XX AAB57781
XX ID AAB57781 standard; Peptide; 12 AA.
XX XX
XX AC AAB57781;
XX XX
XX DT 09-MAR-2001 (first entry)
XX XX
XX DE Bovine DNaseI peptide #5.
XX XX
XX KW Retrotransposon; Genetic defect; cystic fibrosis.
XX OS Bos taurus.
XX
XX XX US6150160-A.
XX PN
XX PD 21-NOV-2000.
XX XX
XX PF 28-APR-1997; 97US-0847844.
XX XX
XX PR 16-NOV-1995; 95US-0006831.
XX PR 15-NOV-1996; 96US-0749805.
XX XX
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (UYPE-) UNIV PENNSYLVANIA.

PI Moran JV, Dombroski BA, Kazazian HH, Boeke JD;
XX WPI; 2001-060015/07.
XX
XX DNAC comprising a promoter P and an L1 cassette sequence having a core
PT retrotransposon element, useful for random insertion of a heterologous
PT or homologous DNA sequence into a cell genome and for correcting
PT genetic defects -
XX
XX Disclosure; Fig 7; 87pp; English.
XX
XX The present invention relates to DNA for a promoter and an L1
CC cassette sequence having a core retrotransposon element. The invention
CC is useful for random insertion of a heterologous or homologous DNA
CC sequence into a cell genome, and for correction of a genetic defect
CC in the cell into which the insertion is made. Genetic defects which
CC may be corrected includes cystic fibrosis, mutations in the
CC dystrophin gene, genetic defects associated with blood clotting and
CC other genetic defects.
XX
XX Sequence 12 AA;
SQ

Query Match 22.2%; Score 4; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0;

QY 9 YPVE 12
Db |||||
5 YPVE 8

RESULT 72
ABB82324
ID ABB82324 standard; peptide; 12 AA.
XX
XX ABB82324;
XX
XX 08-JAN-2003 (first entry)
XX
XX Epitopic peptide binding to a human antibody against C. trachomatis.
XX
XX Epitope; immunostimulant; antibacterial; vaccine; gene therapy.
XX
XX Chlamydia trachomatis.
XX
XX WO200272622-A2.
XX
XX 19-SEP-2002.
XX
XX 12-FEB-2002; 2002WO-GB00597.
XX
XX 12-FEB-2001; 2001GB-0003387.
XX
XX (YABA-) YABA LTD.
XX
XX Jones GE;
XX
XX WPI; 2002-740797/80.
XX
XX New epitopic peptide derived from Chlamydia trachomatis, useful as a
PT vaccine for the induction of protection against Chlamydia trachomatis
PT infections -
XX
XX Claim 1; Page 33; 37pp; English.
XX
XX Sequences ABB82301-340 represent epitopic peptides that bind specifically
CC to a human antibody against Chlamydia trachomatis. The peptides are
CC useful in vaccine preparations for the induction of protection against
CC infection by C. trachomatis. The epitopic sequences or a compound
CC comprising them can be used in medicine, such as in diagnosing,
CC prognosing or treating infections caused by C. trachomatis.
XX
XX Sequence 12 AA;
SQ

Query Match 22.2%; Score 4; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0;

QY 9 YPVE 12
Db |||||
5 YPVE 8

RESULT 73
ABG67387
ID ABG67387 standard; Peptide; 12 AA.
XX
XX ABG67387;
XX
XX 07-OCT-2002 (first entry)
XX
XX Human ADPI tryptic digest peptide #96.
XX
XX Human; Alzheimer's disease; AD; brain tissue; ADPI; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX
XX Homo sapiens.
XX
XX WO200246767-A2.
XX
XX 13-JUN-2002.
XX
XX 29-NOV-2001; 2001WO-GB05289.
XX
XX 08-DEC-2000; 2000US-254431P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAc, Parekh RB, Rohlf C;
XX
XX WPI; 2002-508575/54.
XX
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer's disease-associated features or
PT Alzheimer's disease-associated protein isoforms in brain tissue
PT from the subject -
XX
XX Claim 7; Page 83; 427pp; English.
XX
XX The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in
CC a subject. The method comprises analysing a sample of brain tissue
CC from a subject by 2D electrophoresis to generate a 2D array of
CC Alzheimer's disease-associated features (ADFs), whose relative
CC abundance correlates with the presence, absence, stage or severity of
CC AD and comparing the abundance of each feature with the abundance of
CC that chosen feature in brain tissue from persons free from AD. The
CC invention also describes Alzheimer's disease-associated protein
CC isoforms (ADPIs) detectable in brain tissue. The methods and
CC compositions of the invention are useful for the screening, diagnosis
CC or prognosis of AD in a subject, for determining the stage or severity
CC of AD in a subject, for identifying a subject at risk of developing AD,
CC or for monitoring the effect of therapy administered to a subject
CC having AD. Antibodies capable of binding to ADPIs are useful for
CC treating or preventing AD, and for determining the efficacy of a given
CC treatment regime. An agent that modulates the activity of ADPI is
CC useful in the manufacture of a medicament for the treatment or
CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI
CC tryptic digest peptides.
XX
XX Sequence 12 AA;
SQ

Query Match 22.2%; Score 4; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0;

QY 9 YPVE 12
Db |||||
5 YPVE 8

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
 ||||
 Db 4 TESQ 7

RESULT 74
 AAR63797
 ID AAR63797 standard; Peptide; 13 AA.

XX AAR63797;
 AC
 XX 25-MAR-2003 (updated)
 DT 13-JUL-1995 (first entry)
 XX
 DE Bacillus thuringiensis anion exchange factor N-terminal peptide.
 XX
 KW Vegetative insecticidal protein; VIP; Bacillus thuringiensis;
 KW pesticide; Diabrotica virgifera virgifera; insecticide.
 XX
 OS Bacillus thuringiensis.

XX Key Location/Qualifiers
 FH Misc-difference 1
 FT /note= "any amino acid"
 FT Misc-difference 13
 FT /note= "any amino acid"

XX WO9421795-A1.
 PN
 XX 29-SEP-1994.

XX 23-MAR-1994; 94WO-US03131.
 XX
 XX 25-MAR-1993; 93US-0037057.
 XX
 XX (CIBA) CIBA GEIGY AG.

XX Carr B, Desai N, Kostichka N, Koziel MG, Mullins MA;
 PI Nye GJ, Warren GW;
 XX WPI; 1994-317015/39.

XX Novel pesticidal proteins and Bacillus strains - e.g. useful for
 PT control of Diabrotica virgifera virgifera
 XX
 XX Claim 35; Page 77; 108pp; English.

XX AAR63795-R63802 are auxiliary proteins that enhance the pesticidal
 CC activity of the vegetative insecticidal proteins (VIPs) described
 CC in AAR63792-R63794 and AAR75690. The protein peptide combination can
 CC be used in a variety of systems for controlling plant and non-plant
 CC pests, including insects, fungi, bacteria, nematodes, protozoan
 CC pathogens and animal-parasitic liver flukes. However it is esp.
 CC useful in the control of Diabrotica virgifera virgifera.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 13 AA;

Query Match 22.2%; Score 4; DB 15; Length 13;
 Best Local Similarity 100.0%; Pred.No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
 ||||
 Db 6 VEPF 9

RESULT 75
 AAR91253
 ID AAR91253 standard; Peptide; 13 AA.
 XX

AC AAR91253;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-AUG-1996 (first entry)
 XX
 DE European corn borer-active protein N-terminal peptide.
 XX
 KW Pesticide; insecticide; biological control agent; Lepidoptera;
 KW Coleoptera; transgenic plant; maize; insect resistance;
 KW European corn borer; Ostrinia nubilalis.
 XX
 OS Bacillus thuringiensis strain AB88 (NRRL B-21225).

XX Key Location/Qualifiers
 FH Misc-difference 1
 FT /note= "unidentified amino acid"
 FT Misc-difference 13
 FT /note= "unidentified amino acid"

XX WO9610083-A1.
 PN
 XX 04-APR-1996.

XX 27-SEP-1995; 95WO-EP03826.
 XX
 XX 05-JUN-1995; 95US-0463483.
 XX 28-SEP-1994; 94US-0314594.

XX (CIBA) CIBA GEIGY AG.

XX Warren GW, Koziel MG, Mullins MA, Nye GJ, Carr B, Desai NM;
 PI Kostichka K, Duck NB, Estruch JJ;
 XX WPI; 1996-200921/20.

XX Bacillus strain producing insecticidal protein during vegetative
 PT growth - used in the control of Lepidoptera and Coleoptera pests
 XX
 XX Example 17; Page 75; 242pp; English.

XX N-terminal sequences (AAR91252 and AAR91253) were obtd. from anion
 CC exchange fractions 23 and 28, respectively, of a European corn
 CC borer-active 60 kDa protein of Bacillus thuringiensis AB88. This
 CC strain also produces a protein active against black cutworm (see
 CC also AAR91243).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 13 AA;

Query Match 22.2%; Score 4; DB 17; Length 13;
 Best Local Similarity 100.0%; Pred.No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
 ||||
 Db 6 VEPF 9

Search completed: November 25, 2003, 19:27:09
 Job time : 46.9419 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8837 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKMPFPKYPVBPFTSQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

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12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	15 US-10-281-652-22	Sequence 22, Appl
2	5	27.8	15	15 US-10-281-652-5	Sequence 5, Appli
3	4	22.2	6	12 US-10-441-626-27	Sequence 27, Appl
4	4	22.2	7	9 US-09-997-900-11	Sequence 11, Appl
5	4	22.2	9	10 US-09-780-053-17	Sequence 17, Appl
6	4	22.2	9	10 US-09-780-053-319	Sequence 238, App
7	4	22.2	9	10 US-09-780-053-418	Sequence 319, App
8	4	22.2	9	10 US-09-780-053-418	Sequence 418, App
9	4	22.2	9	12 US-09-932-165-265	Sequence 285, App
10	4	22.2	9	12 US-09-932-165-851	Sequence 851, App
11	4	22.2	9	12 US-09-932-165-1238	Sequence 1238, Ap
12	4	22.2	9	12 US-10-062-109A-4	Sequence 4, Appli
13	4	22.2	9	12 US-10-062-109A-44	Sequence 44, Appli
14	4	22.2	9	12 US-10-005-480A-4	Sequence 4, Appli
15	4	22.2	9	12 US-10-1005-480A-44	Sequence 44, Appli

9	12	US-10-371-069-190	Sequence 190, App
12	9	US-10-371-645-190	Sequence 190, App
10	10	US-09-780-053-68	Sequence 68, Appli
10	10	US-09-780-053-276	Sequence 276, App
20	4	US-09-780-053-398	Sequence 398, App
21	4	US-09-780-053-404	Sequence 404, App
22	4	US-09-780-053-407	Sequence 407, App
23	4	US-09-780-053-495	Sequence 496, App
24	4	US-09-780-053-715	Sequence 715, App
25	4	US-09-932-165-373	Sequence 373, App
26	4	US-09-932-165-395	Sequence 395, App
27	4	US-09-932-165-1339	Sequence 1339, Ap
28	4	US-09-932-165-1351	Sequence 1351, Ap
29	4	US-10-062-109A-55	Sequence 55, Appl
30	4	US-10-062-109A-71	Sequence 71, Appl
31	4	US-10-005-480A-55	Sequence 55, Appl
32	4	US-10-005-480A-71	Sequence 71, Appl
33	4	US-10-062-710-173	Sequence 173, App
34	4	US-10-094-401-148	Sequence 148, App
35	4	US-10-057-789-142	Sequence 142, App
36	4	US-10-212-628-142	Sequence 142, App
37	4	US-10-216-122-89	Sequence 89, Appl
38	4	US-09-966-955A-31	Sequence 31, Appl
39	4	US-09-966-955A-32	Sequence 32, Appl
40	4	US-10-271-078-26	Sequence 26, Appl
41	4	US-09-791-393-100	Sequence 100, App
42	4	US-09-791-389-100	Sequence 100, App
43	4	US-10-271-078-33	Sequence 33, Appl
44	4	US-09-892-877-381	Sequence 381, App
45	4	US-09-991-799-2	Sequence 2, Appli
46	4	US-09-948-783-381	Sequence 381, App
47	4	US-10-001-879-120	Sequence 120, App
48	4	US-10-281-652-8	Sequence 8, Appli
49	4	US-10-264-303-11	Sequence 11, Appl
50	4	US-10-175-270-13	Sequence 13, Appl
51	4	US-10-161-791-181	Sequence 181, App
52	4	US-10-225-567A-1110	Sequence 1110, Ap
53	4	US-10-225-567A-1727	Sequence 1727, Ap
54	4	US-09-864-761-46168	Sequence 46168, A
55	4	US-10-161-791-362	Sequence 362, App
56	4	US-09-864-761-48184	Sequence 48184, A
57	4	US-10-094-401-196	Sequence 196, App
58	4	US-09-841-132-236	Sequence 236, App
59	4	US-09-841-132-237	Sequence 237, App
60	4	US-09-841-132-238	Sequence 238, App
61	4	US-09-841-132-239	Sequence 239, App
62	4	US-09-983-802-664	Sequence 664, App
63	3	US-10-253-532-126	Sequence 126, App
64	3	US-09-982-172-156	Sequence 156, App
65	3	US-09-947-387-27	Sequence 27, Appl
66	3	US-09-994-078-2	Sequence 2, Appli
67	3	US-10-237-160-1	Sequence 1, Appli
68	3	US-10-253-532-122	Sequence 122, App
69	3	US-10-253-532-125	Sequence 125, App
70	3	US-10-087-942-20	Sequence 20, Appl
71	3	US-10-087-942-31	Sequence 31, Appl
72	3	US-10-313-338A-1	Sequence 1, Appli
73	3	US-10-313-790A-1	Sequence 1, Appli
74	3	US-10-138-375-27	Sequence 27, Appl
75	3	US-10-041-030-28	Sequence 28, Appl
76	3	US-10-087-905-20	Sequence 20, Appl
77	3	US-10-087-905-31	Sequence 31, Appl
78	3	US-10-059-261-25	Sequence 25, Appl
79	3	US-10-059-261-133	Sequence 133, App
80	3	US-10-006-869-199	Sequence 199, App
81	3	US-10-253-532-117	Sequence 117, App
82	3	US-10-253-532-121	Sequence 121, App
83	3	US-10-253-532-124	Sequence 124, App
84	3	US-10-226-629A-9	Sequence 9, Appli
85	3	US-10-294-891-49	Sequence 49, Appli
86	3	US-10-276-601-4	Sequence 4, Appli
87	3	US-10-020-354-112	Sequence 112, App
88	3	US-10-145-206-110	Sequence 110, App

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89      3      16.7      5      15      US-10-155-407A-12      Sequence 12, Appl
90      3      16.7      5      15      US-10-006-869-200      Sequence 200, App
91      3      16.7      5      15      US-10-006-869-202      Sequence 202, App
92      3      16.7      5      15      US-10-006-869-1566      Sequence 1566, Ap
93      3      16.7      5      15      US-10-006-869-1568      Sequence 1568, Ap
94      3      16.7      5      15      US-10-096-986-13      Sequence 13, Appl
95      3      16.7      5      15      US-10-058-613-16      Sequence 16, Appl
96      3      16.7      5      15      US-10-281-652-15      Sequence 15, Appl
97      3      16.7      5      15      US-10-206-699-199      Sequence 199, App
98      3      16.7      6      9      US-09-062-113-1      Sequence 1, Appl
99      3      16.7      6      10      US-09-529-759-26      Sequence 26, Appl
100     3      16.7      6      10      US-09-529-759-27      Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-22
; Sequence 22, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-22
Query Match      100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      HKEMPPPKYPVPPFTESQ 18
DB      1      HKEMPPPKYPVPPFTESQ 18

RESULT 2
US-10-281-652-5
; Sequence 5, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-5
Query Match      100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      HKEMPPPKYPVPPFTESQ 18
DB      1      HKEMPPPKYPVPPFTESQ 18

; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-5
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10      PVEPP 14
DB      8      PVEPP 12

RESULT 3
US-10-441-626-27
; Sequence 27, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGIII-like cellulase amino acid string
US-10-441-626-27
Query Match      22.2%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12      EPFT 15
DB      3      EPFT 6

RESULT 4
US-09-997-900-11
; Sequence 11, Application US/09997900
; Patent No. US20020053098A1
; GENERAL INFORMATION:
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; FILE REFERENCE: 043753/241148 (5849-20A)
; CURRENT APPLICATION NUMBER: US/09/997,900
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 09/426,568
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
```

```

; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-11

Query Match      22.2%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 3 VEPF 6

RESULT 5
US-09-780-053-17
; Sequence 17, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-17

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
Db 2 TESQ 5

RESULT 6
US-09-780-053-238
; Sequence 238, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09

```

```

; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-238

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
Db 2 TESQ 5

RESULT 7
US-09-780-053-319
; Sequence 319, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-319

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
Db 2 TESQ 5

RESULT 8
US-09-780-053-418
; Sequence 418, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09

```

```
; ; PRIOR FILING DATE: 2000-02-09
; ; NUMBER OF SEQ ID NOS: 716
; ; SOFTWARE: FastSEQ for Windows Version 4.0
; ; SEQ ID NO 418
; ; LENGTH: 9
; ; TYPE: PRT
; ; ORGANISM: Homo Sapiens
US-09-780-053-418

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches    4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TESQ 18
        |||||
Db       4 TESQ 7

RESULT 9
US-09-932-165-265
; Sequence 265, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENÉ
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-265

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches    4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KYPV 11
        |||||
Db       6 KYPV 9

RESULT 10
US-09-932-165-851
; Sequence 851, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENÉ
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 851
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-851
```

```

; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-4

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      11 VEPF 14
        ||||
Db      4 VEPF 7

```

```

RESULT 13
US-10-062-109A-44
; Sequence 44, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-44

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      2 VEPF 5

```

```

RESULT 14
US-10-005-480A-4
; Sequence 4, Application US/10005480A
; Publication No. US20030191073A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-4

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      4 VEPF 7

```

```

RESULT 15
US-10-005-480A-44
; Sequence 44, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-44

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      2 VEPF 5

```

```

RESULT 16
US-10-371-069-190
; Sequence 190, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.

```

; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-10-371-069-190

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTES 17
Db 2 FTES 5

RESULT 17
US-10-371-645-190
; Sequence 190, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-10-371-645-190

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTES 17
Db 2 FTES 5

RESULT 18
US-09-780-053-68
; Sequence 68, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-68

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db 2 TESQ 5

RESULT 19
US-09-780-053-276
; Sequence 276, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-276

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db 5 TESQ 8

RESULT 20

```

US-09-780-053-398
; Sequence 398, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 398
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-398

```

```

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 TESQ 18
        |||||
Db      3 TESQ 6

```

RESULT 21

```

US-09-780-053-404
; Sequence 404, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 404
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-404

```

```

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 TESQ 18
        |||||
Db      2 TESQ 5

```

RESULT 22

```

US-09-780-053-407
; Sequence 407, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 407
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-407

```

```

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 TESQ 18
        |||||
Db      4 TESQ 7

```

RESULT 23

```

US-09-780-053-496
; Sequence 496, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-496

```

```

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 TESQ 18
        |||||
Db      5 TESQ 8

```

RESULT 24

US-09-780-053-715
; Sequence 715, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129,5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 715
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-715

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||
DB 5 TESQ 8

RESULT 25
US-09-932-165-373
; Sequence 373, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 373
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-373

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11
|||

Db 6 KYPV 9

RESULT 26

US-09-932-165-395
; Sequence 395, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-395

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11
|||
DB 7 KYPV 10

RESULT 27
US-09-932-165-1339
; Sequence 1339, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1339
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1339

```
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1339

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
Db 5 KYPV 8

RESULT 28
US-09-932-165-1351
; Sequence 1351, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1351
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1351

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
Db 1 KYPV 4

RESULT 29
US-10-062-109A-55
; Sequence 55, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
```

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; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-55

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 2 VEPF 5

RESULT 30
US-10-062-109A-71
; Sequence 71, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-71

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 4 VEPF 7

RESULT 31
US-10-005-480A-55
; Sequence 55, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
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; FEATURE:
; OTHER INFORMATION: HIV B Cell Epitopes
US-10-062-710-173

Query Match      22.2%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred.No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      10 PVEP 13
Db      1 PVEP 4
      ||||

RESULT 34
US-10-094-401-148
; Sequence 148, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 148
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
US-10-094-401-148

Query Match      22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      3 EMPF 6
Db      7 EMPF 10
      ||||

RESULT 35
US-10-057-789-142
; Sequence 142, Application US/10057789
; Publication No. US20030082522A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; FILE REFERENCE: NADII.022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

```

```
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-789-142

Query Match          22.2%  Score 4;  DB 15;  Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 11 VEPF 14
Db 2 VEPF 5

RESULT 36
US-10-212-628-142
; Sequence 142, Application US/10212628
; Publication No. US20030087329A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; FILE REFERENCE: NADII.022CPI
; CURRENT APPLICATION NUMBER: US/10/212,628
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2001-01-26 US 60/264,576
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/057,789
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-212-628-142

Query Match          22.2%  Score 4;  DB 15;  Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 11 VEPF 14
Db 2 VEPF 5

RESULT 37
US-10-216-122-89
; Sequence 89, Application US/10216122
; Publication No. US20030121063A1
; GENERAL INFORMATION:
; APPLICANT: Kazazian, Haig H.
; APPLICANT: Osterag, Eric
; APPLICANT: DeBerardinis, Ralph
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
; FILE REFERENCE: 053893-5006-03
; CURRENT APPLICATION NUMBER: US/10/216,122
; CURRENT FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/653,812
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 08/847,844
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: US 08/749,805
```

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; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/006,831
; PRIOR FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-216-122-89

Query Match          22.2%  Score 4;  DB 15;  Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 9 YPVE 12
Db 5 YPVE 8

RESULT 38
US-09-966-955A-31
; Sequence 31, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:
; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clink-related Gene, MIST (Mast Cell Immunoreceptor
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-31

Query Match          22.2%  Score 4;  DB 10;  Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 5 PFPK 8
Db 10 PFPK 13

RESULT 39
US-09-966-955A-32
; Sequence 32, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:
; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clink-related Gene, MIST (Mast Cell Immunoreceptor
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28
```

; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-32

Query Match 22.2%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8
|||
Db 1 PFPK 4

RESULT 40

US-10-271-078-26
; Sequence 26, Application US/10271078
; Publication No. US20030186267A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLLRCH
; FILE REFERENCE: D0157 NP
; CURRENT APPLICATION NUMBER: US/10/271,078
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: U.S. 60/328,478
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-078-26

Query Match 22.2%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEMP 5
|||
Db 8 KEMP 11

RESULT 41

US-09-791-393-100
; Sequence 100, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 14
; TYPE: PRT

; ORGANISM: homo sapien
US-09-791-393-100

Query Match 22.2%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6
|||
Db 2 EMPF 5

RESULT 42

US-09-791-389-100
; Sequence 100, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-100

Query Match 22.2%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6
|||
Db 2 EMPF 5

RESULT 43

US-10-271-078-33
; Sequence 33, Application US/10271078
; Publication No. US20030186267A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLL
; FILE REFERENCE: D0157 NP
; CURRENT APPLICATION NUMBER: US/10/271,078
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: U.S. 60/328,478
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-078-33

Query Match 22.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5
|||||
Db 8 KEMP 11

RESULT 44

US-09-892-877-381
; Sequence 381, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P1
; CURRENT APPLICATION NUMBER: US/09/892,877
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 381
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-877-381

Query Match 22.2%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||||
Db 12 TESQ 15

RESULT 45

US-09-991-799-2
; Sequence 2, Application US/09991799
; Publication No. US20030100012A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Plasma Protease C1 Biopolymer Markers Predictive of Alzheimers Disease
; FILE REFERENCE: 2132.086
; CURRENT APPLICATION NUMBER: US/09/991,799
; CURRENT FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-799-2

Query Match 22.2%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11
|||||
Db 2 KYPV 5

RESULT 46

US-09-948-783-381
; Sequence 381, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 09/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/09847
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/085,093
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,094
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,105
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,928
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,920
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 381
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-948-783-381

Query Match 22.2%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||||
Db 12 TESQ 15

RESULT 47

US-10-001-879-120
; Sequence 120, Application US/10001879
; Publication No. US20020127237A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chonghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 15

; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-120

Query Match 22.2%; Score 4; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPKY 9
|||
Db 8 PPKY 11
|||

RESULT 48

US-10-281-652-8
; Sequence 8, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 2002-10-28
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-8

Query Match 22.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKK 8
|||
Db 3 PPKK 6
|||

RESULT 49

US-10-264-303-11
; Sequence 11, Application US/10264303
; Publication No. US20030124060A1
; GENERAL INFORMATION:
; APPLICANT: Roux, Kenneth
; APPLICANT: Sathé, Shridhar
; APPLICANT: Teuber, Suzanne
; TITLE OF INVENTION: Purified Linear Epitopes from Cashew Nuts, Nucleic Acids Encoding
; TITLE OF INVENTION: Therefor and Associated Methods
; FILE REFERENCE: 28396 and 30728
; CURRENT APPLICATION NUMBER: US/10/264,303
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,793
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/371,774
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Anacardium occidentale

US-10-264-303-11

Query Match 22.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
|||
Db 10 PFTE 13
|||

RESULT 50

US-10-175-270-13
; Sequence 13, Application US/10175270
; Publication No. US20030166549A1
; GENERAL INFORMATION:
; APPLICANT: PETERSON, JOHNNY W.
; APPLICANT: SAINI, SHAMSHER S.
; APPLICANT: WOOD, THOMAS G.
; APPLICANT: CHOPRA, ASHOK K.
; TITLE OF INVENTION: ANTI-INFLAMMATORY AND OTHER THERAPEUTIC PROPHYLACTIC OR DIAGN
; TITLE OF INVENTION: SYNTHETIC MELITTIN AND NE
; TITLE OF INVENTION: W RELATED PEPTIDES
; FILE REFERENCE: UTSG:213
; CURRENT APPLICATION NUMBER: US/10/175,270
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/458,397
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: PCT/US98/12340
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-175-270-13

Query Match 22.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTES 17
|||
Db 3 FTES 6
|||

RESULT 51

US-10-161-791-181
; Sequence 181, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161.791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602.999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 181:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-10-161-791-181

Query Match 22.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFPK 8
Db 5 PFPK 8

RESULT 52

US-10-225-567A-1110
/ Sequence 1110, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenna C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1110
/ LENGTH: 16
/ TYPE: PPT
/ ORGANISM: Homo sapiens
US-10-225-567A-1110

Query Match 22.2%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFPK 8
Db 10 PFPK 13

RESULT 53

US-10-225-567A-1727
/ Sequence 1727, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:

/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenna C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1727
/ LENGTH: 16
/ TYPE: PPT
/ ORGANISM: Homo sapiens
US-10-225-567A-1727

Query Match 22.2%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVS 12
Db 9 YPVS 12

RESULT 54

US-09-864-761-46168
/ Sequence 46168, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharron G.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
/ FILE REFERENCE: Aeomica-x-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21


```
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46168
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL135787.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EST_HUMAN HIT: AA595480.1, EVALUE 2.90e-02
US-09-864-761-46168

Query Match          22.2%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEMP 5
   ||||
Db 10 KEMP 13

RESULT 55
US-10-161-791-362
; Sequence 362, Application US/10161791
; Publication No. US20030186963A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
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; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-362

Query Match          22.2%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
   ||||
Db 10 PVEP 13

RESULT 56
US-09-864-761-48184
; Sequence 48184, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48184
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022238.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
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; OTHER INFORMATION: EST_HUMAN HIT: AL121033.1, EVALUE 3.70e-02
US-09-864-761-48184

Query Match 22.2%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 1 PFTE 4

RESULT 57

US-10-094-401-196
; Sequence 196, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
US-10-094-401-196

Query Match 22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6
Db 10 EMPF 13

RESULT 58

US-09-841-132-236
; Sequence 236, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-236

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 YPVE 12
Db 17 YPVE 20

RESULT 59

US-09-841-132-237
; Sequence 237, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-237

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12
Db 12 YPVE 15

RESULT 60

US-09-841-132-238
; Sequence 238, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-238

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12
Db 7 YPVE 10

RESULT 61
US-09-841-132-239

; Sequence 239, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-239

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 9 YPVE 12
Db 2 YPVE 5

RESULT 62
US-09-883-802-664
; Sequence 664, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-983-802-664

Query Match 22.2%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 5 PFPK 8
Db 16 PFPK 19

RESULT 63
US-10-253-532-126
; Sequence 126, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 126
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-126

Query Match      16.7%; Score 3; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TES 17
      |||
Db      1 TES 3

RESULT 64
US-09-982-172-156
; Sequence 156, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-156

Query Match      16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVE 12
      |||
Db      1 PVE 3

RESULT 65
US-09-947-387-27
; Sequence 27, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-27

Query Match      16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VEP 13
      |||
Db      1 VEP 3

RESULT 66
US-09-994-078-2
; Sequence 2, Application US/09994078
; Publication No. US20030032774A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, WILLIAM
; APPLICANT: DIMAIO, JOHN
; APPLICANT: SCHILLER, PETER
; APPLICANT: MARTEL, RENE
; APPLICANT: MARTEL, FRANCIS
; APPLICANT: MARTEL, DIANE
; APPLICANT: MARTEL, PIERRE
; TITLE OF INVENTION: NOVEL OPIOID PEPTIDES FOR THE TREATMENT OF PAIN
; FILE REFERENCE: MAS/81823/282437
; CURRENT APPLICATION NUMBER: US/09/994,078
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/159,518
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/392,918
; PRIOR FILING DATE: 1995-03-03
; PRIOR APPLICATION NUMBER: 08/718,585
; PRIOR FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-994-078-2

Query Match      16.7%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFT 15
      |||
Db      2 PFT 4

RESULT 67
US-10-237-160-1
; Sequence 1, Application US/10237160
; Publication No. US20030133926A1
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Graybeal Jackson Haley
; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
```

; ZIP: 98004-5117
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 98
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,160
; FILING DATE: 09-Dec-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 1776-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (425) 455-5575
; TELEFAX: (425) 455-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-237-160-1

Query Match 16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFP 7
|||
Db 2 PFP 4

RESULT 68
US-10-253-532-122
; Sequence 122, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; CURRENT APPLICATION NUMBER: US/10/253,532
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-122

Query Match 16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
|||
Db 2 TES 4

RESULT 69
US-10-253-532-125
; Sequence 125, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-125

Query Match 16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
|||
Db 1 TES 3

RESULT 70
US-10-087-942-20
; Sequence 20, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,942
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
; OTHER INFORMATION: peptide
US-10-087-942-20

Query Match 16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ESQ 18
|||
Db 2 ESQ 4

```
RESULT 71
US-10-087-942-31
; Sequence 31, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,942
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
; OTHER INFORMATION: peptide
US-10-087-942-31

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
Db 2 YPV 4

RESULT 72
US-10-313-338A-1
; Sequence 1, Application US/10313338A
; Publication No. US20030170226A1
; GENERAL INFORMATION:
; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF AU
; FILE REFERENCE: 1776-1-7
; CURRENT APPLICATION NUMBER: US/10/313,338A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-338A-1

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db 2 PFP 4

RESULT 73
US-10-313-790A-1
; Sequence 1, Application US/10313790A
; Publication No. US20030170227A1
; GENERAL INFORMATION:
; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF
; FILE REFERENCE: 1776-1-6
; CURRENT APPLICATION NUMBER: US/10/313,790A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-790A-1

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db 2 PFP 4

RESULT 74
US-10-138-375-27
; Sequence 27, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prote
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-27

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3

RESULT 75
US-10-041-030-28
; Sequence 28, Application US/10041030
; Publication No. US20020150934A1
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Mu, David
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
```

```
; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF
; FILE REFERENCE: 1776-1-6
; CURRENT APPLICATION NUMBER: US/10/313,790A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-790A-1
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```
Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db 2 PFP 4
```

```
RESULT 74
US-10-138-375-27
; Sequence 27, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prote
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-27
```

```
Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3
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RESULT 75
US-10-041-030-28
; Sequence 28, Application US/10041030
; Publication No. US20020150934A1
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Mu, David
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
```

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; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
; FILE REFERENCE: 018781-006810US
; CURRENT APPLICATION NUMBER: US/10/041,030
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/259,502
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence identity in comparison of pellino 1 and
; OTHER INFORMATION: pellino 2
US-10-041-030-28

Query Match      16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 FTE 16
      |||
Db      2 FTE 4

Search completed: November 25, 2003, 20:37:00
Job time : 29.8837 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVRFETESQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	4	US-09-641-803-22
2	5	27.8	15	4	US-09-641-803-5
3	4	22.2	6	3	US-09-216-295-27
4	4	22.2	7	1	US-08-261-206A-22
5	4	22.2	7	4	US-09-426-568A-11
6	4	22.2	8	1	US-08-259-550A-30
7	4	22.2	8	2	US-08-929-922B-7
8	4	22.2	8	3	US-09-342-394-7
9	4	22.2	8	3	US-09-580-064-7
10	4	22.2	8	4	US-09-718-709-7
11	4	22.2	9	4	US-09-311-784A-190
12	4	22.2	11	1	US-08-158-351-3
13	4	22.2	11	1	US-08-482-576-3
14	4	22.2	12	3	US-08-847-844A-89
15	4	22.2	13	1	US-08-471-033-11
16	4	22.2	13	2	US-08-471-044-11
17	4	22.2	13	2	US-08-463-483A-11
18	4	22.2	13	2	US-08-471-046A-11
19	4	22.2	13	2	US-08-470-566B-11
20	4	22.2	13	2	US-08-838-219B-11
21	4	22.2	13	2	US-08-469-334-11
22	4	22.2	13	3	US-09-300-529-11
23	4	22.2	13	3	US-09-233-336A-11
24	4	22.2	13	3	US-09-233-752A-11
25	4	22.2	13	3	US-09-402-036-11
26	4	22.2	13	4	US-09-904-226-11
27	4	22.2	14	6	5171684-21

Patent No. 5171684

ALIGNMENTS

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RESULT 1
US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22

Query Match          100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKMPFPKYPVPEPTESQ 18
Db 1 HKMPFPKYPVPEPTESQ 18

RESULT 2
US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5

Query Match          27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEPF 14
Db 8 PVEPF 12
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RESULT 3
US-09-216-295-27
; Sequence 27, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-216-295-27

Query Match          22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
Db 3 EPFT 6

RESULT 4
US-08-261-206A-22
; Sequence 22, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 22:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-22
;
; Query Match 22.2% Score 4; DB 1; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 10 PVEP 13
; Db 2 PVEP 5
;
; RESULT 5
; US-09-426-568A-11
; Sequence 11, Application US/09426568A
; Patent No. 6348643
; GENERAL INFORMATION:
; APPLICANT: Kakufuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 008103/195497
; CURRENT APPLICATION NUMBER: US/09/426,568A
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
; US-09-426-568A-11
;
; Query Match 22.2% Score 4; DB 4; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 11 VEPF 14
; Db 3 VEPF 6
;
; RESULT 6
; US-08-259-550A-30
; Sequence 30, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-22
;
; Query Match 22.2% Score 4; DB 1; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 10 PVEP 13
; Db 2 PVEP 5
;
; RESULT 5
; US-09-426-568A-11
; Sequence 11, Application US/09426568A
; Patent No. 6348643
; GENERAL INFORMATION:
; APPLICANT: Kakufuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 008103/195497
; CURRENT APPLICATION NUMBER: US/09/426,568A
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
; US-09-426-568A-11
;
; Query Match 22.2% Score 4; DB 4; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 11 VEPF 14
; Db 3 VEPF 6
;
; RESULT 6
; US-08-259-550A-30
; Sequence 30, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-259-550A-30
;
; Query Match 22.2% Score 4; DB 1; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 15 TESQ 18
; Db 1 TESQ 4
;
; RESULT 7
; US-08-929-922B-7
; Sequence 7, Application US/08929922B
; Patent No. 5994113
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5994113o No. 5994113disk of No. 5994113th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922B
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
```

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-929-922B-7

Query Match 22.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 4 VEPF 7

RESULT 8

US-09-342-394-7

; Sequence 7, Application US/09342394

; Patent No. 6143546

; GENERAL INFORMATION:

; APPLICANT: Kauppinen, Sakari

; APPLICANT: Si, Joan Qi

; APPLICANT: Spandler, Tina

; APPLICANT: Dammann, Claus

; APPLICANT: Halkier, Torben

; APPLICANT: Ostergaard, Peter Rahbek

; APPLICANT: Patkar, Shamkant Anant

; APPLICANT: Hansen, Kim

; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6143546o No. 6143546disk of No. 6143546th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/342,394

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/929,922

; FILING DATE: 15-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4355.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal

US-09-342-394-7

Query Match 22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 4 VEPF 7

RESULT 9

US-09-580-064-7

; Sequence 7, Application US/09580064

; Patent No. 6200792

; GENERAL INFORMATION:

; APPLICANT: Kauppinen, Sakari

; APPLICANT: Si, Joan Qi

; APPLICANT: Spandler, Tina

; APPLICANT: Dammann, Claus

; APPLICANT: Halkier, Torben

; APPLICANT: stergaard, Peter Rahbek

; APPLICANT: Patkar, Shamkant Anant

; APPLICANT: Hansen, Kim

; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6200792o No. 6200792disk of No. 6200792th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/580,064

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/929,922

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4355.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal

US-09-580-064-7

Query Match 22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 4 VEPF 7

RESULT 10

US-09-718-709-7

; Sequence 7, Application US/09718709

Patent No. 6413559
GENERAL INFORMATION:
APPLICANT: Kauppinen, Sakari
Si, Joan Qi
Spendler, Tina
Dambmann, Claus
Halkier, Torben
stergaard, Peter Rahbek
Patkar, Shankant Anant
Hansen, Kim
TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6413559o No. 6413559disk of No. 6413559th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/718,709
FILING DATE: 22-No. 6413559-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/929,922
FILING DATE: 15-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4355.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-718-709-7
Query Match 22.2%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 VEPF 14
Db 4 VEPF 7
RESULT 11
US-09-311-784A-190
Sequence 190, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same

FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 190
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-09-311-784A-190
Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 FTES 17
Db 2 FTES 5
RESULT 12
US-08-158-351-3
Sequence 3, Application US/08158351
Patent No. 5445820
GENERAL INFORMATION:
APPLICANT: SEIDEL, Christoph
APPLICANT: BURNS, Geoffrey
APPLICANT: ENGEL, Wolf-Dieter
TITLE OF INVENTION: STREPTOLYSIN O PEPTIDE ANTIGENS AND
METHODS FOR THE DETERMINATION OF STREPTOLYSIN ANTIBODIES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
STREET: 655 Fifteenth Street N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,351
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 40 056.2
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 1614-3052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-158-351-3
Query Match 22.2%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 KEMP 5
      ||||
Db      6 KEMP 9

RESULT 13
US-08-482-576-3
; Sequence 3, Application US/08482576
; Patent No. 5688659
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, Christoph
; APPLICANT: BURNS, Geoffrey
; APPLICANT: ENGEL, Wolf-Dieter
; TITLE OF INVENTION: STREPTOLYSIN O PEPTIDE ANTIGENS AND
; TITLE OF INVENTION: METHODS FOR THE DETERMINATION OF STREPTOLYSIN
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W., Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.576
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 40 056.2
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-3052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-576-3

Query Match      22.2%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KEMP 5
      ||||
Db      6 KEMP 9

RESULT 14
US-08-847-844A-89
; Sequence 89, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMEROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS
```

```
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-2302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-844A-89

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      5 YPVE 8

RESULT 15
US-08-471-033-11
; Sequence 11, Application US/08471033
; Patent No. 5770696
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,033
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: P-40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-471-033-11

Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 16
US-08-471-044-11
; Sequence 11, Application US/08471044
; Patent No. 5840868
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,044
; FILING DATE: 06-JUN-1995

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-471-044-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 17
US-08-463-483A-11
; Sequence 11, Application US/08463483A
; Patent No. 5849870
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,483A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594

```

; FILING DATE: 09-SEP-1994
; APPLICATION NUMBER: US 08/218,018
; PRIOR APPLICATION DATA:
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murry
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-463-483A-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
DB 6 VEPF 9

RESULT 18
US-08-471-046A-11
; Sequence 11, Application US/08471046A
; Patent No. 5866326
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Estruch, Juan J
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
; TITLE OF INVENTION: Protein Genes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 5866326artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,046A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SQLV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-471-046A-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
DB 6 VEPF 9

RESULT 19
US-08-470-566B-11
; Sequence 11, Application US/08470566B
; Patent No. 5872212
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 5872212artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV4 - SQLV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-08-470-566B-11
Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

; RESULT 20
; US-08-838-219B-11
; Sequence 11, Application US/08838219B
; Patent No. 5877012
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/838,219B
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993

; RESULT 21
; US-08-469-334-11
; Sequence 11, Application US/08469334
; Patent No. 5990383
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5990383el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/469,334
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,483
; FILING DATE:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
```


; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-08-469-334-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 22

US-09-300-529-11
; Sequence 11, Application US/09300529

; Patent No. 6066783
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Genes Encoding Insecticidal Proteins
; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066783artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,529
; FILING DATE: TBA

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,334
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19506L

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-09-300-529-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 23

US-09-233-336A-11
; Sequence 11, Application US/09233336A

; Patent No. 6107279
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6107279el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,336A
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,219
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582

; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-09-233-336A-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 24
US-09-233-752A-11
; Sequence 11, Application US/09233752A
; Patent No. 6137033
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
; CONTROL OF PLANT PESTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,752A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,219
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-09-233-752A-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 25
US-09-402-036-11
; Sequence 11, Application US/09402036
; Patent No. 6291156
; GENERAL INFORMATION:
; APPLICANT: Estruch, Juan J.
; APPLICANT: Yu, Cao-Guo
; APPLICANT: Warren, Gregory W.
; APPLICANT: Desai, Nalini
; APPLICANT: Kozziel, Michael
; APPLICANT: Nye, Gordon
; TITLE OF INVENTION: Plant Pest Control
; FILE REFERENCE: S-21284C
; CURRENT APPLICATION NUMBER: US/09/402,036
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: PCT/EP98/01952
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 08/838,219
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,263
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,265
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/463,483
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/314,594
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: 08/218,018
; PRIOR FILING DATE: 1994-03-24
; PRIOR APPLICATION NUMBER: 08/037,057
; PRIOR FILING DATE: 1993-03-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
; OTHER INFORMATION: Xaa represents any amino acid
; US-09-402-036-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 26
US-09-904-226-11
; Sequence 11, Application US/09904226

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; Patent No. 6429360
; GENERAL INFORMATION:
; APPLICANT: Estruch, Juan J.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Desai, Nalini
; APPLICANT: Kosiel, Michael
; APPLICANT: Nye, Gordon
; TITLE OF INVENTION: Plant Pest Control
; FILE REFERENCE: S-21284D
; CURRENT APPLICATION NUMBER: US/09/904,226
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP98/01952
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 08/838,219
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,263
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,265
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/463,483
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/314,594
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: 08/218,018
; PRIOR FILING DATE: 1994-03-24
; PRIOR APPLICATION NUMBER: 08/037,057
; PRIOR FILING DATE: 1993-03-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE: <221> SITE<222> (1)..(13)<223> Xaa represents any amino acid
US-09-904-226-11

Query Match      22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VEPF 14
DB      6 VEPF 9

RESULT 27
5171684-21
; Patent No. 5171684
; APPLICANT: YEN, KWANG-MU;BLATT, LAWRENCE M.;KARL, MICHAEL R.
; TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
; MONOOXYGENASE OF PSEUDOMONAS MENDOCINA KR-1
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,374
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 177,631
; FILING DATE: 05-APR-1988
; SEQ ID NO:21:
; LENGTH: 14
5171684-21

Query Match      22.2%; Score 4; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPEF 12
DB      9 YPEF 12

RESULT 28
US-08-080-073-25

```

```

; Sequence 25, Application US/08080073
; Patent No. 5384255
; GENERAL INFORMATION:
; APPLICANT: Ciechanover, Aaron J.
; APPLICANT: Blumenfeld, Nava
; APPLICANT: Gonen, Hedva
; TITLE OF INVENTION: Ubiquitin Carrier Enzyme E2-F1,
; TITLE OF INVENTION: Purification, Production, and Use
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/080,073
; FILING DATE: 21-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1448.0050000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-080-073-25

Query Match      22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PKYP 10
DB      7 PKYP 10

RESULT 29
US-08-967-101-168
; Sequence 168, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101

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; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-101-168

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFTE 16
Db      9 PFTE 12

RESULT 30
US-08-687-956A-7
; Sequence 7, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-8

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
Db      11 PVEP 14

RESULT 31
US-08-687-956A-8
; Sequence 8, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-8

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
Db      11 PVEP 14
```

```

RESULT 32
US-08-592-541-168
; Sequence 168, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-592-541-168

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFTE 16
DB 9 PFTE 12

RESULT 33
US-08-591-629-5
; Sequence 5, Application US/08591629
; Patent No. 5993808
; GENERAL INFORMATION:
; APPLICANT: MELCHERS, Leo Sjoerd
; APPLICANT: APOTHEKER-DE GROOT, Marion
; APPLICANT: BOL, John Ferdinand
; APPLICANT: CORNELISSEN, Bernardus Johannes Clemens
; APPLICANT: LINTHORST, Hubertus Josephus Maria
; APPLICANT: PONSTEIN, Anne Silene
; APPLICANT: SELA-BUURLAGE, Marianne Beatrix
; TITLE OF INVENTION: plant chitinases, DNA coding therefor and
; TITLE OF INVENTION: plants containing same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: NY
; COUNTRY: USA

```

```

; ZIP: 10023-7604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC 4.86 SX 50 Mhz
; OPERATING SYSTEM: DOS 6.20
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,629
; FILING DATE: 15-FEB-96
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02761
; FILING DATE: 17-AUG-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93202425.0
; FILING DATE: 17-AUG-93
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS. CLIFFORD J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010627-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; DEVELOPMENTAL STAGE: TMV-induced
; TISSUE TYPE: leaf
US-08-591-629-5

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
DB 4 YPVE 7

RESULT 34
US-09-124-698-168
; Sequence 168, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-124-698-168

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 35
US-09-127-480-168
; Sequence 168, Application US/09127480
; Patent No. 6194153
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,480
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-127-480-168

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 36
US-08-496-841C-165
; Sequence 165, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,841C
; FILING DATE: 28-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehlner, Ph.D.
; REGISTRATION NUMBER: 35,135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-08-496-841C-165

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 37
US-09-124-523-168
; Sequence 168, Application US/09124523
; Patent No. 6395960
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
```

```
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-124-523-168

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 39
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-09-641-803-8

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8
Db 3 PFPK 6

RESULT 40
US-08-602-999A-181
; Sequence 181, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```

```

; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-181

```

```

Query Match      22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

Qy 5 PPKK 8
Db 5 PPKK 8

```

```

RESULT 41
; Sequence 181, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-181

```

```

Query Match      22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

Qy 5 PPKK 8
Db 5 PPKK 8

```

```

RESULT 42
; Sequence 362, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-362

```

```

Query Match      22.2%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

```


Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
||||
Db 10 PVEP 13

RESULT 43

US-09-500-124-362
; Sequence 362, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Miarock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-362

Query Match 22.2%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
||||
Db 10 PVEP 13

RESULT 44

US-08-105-454-4
; Sequence 4, Application US/08105454
; Patent No. 6071715
; GENERAL INFORMATION:
; APPLICANT: Qian, Yue-Wei
; APPLICANT: Lee, Eva Y.-H. P.

; TITLE OF INVENTION: No. 6071715el Proteins Which Bind to
; TITLE OF INVENTION: Retinoblastoma Proteins and Their
; TITLE OF INVENTION: Encoding DNA Sequences
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 2300 One American Center
; CITY: Austin
; STATE: TX
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,454
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSK:196/XIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-105-454-4

Query Match 22.2%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5
||||
Db 7 KEMP 10

RESULT 45

US-09-407-687-8
; Sequence 8, Application US/09407687
; Patent No. 6548634
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; APPLICANT: Kavanaugh, Michael
; TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
; TITLE OF INVENTION: Affinity
; FILE REFERENCE: 1517.001
; CURRENT APPLICATION NUMBER: US/09/407,687
; CURRENT FILING DATE: 1999-09-28
; EARLIER APPLICATION NUMBER: 60/102,667
; EARLIER FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-407-687-8

Query Match 22.2%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPPK 7
 ||||
 Db 2 MPPK 5

RESULT 46
 US-09-227-357-664
 ; Sequence 664, Application US/09227357
 ; Patent No. 6342581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer et al.
 ; TITLE OF INVENTION: 123 Human Secreted Proteins
 ; FILE REFERENCE: P2010P1
 ; CURRENT APPLICATION NUMBER: US/09/227,357
 ; EARLIER FILING DATE: 1999-01-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684
 ; EARLIER FILING DATE: 1998-07-07
 ; EARLIER APPLICATION NUMBER: 60/051,926
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,793
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,925
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,929
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,803
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,732
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,931
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,932
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,916
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,930
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,918
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,920
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,733
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,795
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,919
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,928
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/055,722
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,723
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,948
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,949
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,953
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,950
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,947
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,964
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/056,360
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,684
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,984
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,954
 ; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/058,785
 ; EARLIER FILING DATE: 1997-09-12
 ; EARLIER APPLICATION NUMBER: 60/058,664
 ; EARLIER FILING DATE: 1997-09-12
 ; EARLIER APPLICATION NUMBER: 60/058,660
 ; EARLIER FILING DATE: 1997-09-12
 ; EARLIER APPLICATION NUMBER: 60/058,661
 ; EARLIER FILING DATE: 1997-09-12
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 664
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-227-357-664
 Query Match 22.2%; Score 4; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 PPK 8
 ||||
 Db 16 PPK 19

RESULT 47
 US-09-556-877-236
 ; Sequence 236, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C5
 ; CURRENT APPLICATION NUMBER: US/09/556,877
 ; CURRENT FILING DATE: 2000-04-19
 ; NUMBER OF SEQ ID NOS: 305
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 236
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-556-877-236
 Query Match 22.2%; Score 4; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 YPVE 12
 ||||
 Db 17 YPVE 20

RESULT 48
 US-09-556-877-237
 ; Sequence 237, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C5
 ; CURRENT APPLICATION NUMBER: US/09/556,877

```
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 12 YPVE 15

RESULT 49
US-09-556-877-238
; Sequence 238, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-238

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 7 YPVE 10

RESULT 50
US-09-556-877-239
; Sequence 239, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-239

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 12 YPVE 15

RESULT 51
US-09-620-412C-236
; Sequence 236, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-236

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 17 YPVE 20

RESULT 52
US-09-620-412C-237
; Sequence 237, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 12 YPVE 15
```

```
RESULT 53
US-09-620-412C-238
; Sequence 238, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-238

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
      ||||
Db      7 YPVE 10

RESULT 54
US-09-620-412C-239
; Sequence 239, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-239

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
      ||||
Db      2 YPVE 5

RESULT 55
US-09-598-419-236
; Sequence 236, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
```

```
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-236

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
      ||||
Db      17 YPVE 20

RESULT 56
US-09-598-419-237
; Sequence 237, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
      ||||
Db      12 YPVE 15

RESULT 57
US-09-598-419-238
; Sequence 238, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-238
```

```
Query Match          22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 7 YPVE 10

RESULT 58
US-09-598-419-239
; Sequence 239, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.46906
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-239

Query Match          22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 2 YPVE 5

RESULT 59
US-08-224-868-5
; Sequence 5, Application US/08224868
; Patent No. 5698448
; GENERAL INFORMATION:
; APPLICANT: Soldin, Steven J.
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,868
; FILING DATE: 08-APR-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/200,404
; FILING DATE: 23-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/782,761
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,115

Query Match          22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 2 YPVE 5

RESULT 60
US-08-747-137-163
; Sequence 163, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: Yen, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991

Query Match          16.7%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
Db 2 EPF 4
```

ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Pro-Amide"
US-08-747-137-163

Query Match 16.7%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11
Db 1 YPV 3

RESULT 61

US-08-415-655-3
; Sequence 3, Application US/08415655
; Patent No. 6025480
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Lee, Mong-hong
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,655
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/47418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-415-655-3

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PVE 12
Db 2 PVE 4
RESULT 62
US-09-330-970-19
; Sequence 19, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; EARLIER FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-19

Query Match 16.7%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
Db 1 TES 3

RESULT 63

US-09-357-952-27
; Sequence 27, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Who
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protea
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-27

Query Match 16.7%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13

Db 1 VEP 3

RESULT 64

US-09-411-531A-1

; Sequence 1, Application US/09411531A

; Patent No. 6251391

; GENERAL INFORMATION:

; APPLICANT: Wilkinson, Randall

; Houston, Devin

; TITLE OF INVENTION: Inhibition of casomorphin and glutuomorphin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Graybeal Jackson Haley

; STREET: 777-108th Ave. NE, Suite 2460

; CITY: Bellevue

; STATE: Washington

; COUNTRY: USA

; ZIP: 98004-5117

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 98

; SOFTWARE: Microsoft Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/411,531A

; FILING DATE: 01-Oct-1999

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: King, Joshua

; REGISTRATION NUMBER: 35,570

; REFERENCE/DOCKET NUMBER: 1776-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (425) 455-5575

; TELEFAX: (425) 455-1046

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-411-531A-1

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPP 7

Db 2 PPP 4

RESULT 65

US-09-521-650-27

; Sequence 27, Application US/09521650

; Patent No. 6335429

; GENERAL INFORMATION:

; APPLICANT: Weber, Eckard

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Keana, John F.W.

; APPLICANT: Drewe, John A.

; APPLICANT: Zhang, Han-Zhong

; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and

; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735.0290002

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPP 7

Db 2 PPP 4

; CURRENT APPLICATION NUMBER: US/09/521,650

; CURRENT FILING DATE: 2000-03-08

; EARLIER APPLICATION NUMBER: 09/168,888

; EARLIER FILING DATE: 1998-10-09

; EARLIER APPLICATION NUMBER: US 60/061,582

; EARLIER FILING DATE: 1997-10-10

; EARLIER APPLICATION NUMBER: US 09/033,661

; EARLIER FILING DATE: 1998-03-03

; NUMBER OF SEQ ID NOS: 142

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-521-650-27

Query Match 16.7%; Score 3; DB 4; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

Db 1 VEP 3

RESULT 66

US-09-168-888-27

; Sequence 27, Application US/09168888

; Patent No. 6342611

; GENERAL INFORMATION:

; APPLICANT: Weber, Eckard

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Keana, John F.W.

; APPLICANT: Drewe, John A.

; APPLICANT: Zhang, Han-Zhong

; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules a:

; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735.0290002

; CURRENT APPLICATION NUMBER: US/09/168,888

; CURRENT FILING DATE: 1998-10-09

; EARLIER APPLICATION NUMBER: US 60/061,582

; EARLIER FILING DATE: 1997-10-10

; EARLIER APPLICATION NUMBER: US 09/033,661

; EARLIER FILING DATE: 1998-03-03

; NUMBER OF SEQ ID NOS: 142

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-168-888-27

Query Match 16.7%; Score 3; DB 4; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

Db 1 VEP 3

RESULT 67

US-09-187-859-199

; Sequence 199, Application US/09187859A

; Patent No. 6358920

```
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-187-859-199

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEP 13
      |||
Db      1 VEP 3

RESULT 68
US-09-411-605A-1
; Sequence 1, Application US/09411605A
; Patent No. 6447772
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of Symptoms Of Au
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/411,605A
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-605A-1

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PFP 7
      |||
Db      2 PFP 4

RESULT 69
US-09-839-542B-199
; Sequence 199, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-199

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEP 13
      |||
Db      1 VEP 3

RESULT 70
5215966-12
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER; RADDATZ, PETER; SCHMITGES,
; CLAUS J.; MINCK, KLAUS OTTO; JONCZYK, ALFRED; SOMBROEK,
; JOHANNES; GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO: 12
; LENGTH: 4
5215966-12

Query Match          16.7%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PFP 7
      |||
Db      2 PFP 4

RESULT 71
5215966-14
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER; RADDATZ, PETER; SCHMITGES,
; CLAUS J.; MINCK, KLAUS OTTO; JONCZYK, ALFRED; SOMBROEK,
; JOHANNES; GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO: 14
; LENGTH: 4
5215966-14

Query Match          16.7%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 PFT 15
      |||
Db      2 PFT 4

RESULT 72
US-07-708-035-14
; Sequence 14, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohmad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; and Nervous Systems
```



```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/708,035
; FILING DATE: 19910603
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRIP-US40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; TELEX: 910-250-6892
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; OTHER INFORMATION: /note= "Acetyl is attached to the amino terminus
; OTHER INFORMATION: of the peptide."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= NH2
; OTHER INFORMATION: /note= "NH2 is attached to the carboxy terminus of
; OTHER INFORMATION: the peptide."
;
US-07-708-035-14

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
Db 3 EPF 5

RESULT 73
US-07-657-769B-28
; Sequence 28, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-657-769B-67

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3

RESULT 74
US-07-657-769B-67
; Sequence 67, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-657-769B-28

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDVKEHLPLPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR_76:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	27.8	18	2	S04229
2	4	22.2	15	2	S66419
3	4	22.2	15	2	S20410
4	4	22.2	16	2	S66613
5	4	22.2	19	2	S60633
6	4	22.2	20	1	LFBSIU
7	4	22.2	20	2	S23742
8	4	22.2	20	2	S56046
9	4	22.2	20	2	S56005
10	3	16.7	6	2	B33932
11	3	16.7	7	2	P00663
12	3	16.7	8	2	T14906
13	3	16.7	8	2	S10783
14	3	16.7	9	2	P00080
15	3	16.7	10	2	C26997
16	3	16.7	10	2	I36893
17	3	16.7	10	2	S18396
18	3	16.7	10	2	C35389
19	3	16.7	10	2	C39745
20	3	16.7	10	2	A61007
21	3	16.7	10	2	A56633
22	3	16.7	10	2	C39111
23	3	16.7	10	2	B45482
24	3	16.7	10	2	C39388
25	3	16.7	10	2	A47364
26	3	16.7	10	2	A61354
27	3	16.7	10	2	PX0060
28	3	16.7	10	2	T13838
29	3	16.7	10	2	T14219
30	3	16.7	10	2	C54226
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32	3	16.7	10	2	P50220
33	3	16.7	11	2	S42449
34	3	16.7	11	2	D58502
35	3	16.7	11	2	I33098
36	3	16.7	11	2	I52304
37	3	16.7	11	2	T17081
38	3	16.7	11	2	P00034
39	3	16.7	12	2	S29764
40	3	16.7	12	2	S65136
41	3	16.7	12	2	P00663
42	3	16.7	12	2	B60228
43	3	16.7	12	4	JX0315
44	3	16.7	12	4	S49073
45	3	16.7	13	2	P00491
46	3	16.7	13	2	A60856
47	3	16.7	13	2	S15755
48	3	16.7	13	2	JZVHP1
49	3	16.7	13	2	P00125
50	3	16.7	13	2	PC4055
51	3	16.7	13	2	D56661
52	3	16.7	13	2	S09019
53	3	16.7	13	2	I84603
54	3	16.7	13	2	A61458
55	3	16.7	13	2	S57571
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58	3	16.7	14	2	S19803
59	3	16.7	14	2	B29743
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61	3	16.7	14	2	D61308
62	3	16.7	14	2	PT0259
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65	3	16.7	15	2	A26997
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69	3	16.7	15	2	B39109
70	3	16.7	15	2	A35232
71	3	16.7	15	2	S61284
72	3	16.7	15	2	S62620
73	3	16.7	15	2	PA0051
74	3	16.7	15	2	PA0060
75	3	16.7	15	2	PA0106
76	3	16.7	15	2	PA0063
77	3	16.7	15	2	P80221
78	3	16.7	15	2	PH1788
79	3	16.7	15	2	A56049
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82	3	16.7	16	2	A61268
83	3	16.7	16	2	S29631
84	3	16.7	16	2	B58503
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86	3	16.7	16	2	H49039
87	3	16.7	16	2	G24687
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89	3	16.7	16	2	I46275
90	3	16.7	16	2	PH1637
91	3	16.7	16	2	B40291
92	3	16.7	16	2	F54226
93	3	16.7	17	2	S66198
94	3	16.7	17	2	JP0046
95	3	16.7	17	2	S15754
96	3	16.7	17	2	B44873
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98	3	16.7	17	2	A59069
99	3	16.7	17	2	S60171
100	3	16.7	17	2	A42920

light-harvesting p
ferredoxin-NADP re
ferredoxin-NADP re
ant1 protein - pha
27K bile and gallb
173K exoantigen -
gene RSSR4 protei
cytochrome-c oxida
dextranucrase (EC
alpha-macroglobuli
kallikrein K2 - hu
dystrophin-associa
Fc mu (IgM) recept
aminotransferase c
frame shifted cyta
self-incompatibili
inhibin alpha chai
actin 7 - soybean
crabroline - Europe
serine proteinase
hypothetical 13 pr
S-locus specific g
hemolytic protein
deoxynucleotidyltr
Ig kappa chain V-I
T-cell receptor al
histamine-releasein
ubiquitin - potato
translocation initia
223K exoantigen -
hemocyanin chain 5
Ig heavy chain CRD
T-cell receptor V-
dehydrin 4.5K poly
unspecific monooxy
S-locus specific g
photosystem I 19,0
capsid protein vp1
hypothetical 1.5K
gentisate 1,2-diox
phosphoprotein, 80
protein disulfide-
protein QF200016 -
protein QF200037 -
protein QF200076 -
ubiquitin - fungus
gastrin-releasing
T cell receptor al
urinary tract ston
hypothetical TEL/M
gene c-fms protein
cytochrome P450-th
beta-glucosidase (
superoxide dismuta
photosystem I chai
T-cell receptor be
insulin-like growt
hemoglobin beta-x
Ig H chain V-D-J r
cytochrome P450mtf
light-harvesting p
alcohol dehydrogen
ribosomal protein
actin 6 - soybean
caldesmon - rabbit
vitamin D binding
excretory gland al
sex-lethal protein
fatty acid ethyl e

ALIGNMENTS

RESULT 1

S04229
 N4: (beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)
 N:Alternate names: glycosylasparaginase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
 C:Accession: S04229

R:Tollersrud, O.K.; Aronson Jr., N.N.

Biochem. J. 260, 101-108, 1989

A:Title: Purification and characterization of rat liver glycosylasparaginase.

A:Reference number: S04228; MUID:89374025; PMID:2775174

A:Accession: S04229

A:Molecule type: protein

A:Residues: 1-18 <TOL>

C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase

C:Keywords: hydrolase

Query Match 27.8%; Score 5; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17

Db 3 PLPLV 7

RESULT 2

S66419

tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)

C:Species: Spinacia oleracea (spinach)

C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997

C:Accession: S66419

R:Kuwabata, T.

FEBS Lett. 371, 195-198, 1995

A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric proteinase of spi

A:Reference number: S66419; MUID:95402209; PMID:7672127

A:Accession: S66419

A:Molecule type: protein

A:Residues: 1-9 <KUM>

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QY 6 DVEK 9

Db 6 DVEK 9

RESULT 3

S20410

protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)

N:Alternate names: LHCI protein kinase

C:Species: chloroplast Spinacia oleracea (spinach)

C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C:Accession: S20410

R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.

FEBS Lett. 298, 33-35, 1992

A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyto

A:Reference number: S20410; MUID:92183823; PMID:1544419

A:Accession: S20410

A:Molecule type: protein

A:Residues: 1-15 <GAL>

C:Genetics:

A:Genome: chloroplast

C:Function:

A:Description: is responsible for the regulation of energy distribution between photosys

A>Note: does not exhibit redox-controlled activation

C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match 22.2%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9

Db 6 DVEK 9

RESULT 4

S66613

protein p12E - Friend murine leukemia virus (fragments)

C:Species: Friend murine leukemia virus

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S66613

R:Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.

Eur. J. Biochem. 232, 373-380, 1995

A:Title: Localization of the palmitoylation site in the transmembrane protein p12E of

A:Reference number: S66613; MUID:96035869; PMID:7556184

A:Accession: S66613

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-9;10-16 <HEN>

Query Match 22.2%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4

Db 4 SLTL 7

RESULT 5

S60633

H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion

C:Species: mitochondrion Artemia sp. (brine shrimp)

A:Variety: Strain La Mata

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002

C:Accession: S60633

R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.

J. Mol. Evol. 38, 156-168, 1994

A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and i

A:Reference number: S60624; MUID:94223692; PMID:8169960

A:Accession: S60633

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-19 <PER>

A:Cross-references: EMBL:X67263; NID:gl1210; PIDN:CAA47685.1; PID:gl1211

A:Experimental source: strain La Mata

A>Note: the source is designated as Artemia parthenogenetica

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

C:Genetics:

A:Gene: ATP8

A:Genome: mitochondrion

A:Genetic code: SGC4

C:Superfamily: H+-transporting ATP synthase protein 8

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 22.2%; Score 4; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLP 15

Db 5 LPLP 8

RESULT 6

LFESTU

tet leader peptide - Bacillus cereus plasmid pBC16

C:Species: Bacillus cereus

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S09233
 R;Palva, A.; Vidgren, G.; Simonen, M.; Rintala, H.; Laamanen, P.
 Nucleic Acids Res. 18, 1635, 1990
 A;Title: Nucleotide sequence of the tetracycline resistance gene of pBC16 from *Bacillus*
 A;Reference number: S09233; MUID:90221899; PMID:2109312
 A;Accession: S09233
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-20 <PAL>
 A;Cross-references: EMBL:X51366; NID:G39459; PIDN:CAA35750.1; PID:G39460
 C;Genetics:
 A;Genome: plasmid
 C;Superfamily: tet leader peptide

Query Match 22.2%; Score 4; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTL 4
 ||||
 Db 17 SLTL 20

RESULT 7
 S23742
 tet leader peptide - *Staphylococcus hyicus*
 C;Species: *Staphylococcus hyicus*
 C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
 C;Accession: S23742
 R;Schwarz, S.; Cardoso, M.; Wegener, H.C.
 Antimicrob. Agents Chemother. 36, 580-588, 1992
 A;Title: Nucleotide sequence and phylogeny of the tet (L) tetracycline resistance determi
 A;Reference number: S23742; MUID:92321725; PMID:1622166
 A;Accession: S23742
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-20 <SCH>
 A;Cross-references: EMBL:X60828; NID:G43682; PIDN:CAA43219.1; PID:G43683
 A;Note: the authors translated the codon GGA for residue 14 as Ala
 C;Superfamily: tet leader peptide

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTL 4
 ||||
 Db 17 SLTL 20

RESULT 8
 F56046
 urinary tract stone matrix protein 8, 14K - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
 C;Accession: F56046
 R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
 Submitted to the Protein Sequence Database, February 1995
 A;Description: Isolation, characterization and sequence of stone proteins.
 A;Reference number: A56046
 A;Accession: F56046
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <BIN>

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TLTD 6
 ||||
 Db 12 TLTD 15

RESULT 9
 S56005
 lysosomal protein 22K - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C;Accession: S56005
 R;Kuwana, T.; Mullock, B.M.; Luzio, J.P.
 Biochem. J. 308, 937-946, 1995
 A;Title: Identification of a lysosomal protein causing lipid transfer, using a fluores
 A;Reference number: S56005; MUID:97104296; PMID:8948454
 A;Accession: S56005
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <KUW>

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTL 4
 ||||
 Db 17 SLTL 20

RESULT 10
 B33932
 Ig mu chain D region (D23) - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
 C;Accession: B33932
 R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
 A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ
 A;Reference number: A33932; MUID:89282823; PMID:2499887
 A;Accession: B33932
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-6 <BAC>
 A;Cross-references: GB:M27107
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 EKL 10
 ||||
 Db 1 EKL 3

RESULT 11
 PQ0663
 membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
 C;Species: porcine epidemic diarrhea virus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
 C;Accession: PQ0663
 R;Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
 J. Gen. Virol. 74, 1795-1804, 1993
 A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epidem
 issible gastroenteritis virus.
 A;Reference number: JQ2191; MUID:93389433; PMID:8397280
 A;Accession: PQ0663
 A;Molecule type: mRNA
 A;Residues: 1-7 <BRI>
 A;Cross-references: GB:Z14976; NID:G311650; PIDN:CAA78699.1; PID:G584083
 C;Comment: This virus is coronavirus related to human coronavirus 229E.
 C;Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12
|||
Db 4 LHL 6

RESULT 12

T14906
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14906
R;Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weisshaar, B.
Plant Cell 6, 1607-1621, 1994
A;Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.
A;Reference number: Z18259; MUID:95128172; PMID:7827494
A;Accession: T14906
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-8 <FE>
A;Cross-references: EMBL:S75395; NID:g913201; PID:el94245

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 4 TLT 6

RESULT 13

S10783
enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10783
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10783
A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 2 PLP 4

RESULT 14

PT0080
60K Ca binding protein - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PT0080
R;Treveso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A;Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calreti
A;Reference number: PT0080; MUID:91207333; PMID:2018493
A;Accession: PT0080
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <TR>

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 2 PLV 4

RESULT 15

C26997
unspecific monooxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic -
N;Alternate names: cytochrome P450
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Mar-1999
C;Accession: C26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha
A;Reference number: A26997; MUID:8800604; PMID:3651420
A;Accession: C26997
A;Molecule type: protein
A;Residues: 1-10 <GRA>
A;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembr

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 7 LTL 9

RESULT 16

I36893
apolipoprotein A-I - green monkey (fragment)
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I36893
R;Sorci-Thomas, M.; Kearns, M.W.
J. Biol. Chem. 266, 18045-18050, 1991
A;Title: Transcriptional regulation of the apolipoprotein A-I gene.
A;Reference number: A57766; MUID:92011532; PMID:1917942
A;Accession: I36893
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: GB:M69224; NID:g176486; PIDN:AAA35357.1; PID:g553152
C;Superfamily: apolipoprotein A-I

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 6 LTL 8

RESULT 17

S18396
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fr.
C;Species: Acetobacter hansenii
C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C;Accession: S18396
R;Levy, H.R.; Cook, C.
Arch. Biochem. Biophys. 291, 161-167, 1991
A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase
A;Reference number: S18396; MUID:92027789; PMID:1929428
A;Accession: S18396
A;Molecule type: protein
A;Residues: 1-10 <LEV>
A;Experimental source: ATCC 23769
C;Function:
A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phospha

A;Pathway: pentose phosphate pathway
C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
|||
Db 2 HLP 4

RESULT 18
C35389
urease (BC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C;Accession: C35389
R;Hu, L.F.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of gene
A;Reference number: A35389; PMID:90264298; PMID:2345135
A;Accession: C35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HUA>
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
|||
Db 8 VEK 10

RESULT 19
C39745
sphingomyelinase - Rhodococcus sp. (fragment)
C;Species: Rhodococcus sp.
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: C39745
R;Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidas. Evidence using these activator proteins.
A;Reference number: A39745; PMID:91210321; PMID:1850427
A;Accession: C39745
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ITO>

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 3 PLP 5

RESULT 20
A61007
hementin (BC 3.4.-.-) - Amazon leech (fragment)
C;Species: Haementeria ghilianii (Amazon leech)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 359-369, 1990
A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from
A;Reference number: A61007; PMID:90256973; PMID:2187898
A;Accession: A61007

A;Molecule type: protein
A;Residues: 1-10 <SWA>
C;Keywords: anticoagulant; hydrolase; saliva

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 2 TLT 4

RESULT 21
A56633
neomysuppressin - flesh fly (Sarcophaga bullata)
N;Alternate names: Neb-MS
C;Species: Sarcophaga bullata
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Accession: A56633
R;Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; Bueds, H.; De Loof, A.
Comp. Biochem. Physiol. C 102, 239-245, 1992
A;Title: Isolation, primary structure and synthesis of neomysuppressin, a myoinhibitory peptide
A;Reference number: A56633; PMID:93047886; PMID:1358537
A;Accession: A56633
A;Molecule type: protein
A;Residues: 1-10 <FON>
A;Experimental source: head
A;Note: sequence extracted from NCBI backbone (NCBIP:119072)
C;Keywords: amidated carboxyl end; neuropeptide
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7
|||
Db 1 TDV 3

RESULT 22
C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stoutii (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: C39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity to Ig heavy chain C region
A;Reference number: A39111; PMID:91156684; PMID:2000382
A;Accession: C39111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAR>
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 7 PLV 9

RESULT 23
B45482
platelet activating factor acetylhydrolase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-May-1995
C;Accession: B45482
R;Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.

J. Biol. Chem. 268, 3857-3865, 1993
 A;Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purified
 A;Reference number: A45482; MUID:93179380; PMID:8440681
 A;Accession: B45482
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <STR>

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
 ||||
 Db 2 PLV 4

RESULT 24

C39398
 FC mu (IgM) receptor surface complex gamma chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 20-Mar-1998
 C;Accession: C39398
 R;Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
 A;Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g
 A;Reference number: A39398; MUID:91219496; PMID:2023945
 A;Accession: C39398
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <CAM>

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 ||||
 Db 4 LPL 6

RESULT 25

A47364
 Placental lactogen-I precursor - mouse (fragment)
 C;Species: Mus sp. (mouse)
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
 R;Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
 Mol. Endocrinol. 7, 181-188, 1993
 A;Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro
 A;Reference number: A47364; MUID:93225959; PMID:8469232
 A;Accession: A47364
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-10 <RES>
 A;Cross-references: GB:S58124; NID:9299449

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
 ||||
 Db 3 LTL 5

RESULT 26

A61354
 carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
 N;Alternate names: endoplasmic reticulum protein ERP61; glucose regulated protein GRP58;
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C;Accession: A61354

R;Murthy, M.S.R.; Pande, S.V.
 Mol. Cell. Biochem. 122, 133-138, 1993
 A;Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the p
 A;Reference number: A61354; MUID:94049728; PMID:8232244
 A;Accession: A61354
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <MUR>
 C;Keywords: acyltransferase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
 ||||
 Db 6 LTD 8

RESULT 27

PX0060
 lysosome-associated membrane glycoprotein 2 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-1995
 C;Accession: PX0060
 R;Akasaki, K.; Yamaguchi, Y.; Furuno, K.; Tsuji, H.
 J. Biochem. 110, 922-927, 1991
 A;Title: Purification, some properties, and tissue distribution of a major lysosome-
 A;Reference number: PX0060; MUID:92176167; PMID:1794981
 A;Accession: PX0060
 A;Molecule type: protein
 A;Residues: 1-10 <AKA>
 A;Experimental source: liver
 C;Keywords: glycoprotein; membrane protein

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
 ||||
 Db 5 LTD 7

RESULT 28

T13838
 cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
 C;Species: mitochondrion Bipes biporus
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
 C;Accession: T13838
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A;Title: Two novel gene orders and the role of light-strand replication in rearrange
 A;Reference number: Z17789; MUID:97153826; PMID:9000757
 A;Accession: T13838
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-10 <MAC>
 A;Cross-references: EMBL:U71335; NID:gl753232; PID:gl753235; PIDN:AAB48271.1
 C;Genetics:
 A;Genome: mitochondrion
 A;Note: COI
 C;Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
 ||||
 Db 2 SLT 4

RESULT 29
 T14219
 Cytochrome-c oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment)
 C:Species: mitochondrion Xenosaurus grandis
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T14219
 R:Wacey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A>Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A:Reference number: Z17789; MUID:97153826; PMID:9000757
 A:Accession: T14219
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <MAC>
 A:Cross-references: EMBL:U71333; NID:g5739536; PIDN:AAC62821.1; PID:g1753275
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: Col
 C:Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 |||
 Db 2 TLT 4

RESULT 30
 C54226
 light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)
 C:Species: Chromatium purpuratum
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C:Accession: C54226
 R:Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
 Biochemistry 33, 2178-2184, 1994
 A>Title: Purification and characterization of the peripheral antenna of the purple-sulfur
 A:Reference number: A54226; MUID:94162224; PMID:8117674
 A:Accession: C54226
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <KER>
 C:Keywords: antenna complex; light-harvesting polypeptide

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LVQ 18
 |||
 Db 7 LVQ 9

RESULT 31
 PA0116
 ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)
 C:Species: Oryza sativa (rice)
 C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 03-Jun-2002
 C:Accession: PA0116
 R:Kamo, M.; Tsugita, A.
 submitted to JIPID, March 1995
 A:Reference number: PA0114
 A:Accession: PA0116
 A:Molecule type: protein
 A:Residues: 1-10 <KAM>
 A:Experimental source: leaf
 C:Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9
 |||
 Db 1 VEX 3

RESULT 32
 PS0220
 ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)
 C:Species: Oryza sativa (rice)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
 C:Accession: PS0220
 R:Uchiyama, Y.; Tsugita, A.
 submitted to JIPID, August 1991
 A:Reference number: PS0205
 A:Accession: PS0220
 A:Molecule type: protein
 A:Residues: 1-10 <UCH>
 C:Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9
 |||
 Db 1 VEX 3

RESULT 33
 S42449
 ant1 protein - phage P7
 C:Species: phage P7
 C>Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
 C:Accession: S42449
 R:Citron, M.; Schuster, H.
 Cell 62, 591-598, 1990
 A>Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
 A:Reference number: S42448; MUID:90335969; PMID:1696181
 A:Accession: S42449
 A>Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-11 <CIT>
 A:Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
 |||
 Db 4 PLV 6

RESULT 34
 D58502
 27K bile and gallbladder stone protein - unidentified bacterium (fragment)
 C:Species: unidentified bacterium
 C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 C:Accession: D58502
 R:Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A>Description: The proteins of kidney and gallbladder stones.
 A:Reference number: A58501
 A:Accession: D58502
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <BIN>
 A:Experimental source: human bile and gallbladder stones

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
|||
Db 4 LTD 6

RESULT 35

I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: I33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: I33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 6 LPL 8

RESULT 36

I52304
gene rSSTR4 protein - rat (fragment)
C:Species: Rattus sp. (rat)
C>Date: 23-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
C:Accession: I52304
R;Xu, Y.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 206, 935-941, 1995
A:Title: Characterization of the proximal promoter region of the rat somatostatin receptor
A:Reference number: I52304; MUID:95134278; PMID:7832807
A:Accession: I52304
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S75475; NID:g914315
C:Genetics:
A:Gene: rSSTR4

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 7 LPL 9

RESULT 37

T17081
Cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynocephalus raddei mitochondrion (fragment)
C:Species: mitochondrion Phrynocephalus raddei
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C:Accession: T17081
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A:Reference number: Z18674; MUID:97315309; PMID:9169559
A:Accession: T17081
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <MAC>
A:Cross-references: EMBL:U82691; NID:g3603148; PID:g3603151; PIDN:AAC62302.1
C:Genetics:
A:Genome: mitochondrion
A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 3 TLT 5

RESULT 38

PU0034
dextranase (EC 2.4.1.5) - Streptococcus bovis (fragment)
C:Species: Streptococcus bovis
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996
C:Accession: PU0034
R;Uezono, Y.; Tsumori, H.; Mukasa, H.
submitted to JIPID, October 1993
A:Description: Purification and properties of glucosyltransferase synthesizing 1,6-a
A:Reference number: PU0034
A:Accession: PU0034
A:Molecule type: protein
A:Residues: 1-11 <UEZ>
A:Experimental source: ATCC 9809
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 7 TLT 9

RESULT 39

S29764
alpha-macroglobulin proteinase inhibitor - bullfrog (fragment)
C:Species: Rana catesbeiana (bullfrog)
C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 07-May-1999
C:Accession: S29764
R;Rubenstein, D.S.; Thøgersen, I.B.; Pizzo, S.V.; Engchild, J.J.
Biochem. J. 290, 85-95, 1993
A:Title: Identification of monomeric alpha-macroglobulin proteinase inhibitors in bi
teasin inhibitor from the American bullfrog Rana catesbeiana.
A:Reference number: S29764; MUID:93176138; PMID:7679897

A:Accession: S29764
A:Molecule type: protein
A:Residues: 1-12 <RUB>
A:Experimental source: plasma
C:Function:

A:Description: inhibits the proteinases of different catalytic class
C:Superfamily: alpha-2-macroglobulin
C:Keywords: monomer; proteinase inhibitor

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
|||
Db 3 HLP 5

RESULT 40

S65136
kalikrein K2 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
A:Accession: S65136
R;Deperthes, D.; Chapdelaine, P.; Tremblay, R.R.; Brunet, C.; Berton, J.; Hebert, J.
Biochim. Biophys. Acta 1245, 311-316, 1995

A:Title: Isolation of prostatic kallikrein hK2, also known as hGK-1, in human seminal plasma
 A:Reference number: S65136; MUID:96125726; PMID:8541306
 A:Accession: S65136
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <DEP>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12
 |||
 Db 7 LHL 9

RESULT 41

PN0663
 dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C:Accession: PN0663
 R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the Golgi apparatus of skeletal muscle
 A:Reference number: PN0662; MUID:94156881; PMID:8113213
 A:Accession: PN0663
 A:Molecule type: protein
 A:Residues: 1-12 <VS>
 C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C:Keywords: glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
 |||
 Db 3 PLP 5

RESULT 42

B60228
 FC mu (IgM) receptor surface complex beta chain - mouse (fragment)
 N:Alternate names: membrane protein B29
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 20-Mar-1998
 C:Accession: B60228; B39398
 R:Hombach, J.; Lottspeich, F.; Reth, M.
 Eur. J. Immunol. 20, 2795-2799, 1990
 A:Title: Identification of the genes encoding the IGM-alpha and Ig-beta components of the B cell receptor
 A:Reference number: A60228; MUID:91099432; PMID:2269334
 A:Accession: B60228
 A:Molecule type: protein
 A:Residues: 1-12 <HOM>
 R:Cambieri, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
 A:Title: IGM antigen receptor complex contains phosphoprotein products of B29 and mb-1 genes
 A:Reference number: A39398; MUID:91219496; PMID:20233945
 A:Accession: B39398
 A:Molecule type: protein
 A:Residues: 'XX', 3-10 <CAM>
 C:Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 |||
 Db 4 LPL 6

RESULT 43

JX0315
 aminotransferase chimera DY18 - synthetic (fragment)
 C:Species: synthetic
 C:Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
 C:Accession: JX0315
 R:Miyaizawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
 J. Biochem. 115, 568-577, 1994
 A:Title: Construction of aminotransferase chimeras and analysis of their substrate specificity
 A:Reference number: JX0315; MUID:94334304; PMID:8056774
 A:Accession: JX0315
 A:Molecule type: DNA
 A:Residues: 1-12 <MY>
 C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransferase and aminotransferase
 C:Keywords: aminotransferase

Query Match 16.7%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
 |||
 Db 7 LTL 9

RESULT 44

S49073
 frame shifted cytochrome c oxidase subunit II - Mycoplasma pneumoniae (fragment)
 N:Alternate names: H-transferring ATP synthase (EC 3.6.3.14) alpha chain (misidentified)
 C:Species: Mycoplasma pneumoniae
 C:Date: 28-Aug-1998 #sequence_revision 28-Aug-1998 #text_change 19-Apr-2002
 C:Accession: S49073
 R:Proft, T.; Herrmann, R.
 Mol. Microbiol. 13, 337-348, 1994
 A:Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae cytochrome c oxidase subunit II
 A:Reference number: S49059; MUID:95075318; PMID:7984111
 A:Accession: S49073
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-12 <PRO>
 A:Cross-references: EMBL:Z32665; NID:G474163; PIDN:CAA83583.1; PID:G581348
 A:Experimental source: clone D2-16
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
 A:Note: the GenBank entry MPDASAL, release 106.0, translates the ATC codon, 1 in this sequence, to a stop codon. The nucleotide sequence translated in an alternative reading frame is identical to the one in this sequence.
 C:Genetics: SGC3
 A:Genetic code: SGC3

Query Match 16.7%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 |||
 Db 3 TLT 5

RESULT 45

PQ0491
 self-incompatibility locus glycoprotein delta - wild cabbage (fragment)
 C:Species: Brassica oleracea (wild cabbage)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Oct-1997
 C:Accession: PQ0491
 R:Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
 Plant Cell 5, 75-86, 1993
 A:Title: Expression of a self-incompatibility gene in a self-compatible line of Brassica oleracea
 A:Reference number: JQ1733; MUID:93177215; PMID:8439745
 A:Accession: PQ0491
 A:Molecule type: protein
 A:Residues: 1-13 <GAU>
 A:Experimental source: stigma, var. acephala p57S1
 C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein

C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
|||
Db 9 SLT 11

RESULT 46

A60856
inhibin alpha chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60856
R;Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wattenhall
J. Endocrinol. 113, 213-221, 1987
A;Title: Isolation of inhibin from ovine follicular fluid.
A;Reference number: A60856; MUID:87224684; PMID:3585232
A;Accession: A60856
A;Molecule type: protein
A;Residues: 1-13 <LSV>
C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C;Superfamily: inhibin
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 4 PLP 6

RESULT 47

S15755
actin 7 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Accession: S15755
R;Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A;Reference number: S15754; MUID:91346640; PMID:2102831
A;Accession: S15755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <PEA>
A;Cross-references: EMBL:X17120; NID:gl18527; PIDN:CAA34980.1; PID:gl18528
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 9 PLV 11

RESULT 48

JZVHP1
crabrolin - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A01781
R;Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A;Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,

A;Reference number: A92441; MUID:84289390; PMID:6206053

A;Accession: A01781

A;Molecule type: protein

A;Residues: 1-13 <ARG>

C;Comment: This cytotoxic peptide from hornet venom induces mast cell degranulation

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; venom

F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 2 LPL 4

RESULT 49

PN0125
serine proteinase (BC 3.4.21.-) - Actinomyces sp. (fragment)
C;Species: Actinomyces sp.
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 27-Jan-1995
C;Accession: PN0125
R;Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.
Biochimia 52, 414-422, 1987
A;Title: Glu, Asp-specific proteinase from Actinomycetes.
A;Reference number: PN0125
A;Accession: PN0125
A;Molecule type: protein
A;Residues: 1-13 <MOS>
A;Note: article in Russian with English abstract
C;Keywords: hydrolase; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7
|||
Db 5 TDV 7

RESULT 50

PC4055
hypothetical 13 protein - Frankia sp. (fragment)
C;Species: Frankia sp.
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 27-Oct-1995
C;Accession: PC4055
R;Harriott, O.T.; Hosted, T.J.; Benson, D.R.
Gene 161, 63-67, 1995
A;Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fix
A;Reference number: JC4203; MUID:95369734; PMID:7642138
A;Accession: PC4055
A;Molecule type: DNA
A;Residues: 1-13 <HAR>
A;Cross-references: GB:L29299

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
|||
Db 10 LTD 12

RESULT 51

D56661
S-locus specific glycoprotein (allele S3) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: D56661

R;Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal seq
A;Reference number: A56661; MUID:92090397; PMID:1752245
A;Accession: D56661
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <GAU>
A;Experimental source: stigma extracts, var. acephala
A;Note: sequence extracted from NCBI backbone (NCBIP:72300)
C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in the
C;Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SUT 3
|||
Db 9 SUT 11

RESULT 52
S03019
hemolytic protein B9 - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S03019
R;Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erpamer, G.P.; Barra, D.; Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A;Title: Purification and characterization of bioactive peptides from skin extracts of R
A;Reference number: S03018; MUID:90198965; PMID:2317508
A;Accession: S03019
A;Molecule type: protein
A;Residues: 1-13 <SIM>

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 2 LPL 4

RESULT 53
I84603
deoxynucleotidyltransferase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I84603
R;Koiwai, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A;Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A;Reference number: I45884; MUID:87213162; PMID:3579900
A;Accession: I84603
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-13 <RES>
A;Cross-references: GB:M26144; NID:G951194; PIDN:AAA74588.1; PID:G951195
C;Genetics:
A;Gene: GDB:DNTT
A;Cross-references: GDB:119100; OMIM:187410
A;Map position: 10q23-10q24

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 9 PLP 11

RESULT 54
A61458
Ig kappa chain V-L region (BOU) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C;Accession: A61458; PLO156
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: A61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This protein is one of monoclonal IGM reactive with myeloma-associated gly
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 10 TLT 12

RESULT 55
T cell receptor alpha chain V-J region (clone pp7 and others) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57571; S57573; S57576
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaeet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversifie
A;Reference number: S57494
A;Accession: S57571
A;Molecule type: mRNA
A;Residues: 1-13 <BUR>
A;Cross-references: EMBL:Z49948; NID:g887496; PIDN:CAA90219.1; PID:g887497
A;Experimental source: clone pp7
A;Accession: S57573
A;Molecule type: mRNA
A;Residues: 1-13 <BUL>
A;Cross-references: EMBL:Z49950; NID:g887500; PIDN:CAA90221.1; PID:g887501
A;Experimental source: clone TFI
A;Accession: S57576
A;Molecule type: mRNA
A;Residues: 1-13 <BUW>
A;Cross-references: EMBL:Z49952; NID:g887512; PIDN:CAA90223.1; PID:g887513
A;Experimental source: clone RL16
C;Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 8 EKL 10

RESULT 56
PH0138
T-cell receptor beta chain V-D-J region C8 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C;Accession: PH0138
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S.;
J. Exp. Med. 173, 19-24, 1991
A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the cor
A;Reference number: PH0135; MUID:91086843; PMID:1702137
A;Accession: PH0138

A:Molecule type: mRNA
 A:Residues: 1-13 <MAR>
 C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
 |||
 Db 11 EKL 13

RESULT 57

JN0390
 histamine-releasing peptide II - oriental hornet
 N:Alternate names: venom protein HR-2
 C:Species: Vespa orientalis (oriental hornet)
 C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
 C:Accession: JN0390; S10919
 R:Miroschnikov, A.I.; Shezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus
 Bioorg. Khim. 7, 1467-1477, 1981
 A:Title: Structure and properties of histamine releasing peptides from the venom of Vesp
 A:Reference number: JN0389
 A:Accession: JN0390
 A:Molecule type: protein
 A:Residues: 1-14 <MIR>
 R:Tuichibaev, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
 Biochemistry (N.Y.) 53, 183-190, 1988
 A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S
 A:Reference number: S06445
 A:Accession: S10919
 A:Molecule type: protein
 A:Residues: 1-14 <TUI>
 C:Superfamily: crabrolin
 C:Keywords: amidated carboxyl end; venom
 F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 |||
 Db 2 LPL 4

RESULT 58

S19803
 ubiquitin - potato (fragment)
 C:Species: Solanum tuberosum (potato)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Sep-1993
 C:Accession: S19803
 R:Belknap, W.
 submitted to the EMBL Data Library, January 1992
 A:Reference number: S19798
 A:Accession: S19803
 A:Molecule type: mRNA
 A:Residues: 1-14 <BEL>
 A:Cross-references: EMBL:Z11667
 C:Superfamily: ubiquitin; ubiquitin homology

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 |||
 Db 7 TLT 9

RESULT 59

B29743
 Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)

translation initiation factor eIF-2 alpha chain-associated kinase phosphopeptide - r.
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Oct-1997
 C:Accession: B29743

R:Rose, D.W.; Wettenhall, R.E.H.; Kudlicki, W.; Kramer, G.; Hardesty, B.
 Biochemistry 26, 6593-6597, 1987
 A:Title: The 90-kilodalton peptide of the heme-regulated eIF-2-alpha kinase has sequ
 A:Reference number: A90521; MUID:88107571; PMID:3427028
 A:Accession: B29743
 A:Molecule type: protein
 A:Residues: 1-14 <ROS>
 A:Experimental source: reticulocyte
 C:Superfamily: heat shock protein 90

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
 |||
 Db 3 SLT 5

RESULT 60

C33098
 223k exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: C33098

R:Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: C33098
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
 |||
 Db 6 EKL 8

RESULT 61

D61308
 hemocyanin chain 5A - Sahara scorpion (fragment)
 C:Species: Androctonus australis (Sahara scorpion)
 C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C:Accession: D61308
 R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
 FEBS Lett. 106, 283-291, 1979
 A:Title: Structural characterization of seven different subunits in Androctonus aust
 A:Reference number: A61308; MUID:80047238; PMID:499512
 A:Accession: D61308
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 |||
 Db 10 LPL 12

RESULT 62

PT0259
 Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0259
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A:Reference number: PT0222; M01D:91108337; PMID:1899102
 A:Accession: PT0259
 A:Molecule type: DNA
 A:Residues: 1-14 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
 |||
 Db 2 TLT 4
 |||

RESULT 63
 S57572
 T cell receptor V-J junctional alpha chain region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
 C:Accession: S57572
 R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
 submitted to the EMBL Data Library, June 1995
 A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b
 A:Reference number: S57494
 A:Accession: S57572
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-14 <BUR>
 A:Cross-references: EMBL:249957; NID:g887478; PIDN:CAA90228.1; PID:g887479
 C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
 |||
 Db 10 PLV 12
 |||

RESULT 64
 PC4382
 dehydrin 4.5K polypeptide - Soybean (fragment)
 N:Alternate names: acid soluble 26K protein
 C:Species: Glycine max
 C:Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 18-Jul-2001
 C:Accession: PC4382
 R:Momma, M.; Haraguchi, K.; Saito, M.; Chikuni, K.; Harada, K.
 Biosci. Biotechnol. Biochem. 61, 1286-1291, 1997
 A:Title: Purification and characterization of the acid soluble 26-kDa polypeptide from s
 A:Reference number: PC4380; M01D:97446521; PMID:9301109
 A:Accession: PC4382
 A:Molecule type: protein
 A:Residues: 1-14 <MOM>
 A:Experimental source: seed
 C:Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKL 10
 |||
 Db 6 EKL 8
 |||

RESULT 65
 A26997
 unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
 N:Alternate names: cytochrome P450b
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Mar-1999
 C:Accession: A26997
 R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
 Biochemistry 26, 3887-3894, 1987
 A:Title: Evidence for functional and structural multiplicity of pregnenolone-16- α -
 A:Reference number: A26997; M01D:88000604; PMID:3651420
 A:Accession: A26997
 A:Molecule type: protein
 A:Residues: 1-15 <GRA>
 A:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembr

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4
 |||
 Db 7 LTL 9
 |||

RESULT 66
 B56661
 S-locus specific glycoprotein P57 beta - wild cabbage (fragment)
 C:Species: Brassica oleracea (wild cabbage)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 31-Oct-1997
 C:Accession: B56661
 R:Gaude, I.; Denoroy, L.; Dumas, C.
 Electrophoresis 12, 646-653, 1991
 A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal
 A:Reference number: A56661; M01D:92090397; PMID:1752245
 A:Accession: B56661
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <GAU>
 A:Experimental source: stigma extracts, var. acephala, self-compatible line P57
 A:Note: sequence extracted from NCBI backbone (NCBI:72302)
 C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in
 C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
 C:Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3
 |||
 Db 11 SLT 13
 |||

RESULT 67
 PQ0681
 Photosystem I 19.0K D1 chain - common tobacco (fragment)
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
 C:Accession: PQ0681
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
 Plant Physiol. 102, 1259-1267, 1993
 A:Title: Molecular heterogeneity of photosystem I. psal, psae, psaf, psah and psal a;
 A:Reference number: PQ0667; M01D:94105345; PMID:8278548
 A:Accession: PQ0681
 A:Molecule type: protein
 A:Residues: 1-15 <OBO>
 C:Superfamily: photosystem I chain II
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEX 9
|||
Db 2 VEX 4

RESULT 68

PQ0545
capsid protein VP19C - human herpesvirus 1 (fragment)
C;Species: human herpesvirus 1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PQ0545
R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
A;Reference number: PQ0544; MUID:93019027; PMID:1328483
A;Accession: PQ0545
A;Molecule type: protein
A;Residues: 1-15 <DAV>
A;Experimental source: strain 17
C;Genetics:
A;Gene: UL38
C;Keywords: capsid protein

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15
|||
Db 5 PLP 7

RESULT 69

B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; JQ1585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
A;Cross-references: GB:M58406
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of putative core
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15
|||
Db 10 PLP 12

RESULT 70

A35232
gentisate 1,2-dioxygenase (EC 1.13.11.4) - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni

C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 23-Jun-1993
C;Accession: A35232
R;Harpel, M.R.; Lipscomb, J.D.
J. Biol. Chem. 265, 6301-6311, 1990
A;Title: Gentisate 1,2-dioxygenase from Pseudomonas. Purification, characterization,
A;Reference number: A35232; MUID:90202907; PMID:2156846
A;Accession: A35232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HAR>
C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LVQ 18
|||
Db 2 LVQ 4

RESULT 71

S61284
Phosphoprotein, 80K - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 25-Apr-1997
C;Accession: S61284
R;Freestone, P.; Grant, S.; Toth, I.; Norris, V.
Mol. Microbiol. 15, 573-580, 1995
A;Title: Identification of phosphoproteins in Escherichia coli.
A;Reference number: S61284; MUID:95302968; PMID:7783627
A;Accession: S61284
A;Molecule type: protein
A;Residues: 1-15 <FRE>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKL 10
|||
Db 3 EKL 5

RESULT 72

S62620
Protein disulfide-isomerase (EC 5.3.4.1) - castor bean (fragment)
C;Species: Ricinus communis (castor bean)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-1999
C;Accession: S62620
R;Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.
Eur. J. Biochem. 235, 215-224, 1996
A;Title: Molecular characterisation of plant endoplasmic reticulum: identification c
A;Reference number: S62620; MUID:96202938; PMID:8631332
A;Accession: S62620
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <COU>
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4
|||
Db 11 LTL 13

RESULT 73

PA0051
protein QF200016 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0051

R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*

A;Reference number: PA0051

A;Accession: PA0051

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9

Db 2 VEK 4

RESULT 74

PA0060

protein QF200037 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0060

R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*

A;Reference number: PA0051

A;Accession: PA0060

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15

Db 4 PLP 6

RESULT 75

PA0106

protein QF200076 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0106

R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*

A;Reference number: PA0051

A;Accession: PA0106

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4

Db 6 LTL 8

Search completed: November 25, 2003, 19:36:09
Job time : 13.3488 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDEVKLHLPLVLQ 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	13	1	TEJA_RANJA
2	4	22.2	17	1	PH3_PERAM
3	4	22.2	20	1	LPTR_BACST
4	3	16.7	8	1	ALL6_CDDPO
5	3	16.7	10	1	ESL_LACCA
6	3	16.7	10	1	NSI_MYCTU
7	3	16.7	10	1	URE3_MORMO
8	3	16.7	11	1	TIN4_HOPTI
9	3	16.7	12	1	PPK4_PERAM
10	3	16.7	12	1	TIN2_HOPTI
11	3	16.7	12	1	TIN3_HOPTI
12	3	16.7	12	1	TM2A_METWA
13	3	16.7	13	1	ACT7_SOYBN
14	3	16.7	13	1	CRBL_VESCR
15	3	16.7	13	1	CRTC_RANES
16	3	16.7	13	1	FR12_PEA
17	3	16.7	13	1	HPB9_RANES
18	3	16.7	13	1	IDHP_RAT
19	3	16.7	13	1	TEMA_RANTE
20	3	16.7	13	1	TEMF_RANTE
21	3	16.7	14	1	CRBL_VESOR
22	3	16.7	14	1	ECDC_LYMDI
23	3	16.7	15	1	CYSK_GLOPA
24	3	16.7	15	1	GTS_ASADI
25	3	16.7	15	1	ONC1_ONCMY
26	3	16.7	15	1	UC29_MAIZE
27	3	16.7	16	1	ARCD_PSEPU
28	3	16.7	16	1	FIBA_MELME
29	3	16.7	16	1	IBPA_PIG
30	3	16.7	16	1	MMFX_SOLTU
31	3	16.7	17	1	ACT6_SOYBN
32	3	16.7	17	1	EPG_THEAQ
33	3	16.7	18	1	RL23_HALCU

34	3	16.7	18	1	UC21_MAIZE
35	3	16.7	19	1	HI790_RAT
36	3	16.7	19	1	LANA_ACTLG
37	3	16.7	19	1	LPGE_ECOLI
38	3	16.7	19	1	MIFB_TRISP
39	3	16.7	20	1	FIBB_SHEEP
40	3	16.7	20	1	FRHA_METBA
41	3	16.7	20	1	HET1_RADMG
42	3	16.7	20	1	M117_BOVIN
43	3	16.7	20	1	TENA_ACTTE
44	3	16.7	20	1	TENB_ACTTE
45	3	16.7	20	1	TL22_SFIOL
46	3	16.7	20	1	YPRB_SERMA
47	2	11.1	5	1	BIOA_CITFR
48	2	11.1	5	1	PRCT_PERAM
49	2	11.1	6	1	TMOF_SARBU
50	2	11.1	6	1	TRPI_PSEPU
51	2	11.1	6	1	VP19_HSV1K
52	2	11.1	7	1	CCF1_ENTFA
53	2	11.1	7	1	MNP1_LEPDE
54	2	11.1	7	1	UN06_PINPS
55	2	11.1	8	1	ACT_CARMA
56	2	11.1	8	1	AKH_TABAT
57	2	11.1	8	1	CAD1_ENTFA
58	2	11.1	8	1	COM2_CONPU
59	2	11.1	8	1	CPD1_ENTFA
60	2	11.1	8	1	HTF2_PERAM
61	2	11.1	8	1	PLP_BRANA
62	2	11.1	8	1	PPK3_PERAM
63	2	11.1	8	1	RT34_BOVIN
64	2	11.1	8	1	UPAA_HUMAN
65	2	11.1	9	1	ALC_CHLRE
66	2	11.1	9	1	BUK_CLOPA
67	2	11.1	9	1	FAR5_PANRE
68	2	11.1	9	1	FAR5_PENMO
69	2	11.1	9	1	FAR9_ASCSU
70	2	11.1	9	1	FIBB_MAFU
71	2	11.1	9	1	MGMT_BOVIN
72	2	11.1	9	1	MOSH_CLYJA
73	2	11.1	9	1	OXYA_SQUAC
74	2	11.1	9	1	OXYT_RABIT
75	2	11.1	9	1	PH1_LYCES
76	2	11.1	9	1	RT33_BOVIN
77	2	11.1	9	1	SAMP_MUSCA
78	2	11.1	9	1	TAL1_PICJA
79	2	11.1	9	1	TAL3_PICJA
80	2	11.1	9	1	UHA2_HUMAN
81	2	11.1	9	1	ULAD_HUMAN
82	2	11.1	9	1	ULAE_HUMAN
83	2	11.1	9	1	UPA3_HUMAN
84	2	11.1	9	1	UPA6_HUMAN
85	2	11.1	9	1	UPA7_HUMAN
86	2	11.1	10	1	AH3_FRUSE
87	2	11.1	10	1	AL19_CARMA
88	2	11.1	10	1	ANGT_BOVIN
89	2	11.1	10	1	ANGT_CHICK
90	2	11.1	10	1	APE_CARGI
91	2	11.1	10	1	BRK_ONCMY
92	2	11.1	10	1	CATE_SHEEP
93	2	11.1	10	1	COXA_ONCMY
94	2	11.1	10	1	COXK_ONCMY
95	2	11.1	10	1	FARP_LOCOMI
96	2	11.1	10	1	FARP_MANSE
97	2	11.1	10	1	GAUJ_HUMAN
98	2	11.1	10	1	GON1_PETMA
99	2	11.1	10	1	GON2_CHEPR
100	2	11.1	10	1	GON3_ONCKE

ALIGNMENTS

RESULT 1

P80527	zea mays (m
P21794	rattus norv
P56650	actinoplane
P33236	escherichia
P14529	trichinella
P14470	ovis aries
P80489	methanosarc
P58689	radianthus
P35451	bos taurus
P30833	actinia ten
P30834	actinia ten
P82796	spinacia ol
P22581	serratia ma
P10371	citrobacter
P01373	periplaneta
P41495	sarcophaga
P36414	pseudomonas
P23210	herpes simp
P20104	enterococcu
P42984	leptinotars
P81675	pinus pinas
P80709	carcinus ma
P14595	tabanus atr
P13268	enterococcu
P58785	conus purpu
P13269	enterococcu
P04549	periplaneta
P81707	brassica na
P82618	periplaneta
P82929	bos taurus
P30096	homo sapien
P82678	chlamydomon
P81337	clostridium
P82661	panagrellus
P83320	penaeus mon
P43172	ascaris suu
P19345	macaca fusc
P29177	bos taurus
P19852	clypeaster
P42999	squalus aca
P82878	oryctolagus
P83380	lycopersico
P82926	bos taurus
P19095	mustelus ca
P17440	pichia jadi
P17441	pichia jadi
P40929	homo sapien
P31929	homo sapien
P31931	homo sapien
P30089	homo sapien
P30092	homo sapien
P30093	homo sapien
P29261	prunus sero
P81822	carcinus ma
P01017	bos taurus
P01018	gallus gall
P80474	capnocytoph
Q9prz1	oncorhynch
P83205	ovis aries
P83328	oncorhynch
P80332	oncorhynch
P38553	locusta mig
P18523	manduca sex
P01358	homo sapien
P04378	petromyzon
P80678	chelyosoma
P20367	oncorhynch

TEJJA_RANJA
ID TEJJA_RANJA STANDARD; PRT; 13 AA.
AC P83307;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporalin-1Ja.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8402;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RC MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RL skin of the Japanese brown frog Rana japonica.";
PEptides 23:419-425(2002).
CC -!- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1405; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13
13
SQ SEQUENCE 13 AA; 1407 MW; 3EF713EA610A2448 CRC64;
Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 LPLV 17
Db 2 LPLV 5

RESULT 2
PH3_PERAM
ID PH3_PERAM STANDARD; PRT; 17 AA.
AC P82696;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide hormone 3 (Pea-VEAacid 1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Abdominal perisymphathetic organs;
RC MEDLINE=20140865; PubMed=10676456;
RA Pradel R., Eckert M., Holman G.M.;
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
RT of insects.";
RL Ann. N.Y. Acad. Sci. 897:282-290(1999).
CC -!- FUNCTION: UNKNOWN.
CC -!- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.
KW Neuropeptide.
SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;
Query Match 22.2%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LTLT 5
Db 3 LTLT 6

RESULT 3
LPTR_BACST
ID LPTR_BACST STANDARD; PRT; 20 AA.
AC P05658;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tetracycline resistance leader peptide.
GN TETL.
OS Bacillus stearothermophilus,
OS Bacillus cereus, and
OS Staphylococcus hyicus.
OG Plasmid pTHT15, Plasmid pBC16, and Plasmid pSTEL.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422, 1396, 1284;
[1] _TaxID=1422, 1396, 1284;
RN SEQUENCE FROM N.A.
RP SPECIES=B.stearothermophilus; PLASMID=pTHT15;
RC MEDLINE=86031344; PubMed=2996983;
RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
RT "Nucleotide sequence of the tetracycline resistance gene of pTHT15, a
RT thermophilic Bacillus plasmid: comparison with staphylococcal Tcr
RT controls.";
RL Gene 37:131-138(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.cereus; PLASMID=pBC16;
RX MEDLINE=90221899; PubMed=2109312;
RA Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
RT "Nucleotide sequence of the tetracycline resistance gene of pBC16
RT from Bacillus cereus.";
RL Nucleic Acids Res. 18:1635-1635(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.hyicus; PLASMID=pSTEL;
RX MEDLINE=92321725; PubMed=1622166;
RA Schwarz S., Cardoso M., Wegener H.C.;
RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline
RT resistance determinant encoded by plasmid pSTEL from Staphylococcus
RT hyicus.";
RL Antimicrob. Agents Chemother. 36:580-588(1992).
CC -----
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CC -----
CC EMBL; D00006; BAA00004.1; -;
DR EMBL; M11036; AAA22850.1; -;
DR EMBL; X51366; CAA35750.1; -;
DR EMBL; X60828; CAA43219.1; -;
DR PIR; S09233; LFBSTU.
DR PIR; S23742; S23742.
KW Leader peptide; Antibiotic resistance; plasmid.
SQ SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA231CA1 CRC64;
Query Match 22.2%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTL 4
Db 17 SLTL 20

RESULT 4
ALL6_CYDPO
ID ALL6_CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 LPL 14
 DB 1 LPL 3
 RESULT 5
 ESL LACCA
 ID ESL LACCA STANDARD; PRT; 10 AA.
 AC P81758;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Putative esterase/lipase (EC 3.1.1.-) (Fragment).
 OS Lactobacillus casei
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1582;
 RN [1]
 RP SEQUENCE
 RC STRAIN=IFPL731;
 RA Lopez de Felipe F.;
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.
 KW Hydrolase; Serine esterase.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TDV 7
 DB 4 TDV 6
 RESULT 6
 NS1 MYCTU
 ID NS1 MYCTU STANDARD; PRT; 10 AA.
 AC P81135;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 1 (Fragment).
 OS Mycobacterium tuberculosis
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE
 RC STRAIN=H37RV;
 RA Prasad H.K., Annappurna P.S.;
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.
 CC -1- CAUTION: We are unable to find this protein in the translation of
 CC the genome of strain H37RV.
 FT NON TER 1
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PLV 17
 DB 4 PLV 6
 RESULT 7
 URE3 MORMO
 ID URE3 MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences."
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 VEK 9
 DB 8 VEK 10
 RESULT 8
 TIN4 HOPTI
 ID TIN4 HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tigerin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;

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RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 13 PLP 15
DB 7 PLP 9

RESULT 9
PK4_PERAM ID PK4_PERAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pea-PK-4) (YXPRU-amide).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
CC Blattidae; Periplaneta.
CC NCBI_TaxID=6978;
RN [1]
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1449 MW; FAYA3049FF42CAA1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 11 HLP 13
DB 2 HLP 4

RESULT 10
TIN2_HOPTI ID TIN2_HOPTI STANDARD; PRT; 12 AA.

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AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerinlin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
CC Hoplobatrachus.
CC NCBI_TaxID=103373;
RN [1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RP TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 13 PLP 15
DB 7 PLP 9

RESULT 11
TIN3_HOPTI ID TIN3_HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerinlin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
CC Hoplobatrachus.
CC NCBI_TaxID=103373;
RN [1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RP TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

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QY      13 PLP 15
      |||
Db      7 PLP 9

RESULT 12
TM2A METMA
ID      TW2A METMA      STANDARD;      PRT;      12 AA.
AC      PS0652;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE      (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE      methyltransferase 28 kDa subunit) (Fragment).
OS      Methanosarcina mazei (Methanosarcina frisia).
OS      Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC      Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX      NCBI_TaxID=2209;
RN      [1]
RP      SEQUENCE.
RC      STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX      MEDLINE=96370840; PubMed=8774736;
RA      Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT      "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT      coenzyme M methyltransferase from Methanosarcina mazei G01
RT      reconstituted in ether lipid liposomes.";
RL      Eur. J. Biochem. 239:857-864 (1996).
CC      -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC      METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC      TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC      TETRAHYDROMETHANOPTERIN.
CC      -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC      mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC      (methylthio)ethanesulfonate.
CC      -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW      Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT      NON TER 12
FT      SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

QY      8 EXL 10
      |||
Db      2 EXL 4

RESULT 13
ACT7 SOYBN
ID      ACT7 SOYBN      STANDARD;      PRT;      13 AA.
AC      P15987;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Actin 7 (Fragment).
GN      SACT7.
OS      Glycine max (Soybean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX      NCBI_TaxID=3847;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Wayne;
RX      MEDLINE=91346640; PubMed=2102831;
RA      Pearson L., Meagher R.B.;
RT      "Diverse soybean actin transcripts contain a large intron in the 5'
RT      untranslated leader: structural similarity to vertebrate muscle actin
RT      genes.";

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RL      Plant Mol. Biol. 14:513-526(1990).
CC      -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC      IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC      IN ALL EUKARYOTIC CELLS.
CC      -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC      IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC      CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC      -!- SIMILARITY: Belongs to the actin family.
CC      -----
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CC      -----
DR      EMBL; X17120; CAA34980.1; -.
DR      PIR; S15755; S15755.
DR      InterPro; IPR004001; Actin.
DR      InterPro; IPR004000; Actin-like.
DR      PROSITE; PS00406; ACTINS_1; PARTIAL.
DR      PROSITE; PS00432; ACTINS_2; PARTIAL.
DR      PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW      Structural protein; Multigene family.
FT      NON TER 13
FT      SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PLV 17
      |||
Db      9 PLV 11

RESULT 14
CRBL VESCR
ID      CRBL VESCR      STANDARD;      PRT;      13 AA.
AC      P01518;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Crabrolin.
OS      Vespa crabro (European hornet).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC      Vespidae; Vespinae; Vespa.
OX      NCBI_TaxID=7445;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RX      MEDLINE=84289390; PubMed=6206053;
RA      Argiolas A., Pisano J.J.;
RT      "Isolation and characterization of two new peptides, mastoparan C and
RT      crabrolin, from the venom of the European hornet, Vespa crabro.";
RL      J. Biol. Chem. 259:10106-10111 (1984).
RN      [2]
RP      SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
RX      MEDLINE=97419326; PubMed=9273892;
RA      Krishnakumari V., Nagaraj R.;
RT      "Antimicrobial and hemolytic activities of crabrolin, a 13-residue
RT      peptide from the venom of the European hornet, Vespa crabro, and its
RT      analogs.";
RL      J. Pept. Res. 50:88-93 (1997).
CC      -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC      of neutrophils. Has antimicrobial and hemolytic activity.
DR      PIR; A01781; JZVHP1.
KW      Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.
FT      MOD_RES 13
FT      SEQUENCE 13

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SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 |||
 DB 2 LPL 4

RESULT 15
 CRIC_RANES
 ID CRIC_RANES STANDARD; PRT; 13 AA.
 AC P31832;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Calreticulin (Major microsomal calcium-binding protein) (Fragment).
 OS Rana esculenta (Edible frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=91207333; PubMed=2018493;
 RA Treveso S., Zorzato F., Chiozzi P., Melandri P., Volpe P., Pozzan T.;
 RT "Frog brain expresses a 60 KDa Ca2+ binding protein similar to
 RT mammalian calreticulin.";
 RL Biochem. Biophys. Res. Commun. 175:444-450 (1991).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR InterPro: IPR001580; Calreticulin.
 DR PROSITE: PS00803; CALRETICULIN 1; PARTIAL.
 DR PROSITE: PS00804; CALRETICULIN 2; PARTIAL.
 DR PROSITE: PS00805; CALRETICULIN REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1510 MW; D0F62AD09EAEE339 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
 |||
 DB 2 PLV 4

RESULT 16
 FR12_PEA
 ID FR12_PEA STANDARD; PRT; 13 AA.
 AC P83445;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin 2, chloroplast (Fragment).
 OS Pisum sativum (Garden pea).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RC STRAIN=cv. Laxton's Progress; TISSUE=Leaf;
 RA Shingles R., McCarty R.E.;
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and

CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited.
 CC -!- SUBCELLULAR LOCATION: Chloroplast (inner envelope membrane), and
 CC other plastids.
 CC -!- TISSUE SPECIFICITY: Leaves.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
 CC 4.74, its MW is: 25.7 kDa.
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY.
 DR InterPro: IPR001519; Ferritin.
 DR PROSITE: PS00204; FERRITIN 2; PARTIAL.
 DR PROSITE: PS00540; FERRITIN 1; PARTIAL.
 DR PROSITE: PS0905; FERRITIN LIKE; PARTIAL.
 KW Iron storage; Iron; Metal-binding; Chloroplast.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1246 MW; 26C9DC25F334ADC7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 |||
 DB 8 TLT 10

RESULT 17
 HPB9_RANES
 ID HPB9_RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hemolytic protein B9 (Fragment).
 OS Rana esculenta (Edible frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Skin secretion;
 RX MEDLINE=90198965; PubMed=2317508;
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta.";
 RL Biochim. Biophys. Acta 1033:318-323 (1990).
 CC -!- FUNCTION: Shows hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR: S09019; S09019.
 KW Amphibian defense peptide; Amidation; Hemolysis.
 FT MOD_RES 13
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 |||
 DB 2 LPL 4

RESULT 18
 IDHP_RAT
 ID IDHP_RAT STANDARD; PRT; 13 AA.
 AC P56574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
 CC (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP) (ICD-

```

DE M) (Fragment).
GN IDH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY
CC PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE
CC DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
CC + NADPH.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.
CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
CC InterPro: IPR001804; IsoDh.
DR PROSITE; PS00470; IDH_IDH2; PARTIAL.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
KW Mitochondrion.
FT NON TER 13
FT SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
Db 7 VEK 9

RESULT 19
TEMA_RANTE
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56917;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin A.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13
FT SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
Db 7 VEK 9

RESULT 20
TEMA_RANTE
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13
FT SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
Db 2 LPL 4

RESULT 21
CRBL_VESOR
ID CRBL_VESOR STANDARD; PRT; 14 AA.
AC P17236;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histamine releasing peptide II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Miroshnikov A. I., Snezhkova L. G., Nazimov I. V., Reshetova O. I.,
RA Rozynov B. V., Gushchin I. S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet."
RL Bioorg. Khim. 7:1467-1477(1981).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
DR PIR; JN0390; JN0390.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 14
FT SEQUENCE 14 AA; 1524 MW; 22015B4A6CEDFD38 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 14;

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
Db 2 LPL 4

RESULT 22

ECDC LYMDI STANDARD; PRT; 14 AA.
AC P80940;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide C (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
gonadotropin isolated from brains of Lymantria dispar pupae."
RL Arch. Insect Biochem. Physiol. 36:37-50(1997)
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
OF LARVAE AND PUPAE.
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 9 PLP 11

RESULT 23

CYSK CLOPA STANDARD; PRT; 15 AA.
AC P81340;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulphydrylase) (O-acetylserine (Thiol)-lyase) (CSase) (CP 27) (Fragment).
GN CYSK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -!- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-cysteine +
acetate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Cysteine biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-
SYNTHASE FAMILY.
DR InterPro; IPR001216; Cys_synthase.

DR PROSITE; PS00901; CYS SYNTHASE; PARTIAL.
KW Lyase; Cysteine biosynthesis; Pyridoxal phosphate.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1625 MW; 019658289671A352 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
Db 10 PLV 12

RESULT 24

GTS ASADI STANDARD; PRT; 15 AA.
AC P83246;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST) (Fragment).
DE (Fragment).
OS Asaphis dichotoma.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Tellinoidea; Psammobiidae; Asaphis.
OX NCBI_TaxID=184428;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM ANALYSIS.
RC TISSUE=Intestine, and Liver;
RX MEDLINE=22135252; PubMed=12139969;
RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;
RT "Purification and characterization of a novel glutathione S-transferase from Asaphis dichotoma."
RL Arch. Biochem. Biophys. 403:202-208(2002).
CC -!- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-dinitrobenzene and etharynic acid.
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- SUBUNIT: Homodimer.
CC -!- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.
CC -!- MISCELLANEOUS: In A. dichotoma there are at least two isozymes of glutathione S-transferase.
CC -!- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene as the substrate.
CC -!- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme, respectively.

CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.
DR GO; GO:0004364; F:Glutathione transferase activity; NAS.
DR GO; GO:0006803; P:Glutathione conjugation reaction; NAS.
KW Transferase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB0B9 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KIH 11
Db 4 KIH 6

RESULT 25

ONCL ONCMY STANDARD; PRT; 15 AA.
AC P83287;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Oncorhynchus 1 (Fragment).


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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin;
RA Fernandes J.M.O., Smith V.J., Kemp G.D.;
RT "Purification and N-terminal sequencing of a 3 kDa antibacterial
RT peptide from skin secretions of rainbow trout.";
RL Submitted (MAY-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium P.citreus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003795; P:antimicrobial peptide activity; NAS.
DR GO: GO:0006805; P:xenobiotic metabolism; NAS.
KW Antibiotic.
FT UNSURE 4 4 OR G.
FT UNSURE 9 9 OR T.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1601 MW; 43C25028DBC12B7C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVE 8
Db 9 DVE 11

RESULT 26
UC29 MAIZE STANDARD; PRT; 15 AA.
ID UC29 MAIZE
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 37.6 kDa.
DR Maize-2DPAGE; P80635; COLEOPTILE.
DR MaizeDB; 123960; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
Db 8 PLV 10

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RESULT 27
ARCD PSEPU STANDARD; PRT; 16 AA.
ID ARCD_PSEPU
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine/ornithine antiporter (Fragment).
GN ARCD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGinine
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGinine DEIMINASE PATHWAY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMEASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U07185; AAA16963.1; -.
KW Transport; Antiport; Amino-acid transport; Transmembrane;
KW Inner membrane.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4
Db 14 LTL 16

RESULT 28
FIBA MELME STANDARD; PRT; 16 AA.
ID FIBA MELME
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Meles.
OX NCBI_TaxID=9662;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma. FIBRINOPEPTIDE A.
KW PEPTIDE 1 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7
DB 1 TDV 3

RESULT 29
ID TBP4_PIG STANDARD; PRT; 16 AA.
AC P24954;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Echerton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -|- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Contains 1 IGFBP domain.
CC PIR; JH0517; JH0517. Contains 1 thyroglobulin type-I domain.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR InterPro; IPR000716; Thyroglobulin_1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
DB 12 EKL 14

RESULT 30
ID MMFX_SOLTU STANDARD; PRT; 16 AA.
AC P80501;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Fragment).
OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RC TISSUE=Tuber;
RX MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Kruff V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
RT of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Mitochondrion.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
DB 9 VEK 11

RESULT 31
ID ACT6_SOYBN STANDARD; PRT; 17 AA.
AC P15986;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 6 (Fragment).
GN SACS.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -|- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -|- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -|- SIMILARITY: Belongs to the actin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17119; CAA34979.1; -
DR PIR; S15754; S15754. Actin.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin-like.
DR Pfam; PF00022; actin; 1.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.

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DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+03; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
Db 9 PLV 11

RESULT 32
EFG_THEAQ STANDARD; PRT; 17 AA.
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN FUS1 OR FUS.
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RC MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,
RA Erdmann V.;
RT "Sequence of the tufA gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
CC EMBL; X66322; CAA46997.1; -.
CC HAMAP; MF_00054; -.
CC InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFAC_TGTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2094 MW; EA461E1F05F96E1D CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+03; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
Db 11 EKL 13

RESULT 33
RL23_HALCU STANDARD; PRT; 18 AA.
ID RL23_HALCU

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AC P05975;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S ribosomal protein L23P (HL31) (Fragment).
GN RPL23P.
OS Halobacterium cutirubrum.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP SEQUENCE.
RX MEDLINE=84282108; PubMed=6467081;
RA Matheson A.T., Yaguchi M., Christensen P., Rollin C.F., Hasnain S.;
RT "Purification, properties, and N-terminal amino acid sequence of
RT certain 50S ribosomal subunit proteins from the archaeobacterium
RT Halobacterium cutirubrum.";
RL Can. J. Biochem. Cell Biol. 62:426-433(1984).
CC -1- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S rRNA
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001014; Ribosomal L23.
DR PROSITE; PS00050; RIBOSOMAL L23; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2041 MW; 3E61DC53F9B4DD4C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+03; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
Db 7 PLV 9

RESULT 34
UC21_MAIZE STANDARD; PRT; 18 AA.
ID UC21_MAIZE
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
CC -1- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
DR Maize-2DPAGE; P80627; -.
DR MaizeDB; 123953; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038B8BA CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+03; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
Db 7 PLV 9

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Db 15 VEK 17

RESULT 35

HI70 RAT STANDARD; PRT; 19 AA.

AC P21794;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last annotation update)

DE Hormone-induced protein 70 kDa (HIP-70) (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP MEDLINE=90208308; PubMed=2181662;

RA Mobbs C.V., Fink G., Pfaff D.W.;

RT "HIP-70: a protein induced by estrogen in the brain and LH-RH in the pituitary.";

RL Science 247:1477-1479(1990).

CC -!- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH IN PITUITARY.

FT NON TER 19 19

SQ SEQUENCE 19 AA; 2113 MW; F793A98720B68E3C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LTD 6

Db 5 LTD 7

RESULT 36

LANA ACTLG STANDARD; PRT; 19 AA.

AC P56650;

DT 15-JUL-1999 (Rel. 38, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Lantibiotic actagardine (Gardimycin).

OS Actinoplanes liguariae.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Micromonosporineae; Micromonosporaceae; Actinoplanes.

OX NCBI_TaxID=69484;

RN [1]

RP PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.

RX MEDLINE=91008698; PubMed=2211371;

RA Kettenring J.K., Malabarba A., Vekey K., Cavalleri B.;

RT "Sequence determination of actagardine, a novel lantibiotic, by homonuclear 2D NMR spectroscopy.";

RL J. Antibiot. 43:1082-1088(1990).

RN [2]

RP SEQUENCE AND STRUCTURE BY NMR.

RX MEDLINE=95255286; PubMed=7737178;

RA Zimmermann N., Metzger J.W., Jung G.;

RT "The tetracyclic lantibiotic actagardine. 1H-NMR and 13C-NMR assignments and revised primary structure.";

RL Eur. J. Biochem. 228:786-797(1995).

RN [3]

RP STRUCTURE BY NMR.

RX MEDLINE=97363218; PubMed=9219543;

RA Zimmermann N., Jung G.;

RT "The three-dimensional solution structure of the lantibiotic murein-biosynthesis-inhibitor actagardine determined by NMR.";

RL Eur. J. Biochem. 246:809-819(1997).

CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA. HAS GOOD ANTISTREPTOCOCCAL ACTIVITY.

CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. The 14-19 beta-methylanthionine thioether bond is oxidized to a sulfoxide. This is followed by membrane translocation and cleavage of the modified precursor.

CC PIR; A58700; A58700.

DR PDB; 1AJ1; 15-OCT-97.

KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Oxidation;

3D-structure; Thioether bond.

FT CROSSLNK 1 6 Lanthionine (Ser-Cys).

FT CROSSLNK 7 12 Beta-methylanthionine (Thr-Cys).

FT CROSSLNK 9 17 Beta-methylanthionine (Thr-Cys).

FT CROSSLNK 14 19 Beta-methylanthionine sulfoxide (Cys-Thr).

SQ SEQUENCE 19 AA; 1946 MW; 5C138C7CEB8765B3 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TLT 5

Db 7 TLT 9

RESULT 37

LPGE_ECOLI STANDARD; PRT; 19 AA.

ID LPGE_ECOLI

AC P33236;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Gef leader peptide.

GN GEFL OR B0018.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92048481; PubMed=1943701;

RA Poulsen L.K., Refn A., Molin S., Andersson P.;

RT "The gef gene from Escherichia coli is regulated at the level of translation.";

RL Mol. Microbiol. 5:1639-1648(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=K12 / MG1655;

RC MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

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CC -----

DR EMBL; AB000112; AAC73129.1; ALT_TERM.

DR EcoGene; EGI2074; gefl.

KW Leader peptide; Complete proteome.

SQ SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LTD 6

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Db      |||
        9 LTD 11

RESULT 38
MIFH_TRISP
ID _MIFH_TRISP STANDARD; PRT; 19 AA.
AC P81529;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-dopachrome-methyl ester tautomerase (Macrophage migration inhibitory
DE factor homolog) (Fragment).
OS Trichinella spiralis (Trichina worm).
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
OC Trichinellidae; Trichinella.
OX NCBI_TaxID=6334;
RN [1]
RP SEQUENCE.
RX MEDLINE=99013685; PubMed=9794786;
RA Pennock J.L., Behnke J.M., Bickie Q.D., Devaney E., Grencis R.K.,
RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
RT "rapid purification and characterization of L-dopamine-methyl-ester
RT tautomerase (macrophage migration inhibitory factor) from Trichinella
RT spiralis, Trichuris muris and Brugia pahangi.";
RL Biochem. J. 335:495-498(1998).
CC -!- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
CC -!- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR InterPro; IP001398; MIF.
DR PROSITE; PS01158; MIF; PARTIAL.
KW Cytokine.
FT NON TER 19
SQ SEQUENCE 19 AA; 2106 MW; F7CAA05F112A628D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7
    |||
    12 TDV 14

Db

RESULT 39
FIBB_SHEEP
ID _FIBB_SHEEP STANDARD; PRT; 20 AA.
AC P14470;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Ovis aries (Sheep); and
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR InterPro; IP0002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT MOD RES 5 5 SULFATION.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
    |||
    15 LPL 17

Db

RESULT 40
FRHA_METEA
ID _FRHA_METEA STANDARD; PRT; 20 AA.
AC P80489;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coenzyme F420 hydrogenase alpha subunit [EC 1.12.98.1] (8-hydroxy-5-
DE deazaflavin-reducing hydrogenase alpha subunit) (FRH) (Fragment).
GN FRHA.
OS Methanosarcina barkeri.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2208;
RN [1]
RP SEQUENCE.
RC STRAIN=Fusaro / DSM 804;
RX MEDLINE=96085134; PubMed=8521835;
RA Michel R., Massanz C., Kostka S., Richter M., Fiebig K.;
RT "Biochemical characterization of the 8-hydroxy-5-deazaflavin-reactive
RT hydrogenase from Methanosarcina barkeri Fusaro.";
RL Eur. J. Biochem. 233:727-735(1995)
CC -!- FUNCTION: REDUCES THE PHYSIOLOGICAL LOW-POTENTIAL TWO-ELECTRON
CC ACCEPTOR COENZYME F420, AND THE ARTIFICIAL ONE-ELECTRON ACCEPTOR
CC METHYLVIOLIGEN.
CC -!- CATALYTIC ACTIVITY: H(2) + coenzyme F420 = reduced coenzyme F420.
CC -!- COFACTOR: FRH CONTAINS NICKEL, IRON-SULFUR, AND FAD COFACTORS.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS AND A
CC GAMMA CHAIN.
CC -!- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
CC SUBUNIT FAMILY.
CC PIR; S63483; S63483.
DR InterPro; IP001501; Ni hdl.
DR PROSITE; PS00507; NI_HGENASE_L1; PARTIAL.
DR PROSITE; PS00508; NI_HGENASE_L2; PARTIAL.
KW Oxidoreductase; Metal-binding; Nickel; FAD.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2233 MW; 0D6597417D776D03 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
    |||
    18 LTL 20

Db

RESULT 41
HET1_RADMG
ID _HET1_RADMG STANDARD; PRT; 20 AA.
AC P58689;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Cytolysin I (Hmg I) (Magnificolysin I) (Fragment).
OS Radanthus magnifica (Magnificent sea anemone) (Heteractis magnifica).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Stichodactylidae; Heteractis.
OX NCBI_TaxID=38281;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RX MEDLINE=94196594; PubMed=8146870;
RA Khoo K.S., Kam W.K., Khoo H.E., Gopalakrishnakone P., Chung M.C.;
RT "Purification and partial characterization of two cytolysins from a
RT tropical sea anemone, Heteractis magnifica.";
RL Toxicon 31:1567-1579(1993).
CC -1- FUNCTION: Has both cytolytic and hemolytic activity. Pore forming
CC protein.
CC -1- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -1- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2003 MW; ED9ABD98AC7C4EBC CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLT 3
Db 11 SLT 13
RESULT 42
MI17_BOVIN
ID MI17_BOVIN STANDARD; PRT; 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Sorensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the protease peptone fraction of bovine milk.";
RL J. Dairy Res. 60:199-197(1993).
CC -1- PFM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 LPL 14
Db 12 LPL 14
RESULT 43
TENA_ACTTE
ID TENA_ACTTE STANDARD; PRT; 20 AA.
AC P30833;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tenebrosin A (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
RX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;
RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa.";
RL Toxicon 28:29-41(1990).
CC -1- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -1- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -1- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; A34016; A34016.
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1974 MW; FA32AC8BDAFF5FA CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TLT 5
Db 13 TLT 15
RESULT 44
TENB_ACTTE
ID TENB_ACTTE STANDARD; PRT; 20 AA.
AC P30834;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin B (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
RX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;
RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa.";
RL Toxicon 28:29-41(1990).
CC -1- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -1- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -1- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; B34016; B34016.
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TLT 5
Db 13 TLT 15
RESULT 45
TL22_SPIOL

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ID TL22_SPIOI STANDARD; PRT; 20 AA.
AC P82796;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 22 kDa protein (P22) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RA Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
RL Submitted (SEP-2000) to the SWISS-PROT data bank.
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON TER 20
SQ SEQUENCE 20 AA; 2409 MW; 78F5B50699BEB620 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3
Db 17 SLT 19

RESULT 46
YPRB_SERMA STANDARD; PRT; 20 AA.
AC P22581;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in prob 5'region (Fragment).
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sr41;
RC MEDLINE=91237315; PubMed=1851803;
RX Omori K., Suzuki S., Inai Y., Komatsubara S.;
RA "Analysis of the Serratia marcescens proBA operon and feedback
RT control of proline biosynthesis."
RL J. Gen. Microbiol. 137:509-517(1991).
CC -----
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CC -----
DR EMBL; D90351; BAAL4363.1; -
DR EMBL; X53086; CAA37253.1; -
DR FIR; C49753; C49753.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2248 MW; 4DD7777735276674 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EXL 10
Db 13 EXL 15

RESULT 47
BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-peilargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RA Shiuan D., Campbell A.;
RL "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
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CC -----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TD 6
Db 3 TD 4

RESULT 48
PRCT_PERAM STANDARD; PRT; 5 AA.
ID PRCT_PERAM
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;

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PN RP SEQUENCE.
PC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256 (1975).
RN [2]
RP BIOLOGICAL SOURCE.
PC SPECIES=P.americana;
RX MEDLINE=8125865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569 (1981).
RN [3]
RP SEQUENCE.
PC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211 (1990).
RN [4]
RP SEQUENCE.
PC SPECIES=C.maenas; PubMed=2872661;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72 (1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PTR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LP 13
DB 3 LP 4

RESULT 49
TMOF SARBUBU
ID TMOF SARBUBU STANDARD; PRT; 6 AA.
AC P41455;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
PC TISSUE=Ovary.
RX MEDLINE=94211930; PubMed=8159807;
RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic
factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
(Sarcophaga) bullata.";

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RL Regul. Pept. 50:61-72 (1994).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM AFTER A BLOOD MEAL.
KW Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LP 11
DB 5 LP 6

RESULT 50
TREP_PSEPU
ID TREP_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TrpBA operon transcriptional activator (Fragment).
GN TREP.
OS Pseudomonas putida.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C1S;
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
putida.";
RL Biochimie 71:521-531 (1989).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRAP OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC -----
DR EMBL; X13299; CAA31660.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LP 13
DB 5 LP 6

RESULT 51

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VP19 HSV1K
 ID VP19_HSV1K STANDARD; PRT; 6 AA.
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN UL38.
 OS Herpes simplex virus (type 1 / strain KOS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
 CC
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 CC
 CC EMBL; M57646; AAA45830.1; -
 DR Capsid assembly; Coat protein; DNA-binding.
 KW NON_TER
 FT 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 PL 14
 Db 5 PL 6
 RESULT 52
 CCF1_ENTFA STANDARD; PRT; 7 AA.
 AC P20104;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone cCF10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89008313; PubMed=3139658;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunny G.M., Suzuki A.;
 RT "Structure of cCF10, a peptide sex pheromone which induces
 conjugative transfer of the Streptococcus faecalis tetracycline
 resistance plasmid, pCF10.";
 RL J. Biol. Chem. 263:14574-14578(1988).
 CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 HEMOLYSIN PLASMID PCF10.
 CC PIR: A30812; A30812.
 DR Pheromone.
 KW PHEROMONE
 FT 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
 SQ SEQUENCE

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 TL 4
 Db 3 TL 4
 RESULT 53
 MNP1_LEPDE STANDARD; PRT; 7 AA.
 ID MNP1_LEPDE
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropptide 1 (Led-MNP-1).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 a novel myotropic neuropptide in the Colorado potato beetle,
 Leptinotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 OVIDUCT.
 CC Neuropeptide; Amidation.
 KW MOD_RES
 FT 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 PL 14
 Db 5 PL 6
 RESULT 54
 UN06_PINPS STANDARD; PRT; 7 AA.
 ID UN06_PINPS
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 CC NON_TER
 FT 1
 SQ SEQUENCE 7 AA; 7
 NON_TER

SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LP 13
Db 5 LP 6

RESULT 55
ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]

RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
PT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32 (1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
6.8, ITS MW IS: 46 kDa.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro: IPR004001; Actin-like.
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005A52CAAB3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DV 7
Db 3 DV 4

RESULT 56
AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor 1) (DCC 1).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;

RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
hypotrehalosemic activity isolated from the corpora cardiaca of horse
flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LT 3
Db 2 LT 3

RESULT 57
CAD1_ENTFA STANDARD; PRT; 8 AA.
AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]

RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sakakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CAD1, that
induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100 (1984).
CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2
Db 3 SL 4

RESULT 58
COW2_CONFU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

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OC Neogastropoda; Conoidea; Conidae; Conus.
ON NCBI_TaxID=41690;
RX SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LP 13
Db 5 LP 6

RESULT 59
CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
ON NCBI_TaxID=1351;
RX SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sakakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIIN PLASMID PPDL.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LV 17
Db 2 LV 3

RESULT 60
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
DE (Pep-CH-II) (Lep-CC-II) (Hypertrehalosemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
ON NCBI_TaxID=6978, 7539, 6976;
RX SEQUENCE.
RX SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RP SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RX SCARBOROUGH R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RP SPECIES=L.declineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RX GAEDE G., Keilner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RX GAEDE G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LT 3
Db 2 LT 3

RESULT 61
PLP_BRANA
ID PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).

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OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
[1]
RN SEQUENCE.
RP STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
CC SPECIFIC PLASTIDIAL LIPID ORGANELLE.
CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHEIRS.
FT NON_TER 8
FT SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DV 7
DB 3 DV 4

RESULT 62
PPK3 PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pyrokinin-3 (Pea-PK-3) (FXPRK-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RN TISSUE SPECIFICITY.
RP MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8
FT AMIDATION.
FT SEQUENCE 8 AA; 997 MW; 0B3417749D772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LV 17
DB 1 LV 2

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RESULT 63
RT34_BOVIN STANDARD; PRT; 8 AA.
AC P82929;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
GN MRPS34.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 8
FT SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LT 3
DB 5 LT 6

RESULT 64
UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RP TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
CC SWISS-2DPAGE; P30096; HUMAN.
DR NON_TER 1
DR NON_TER 5
FT VARIANT 5 5 F -> P
FT /FTID=VAR_000004.
FT NON_TER 8
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LT 3
||
Db 3 LT 4

RESULT 65

ALC_CHLRE STANDARD; PRT; 9 AA.
AC P82678;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Allantoicase (EC 3.5.3.4) (Allantoate amidinohydrolase) (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RC STRAIN=6145C;
RX MEDLINE=20318328; PubMed=10860551;
RA Piedras P., Munoz A., Aguilar M., Pineda M.;
RT "Allantoate amidinohydrolase (Allantoicase) from Chlamydomonas reinhardtii: its purification and catalytic and molecular characterization."
RL Arch. Biochem. Biophys. 378:340-348(2000).
CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-ureidoglycolate and (+)-ureidoglycolate to glyoxylate.
CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O = (-)-ureidoglycolate + urea.
CC -!- PATHWAY: Degradation of allantoate (purine catabolism); second step.
CC -!- SUBUNIT: Homohexamer.
CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with allantoate and ureidoglycolate, respectively.
CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.
KW Hydrolyase; Purine metabolism.
FT UNSURE 5 5 OR Y.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 943 MW; D934ADD9D6D871F2 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TL 4
||
Db 8 TL 9

RESULT 66

BUK_CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=96299918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetokinase family.

DR HAMAP; MF 00542; -; 1
DR InterPro; IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KL 10
||
Db 3 KL 4

RESULT 67

FAR5_PANRE STANDARD; PRT; 9 AA.
AC P82661;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF5 (AMRNALVRP-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G., Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRFamide-related peptides (FarPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
CC Neuropeptide; Amidation.
KW MOD RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LV 17
||
Db 6 LV 7

RESULT 68

FAR5_PENMO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP5 (SMPSLRIRP-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

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RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivithangkul P., Sithigorngul W., Petson A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2
DB 4 SL 5

RESULT 69
FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6255;
RN [1]

SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PL 14
DB 6 PL 7

RESULT 70
FIBB MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]

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RP SEQUENCE.
RA MEDLINE=85289140; PubMed=3928610;
RX Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735B1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2
DB 4 SL 5

RESULT 71
MGMT BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

SEQUENCE.
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE IS
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON TER 1 1
FT ACT SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

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Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LT 3
        |||
Db      6 LT 7.

RESULT 72
MOSH CLYJA      STANDARD;      PRT;      9 AA.
AC P19852;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sperm-activating peptide SAP-b ([His6]-mosact).
OS Clypeaster japonicus (Sand dollar). Eleutherozoa; Echinozoa;
OC Eukaryota; Metazoa; Echinodermata;
OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K.I., Kajiuura H., Nomura K.,
RT Yamaguchi M.;
RT "Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
RN [2]
RP BROMINATION OF HIS-6.
RX MEDLINE=91167743; PubMed=2076468;
RA Takao T., Yoshino K., Suzuki N., Shimonishi Y.;
RT "Analysis of post-translational modifications of proteins by accurate
RT mass measurement in fast atom bombardment mass spectrometry.";
RL Biomed. Environ. Mass Spectrom. 19:705-712(1990).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR; JN0026; JN0026.
KW Bromination.
FT MOD RES      6      6      BROMINATION (PARTIAL).
SQ SEQUENCE      9 AA; 914 MW; 93245721EDC5B4B5 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 HL 12
        |||
Db      6 HL 7

RESULT 73
OXYA_SQUAC      STANDARD;      PRT;      9 AA.
AC P42959;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartogocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083037;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]

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RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
KW Hormone; Amidation.
FT DISULFID      1      6      AMIDATION.
FT MOD RES      9      9
SQ SEQUENCE      9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 PL 14
        |||
Db      7 PL 8

RESULT 74
OXYT_RABIT      STANDARD;      PRT;      9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Ocytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus),
OS Balaenoptera physalus (Finback whale) (Common rorqual), and
OS Tachyglus aculeatus aculeatus (Australian echidna), and
OS Oryctolagus colliei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophysial hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H.amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B.physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A.aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophysial hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RC SPECIES=H.colliei;

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RX MEDLINE=7008110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurophysiophysial hormone in the holocephalian
RT elasmobranch fish, *Hydrolagus collei*.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR003981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PL 14
DB 7 PL 8

RESULT 75
PPH1_LYCES
ID PPH1_LYCES STANDARD; PRT; 9 AA.
AC P83380;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LesAP1 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
[1]
RN SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (*Lycopersicon
RT esculentum*) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In *L. esculentum* there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1005 MW; 3F17C04B5042CAA8 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DV 7
DB 11

Db 3 DV 4

Search completed: November 25, 2003, 19:28:22
Job time : 6.45515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDEKHLPLPLVQ 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	27.8	17	4	Q96P96
2	5	27.8	19	4	Q9UC6
3	4	22.2	8	8	P93963
4	4	22.2	8	8	P92384
5	4	22.2	8	8	P93973
6	4	22.2	8	8	P93973
7	4	22.2	8	8	P93957
8	4	22.2	8	8	P92222
9	4	22.2	8	8	P92388
10	4	22.2	8	8	P92441
11	4	22.2	8	8	P92404
12	4	22.2	8	8	P93961
13	4	22.2	8	8	P93970
14	4	22.2	8	8	P93955
15	4	22.2	8	8	P93965
16	4	22.2	8	8	P92394

17	4	22.2	8	8	P92382	P92382 hordeum bra
18	4	22.2	8	8	P93966	P93966 aegilops sp
19	4	22.2	8	8	P92227	P92227 crithopsis
20	4	22.2	8	8	P92373	P92373 haynaldia v
21	4	22.2	8	8	P92211	P92211 agropyron c
22	4	22.2	8	8	P92428	P92428 peridictyon
23	4	22.2	8	8	P93959	P93959 hordeum ere
24	4	22.2	8	8	P92219	P92219 australopyr
25	4	22.2	8	8	P93985	P93985 aegilops co
26	4	22.2	8	8	P92443	P92443 taeniatheru
27	4	22.2	8	8	P92391	P92391 heteranthe
28	4	22.2	8	8	P93981	P93981 crithodum
29	4	22.2	8	8	P93992	P93992 pseudoroegn
30	4	22.2	8	8	P92426	P92426 aegilops ta
31	4	22.2	8	8	P92431	P92431 psathyrosta
32	4	22.2	8	8	P92422	P92422 psathyrosta
33	4	22.2	9	4	Q16220	Q16220 homo sapien
34	4	22.2	11	4	Q9UEL0	Q9UEL0 homo sapien
35	4	22.2	13	12	Q9WMG5	Q9WMG5 sigma virus
36	4	22.2	15	8	Q9T2K8	Q9T2K8 spinacia ol
37	4	22.2	15	12	Q66174	Q66174 human coron
38	4	22.2	16	4	Q9NMZ2	Q9NMZ2 homo sapien
39	4	22.2	16	4	O00497	O00497 homo sapien
40	4	22.2	17	8	Q9TDQ2	Q9TDQ2 macaca sylv
41	4	22.2	17	8	Q9T379	Q9T379 macaca sylv
42	4	22.2	18	4	Q16244	Q16244 homo sapien
43	4	22.2	18	6	Q8WN06	Q8WN06 bos taurus
44	4	22.2	19	8	Q31687	Q31687 artemia par
45	4	22.2	19	15	Q905F5	Q905F5 human immun
46	4	22.2	20	2	Q9R9A5	Q9R9A5 nitrospir
47	4	22.2	20	2	Q9R987	Q9R987 nitrospir
48	4	22.2	20	4	Q96T45	Q96T45 homo sapien
49	4	22.2	20	10	Q9S900	Q9S900 vigna sinen
50	4	22.2	20	11	Q9QW2	Q9QW2 rattus sp.
51	4	22.2	20	15	Q85636	Q85636 moloney mur
52	3	16.7	5	13	P83308	P83308 gallus gall
53	3	16.7	7	10	P93233	P93233 lycopersico
54	3	16.7	7	12	Q66205	Q66205 transmissio
55	3	16.7	7	13	O42564	O42564 fugu rubrip
56	3	16.7	8	2	Q9R9C2	Q9R9C2 borrelia bu
57	3	16.7	8	6	Q9XSY1	Q9XSY1 canis fami
58	3	16.7	8	6	Q9SM23	Q9SM23 sus scrofa
59	3	16.7	8	9	Q8SBJ0	Q8SBJ0 bacterioph
60	3	16.7	8	9	Q8H9K1	Q8H9K1 bacterioph
61	3	16.7	9	2	Q31363	Q31363 borrelia ga
62	3	16.7	9	2	P83157	P83157 anabaena sp
63	3	16.7	9	4	Q16605	Q16605 homo sapien
64	3	16.7	9	5	Q9TW0	Q9TW0 anthopleura
65	3	16.7	9	8	Q94VD8	Q94VD8 varanus nil
66	3	16.7	9	8	Q94VC6	Q94VC6 varanus pil
67	3	16.7	9	8	Q94V61	Q94V61 varanus mer
68	3	16.7	9	10	Q9S8J8	Q9S8J8 oryza sativ
69	3	16.7	9	11	Q61723	Q61723 mus musculu
70	3	16.7	9	15	Q85723	Q85723 simian sarc
71	3	16.7	9	16	Q935G1	Q935G1 salmone
72	3	16.7	10	2	Q9XBH3	Q9XBH3 bacillus ce
73	3	16.7	10	2	Q9R5T2	Q9R5T2 acetobacter
74	3	16.7	10	2	P83154	P83154 anabaena sp
75	3	16.7	10	8	Q9TG86	Q9TG86 diploglossu
76	3	16.7	10	8	Q94V97	Q94V97 varanus spe
77	3	16.7	10	8	Q94VDS	Q94VDS varanus oli
78	3	16.7	10	8	Q94VC9	Q94VC9 varanus pan
79	3	16.7	10	8	Q94VF0	Q94VF0 varanus kin
80	3	16.7	10	8	P92771	P92771 xenosaurus
81	3	16.7	10	8	Q94V85	Q94V85 varanus var
82	3	16.7	10	8	Q94PD8	Q94PD8 varanus sca
83	3	16.7	10	8	Q9TG38	Q9TG38 ophisauru
84	3	16.7	10	8	P92576	P92576 bipes bipor
85	3	16.7	10	8	Q9TG35	Q9TG35 ophisauru
86	3	16.7	10	8	Q94VD2	Q94VD2 varanus pan
87	3	16.7	10	10	Q9F693	Q9F693 silene pent
88	3	16.7	10	11	Q9QVF7	Q9QVF7 rattus sp.
89	3	16.7	10	11	Q9ESU5	Q9ESU5 mus musculu

Q88082 chimpanzee
Q47606 escherichia
Q9K332 staphylococ
Q47569 escherichia
Q8hym4 felis silve
Q8tqb3 homo sapien
Q84v94 varanus sto
Q94v98 varanus gou
Q9G616 ceratophora
Q9G610 lyriocephal
Q9G5v3 phrynoceph

ALIGNMENTS

RESULT 1
Q96P96 PRELIMINARY; PRT; 17 AA.
ID Q96P96;
AC Q96P96;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHP2-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401217; AAL02173.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1948 MW; AB699919BD70BCEFF CRC64;

Query Match 27.8%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
Db 13 LPLPL 17

RESULT 2
Q9UCK6 PRELIMINARY; PRT; 19 AA.
ID Q9UCK6;
AC Q9UCK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Aspartylglucosaminidase beta 1 subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93111925; PubMed=1281977;
RA Rip J.W., Coulter-Mackie M.B., Rupa C.A., Gordon B.A.;
RT "Purification and structure of human liver aspartylglucosaminidase."
RL Biochem. J. 288:1005-1010(1992).
DR HSP; P20933; IAPY.
SQ SEQUENCE 19 AA; 2127 MW; BC2F148525610300 CRC64;

Query Match 27.8%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17

Db 2 PLPLV 6

RESULT 3
P93963 PRELIMINARY; PRT; 8 AA.
ID P93963;
AC P93963;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Peathyrostachys stoloniformis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=58873;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9182; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77754; CAB01341.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 4
P92384 PRELIMINARY; PRT; 8 AA.
ID P92384;
AC P92384;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum murinum subsp. glaucum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=98113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H801; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77762; CAB01365.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
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Db 2 SLTL 5

RESULT 5

P93973 PRELIMINARY; PRT; 8 AA.
AC P93973;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Eremopyrum distans.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Eremopyrum.
OX NCBI_TaxID=58936;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H5552; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77745; CAB01314.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
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Db 2 SLTL 5

RESULT 6

P92215 PRELIMINARY; PRT; 8 AA.
AC P92215;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Amblyopyrum muticum.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H5572; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77756; CAB01347.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
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Db 2 SLTL 5

RESULT 7

P93957 PRELIMINARY; PRT; 8 AA.
AC P93957;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Festucopsis serpentina.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Festucopsis.
OX NCBI_TaxID=72456;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H6511; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z79501; CAB01777.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
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Db 2 SLTL 5

RESULT 8

P92222 PRELIMINARY; PRT; 8 AA.
AC P92222;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Bromus inermis (Smooth brome grass).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Bromaeae; Bromus.
OX NCBI_TaxID=15371;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01356.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Wed Nov 26 09:07:12 2003

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
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Db 2 SLTL 5

RESULT 9

ID P92388 PRELIMINARY; PRT; 8 AA.
AC P92388;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01323.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
|||
Db 2 SLTL 5

RESULT 10

ID P92441 PRELIMINARY; PRT; 8 AA.
AC P92441;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77769; CAB01386.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 SLTL 4
|||
Db 2 SLTL 5

RESULT 11

ID P92404 PRELIMINARY; PRT; 8 AA.
AC P92404;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Lophopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6692; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01308.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
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Db 2 SLTL 5

RESULT 12

ID P93961 PRELIMINARY; PRT; 8 AA.
AC P93961;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Psathyrostachys rupestris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=58938;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6703; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77755; CAB01344.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

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Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
   ||||
Db 2 SLTL 5

RESULT 13
P93970 ID P93970 PRELIMINARY; PRT; 8 AA.
AC P93970;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Eremopyrum triticeum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Eremopyrum.
OC NCBI_TaxID=58937;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=H5553; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RX "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77746; CAB01315.1; -.
DR KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
   ||||
Db 2 SLTL 5

RESULT 14
P93955 ID P93955 PRELIMINARY; PRT; 8 AA.
AC P93955;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Festucopsis festuoides.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Festucopsis.
OC NCBI_TaxID=72455;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=H6731; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RX "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77770; CAB01389.1; -.
DR KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
   ||||
Db 2 SLTL 5

RESULT 15
P93965 ID P93965 PRELIMINARY; PRT; 8 AA.
AC P93965;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Secale strictum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OC NCBI_TaxID=58866;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=H4342; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RX "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77765; CAB01373.1; -.
DR KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
   ||||
Db 2 SLTL 5

RESULT 16
P92394 ID P92394 PRELIMINARY; PRT; 8 AA.
AC P92394;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=H3139; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RX "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77764; CAB01371.1; -.
DR KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

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[illegible]

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KW Chloroplast. 1 1
FT NON_TER 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 21
P92211 ID P92211 PRELIMINARY; PRT; 8 AA.
AC P92211;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01392.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 22
P92428 ID P92428 PRELIMINARY; PRT; 8 AA.
AC P92428;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77749; CAB01326.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 23
P93959 ID P93959 PRELIMINARY; PRT; 8 AA.
AC P93959;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum erectifolium.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=58926;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H1150; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z79500; CAB01776.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 24
P92219 ID P92219 PRELIMINARY; PRT; 8 AA.
AC P92219;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL sequence data.";
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RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77767; CAB01380.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 860 MW; BIC7287731A735AA CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 25
P93985 PRELIMINARY; PRT; 8 AA.
ID P93985;
AC P93985;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops comosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=4485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6673; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77742; CAB01305.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 26
P92443 PRELIMINARY; PRT; 8 AA.
ID P92443;
AC P92443;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Taeniatherum caput-medusae (Medusahead).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01359.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 27
P92391 PRELIMINARY; PRT; 8 AA.
ID P92391;
AC P92391;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Heteranthellium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Heteranthellium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01329.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 28
P93981 PRELIMINARY; PRT; 8 AA.
ID P93981;
AC P93981;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Crithodium monococcum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Crithodium.
OX NCBI_TaxID=72428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4547; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;

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RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."; Evol. 7:217-230 (1997).
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).
 DR EMBL; Z77757; CAB01350.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 Db 2 SLTL 5

RESULT 29

P93992 ID P93992 PRELIMINARY; PRT; 8 AA.
 AC P93992;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Australopyrum velutinum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Australopyrum.
 OX NCBI_TaxID=58935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6724; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G.; Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."; Evol. 7:217-230 (1997).
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).
 DR EMBL; Z77768; CAB01383.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 Db 2 SLTL 5

RESULT 30

P92426 ID P92426 PRELIMINARY; PRT; 8 AA.
 AC P92426;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Pseudoroegneria.
 OX NCBI_TaxID=4604;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H9082; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G.; Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."; Evol. 7:217-230 (1997).
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).
 DR EMBL; Z77744; CAB01311.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 Db 2 SLTL 5

RESULT 31

P92431 ID P92431 PRELIMINARY; PRT; 8 AA.
 AC P92431;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Aegilops tauschii (Aegilops squarrosa).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Aegilops.
 OX NCBI_TaxID=37682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6668; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G.; Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."; Evol. 7:217-230 (1997).
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).
 DR EMBL; Z77758; CAB01353.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 Db 2 SLTL 5

RESULT 32

P92422 ID P92422 PRELIMINARY; PRT; 8 AA.
 AC P92422; P92420;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
 DE Chloroplast RPOA gene (Fragment).
 GN PETD.
 OS Psathyrostachys fragilis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Psathyrostachys.
 OX NCBI_TaxID=37729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H4372, and H917; TISSUE=Leaf;

RA Petersen G., Seberg O.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z77753; CAB01338.1; -;
 DR EMBL; Z77752; CAB01335.1; -;
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 33

Q16220 PRELIMINARY; PRT; 9 AA.
 AC Q16220;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE HGRP protein (Fragment).
 GN HGRP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94320083; PubMed=8044796;

RA Nagalla S.R., Spindel E.R.;
 RT "Functional analysis of the 5'-flanking region of the human gastrin-releasing peptide gene in small cell lung carcinoma cell lines.";
 RL Cancer Res. 54:4461-4467(1994).
 DR EMBL; S73265; AAD14116.1; -;
 FT NON TER
 SQ SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
 ||||
 Db 6 LPLV 9

RESULT 34

Q9UELO PRELIMINARY; PRT; 11 AA.
 AC Q9UELO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE FAS antigen (CD95 antigen) (Fragment).
 GN CD95.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95355401; PubMed=7543095;
 RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T., Nakanishi Y.;
 RT "Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection.";
 RL J. Biol. Chem. 270:18007-18012(1995).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V., Koppers R., Rajewsky K.;
 RA "Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Koppers R.;
 RA "Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22404279; PubMed=12516573;
 RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N., Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
 RT "Lack of deleterious somatic mutations in the CD95 gene of plasmablasts from systemic lupus erythematosus patients and autoantibody-producing cell lines.";
 RL Eur. J. Immunol. 32:3785-3792(2002).
 DR EMBL; D31968; BAA20850.1; -;
 DR EMBL; AJ279011; CAC35539.1; -;
 DR EMBL; AJ279012; CAC35540.1; -;
 DR EMBL; AJ279013; CAC35541.1; -;
 DR EMBL; AJ509179; CAD48929.1; -;
 DR EMBL; AJ509180; CAD48930.1; -;
 FT NON TER
 SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
 ||||
 Db 8 LPLV 11

RESULT 35

Q9WMG5 PRELIMINARY; PRT; 13 AA.
 AC Q9WMG5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE 3 protein (Fragment).
 GN GENE 3.

OS Sigma virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 OX NCBI_TaxID=11301;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=93212481; PubMed=8384742;
 RA Teninges D., Bras F., Dezelee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene overlap.";
 RL Virology 193:1018-1023(1993).
 DR EMBL; S57850; AAD40700.1; -;
 FT NON TER
 SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75832D5 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
 ||||
 Db 8 LPLV 11

RESULT 36

Q9T2K8
ID Q9T2K8 PRELIMINARY; PRT; 15 AA.
AC Q9T2K8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LHCII kinase, 64 kDa kinase (fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE
RX MEDLINE=92183823; PubMed=1544419;
RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
RL F885 Lett. 298:33-35(1992).
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 22.2%; Score 4; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 6 DVEK 9

RESULT 37
Q66174
ID Q66174 PRELIMINARY; PRT; 15 AA.
AC Q66174
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (fragment).
OS Human coronavirus (strain 229E).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Siddell S.;
RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
RL Nucleic Acids Res. 17:6387-6387(1989).
DR EMBL; X15654; CAA33680.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 8 DVEK 11

RESULT 38
Q9NNZ2
ID Q9NNZ2 PRELIMINARY; PRT; 16 AA.
AC Q9NNZ2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE Integrin alpha-2 subunit (fragment).
GN ITGA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98421383; PubMed=9746778;
RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
RA Kunicki T.J.;
RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
RT that are associated with differences in platelet alpha2 beta1
RT density";
RL Blood 92:2382-2388(1998).
DR EMBL; AF062039; AAF77577.1; -.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 10 PLPL 13

RESULT 39
O00497
ID O00497 PRELIMINARY; PRT; 16 AA.
AC O00497
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA mismatch repair protein (fragment).
GN HMLH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Palmirota R., Veri M.C., Curia M.C., Aceto G., D'Amico F.,
RA Esposito D.L., Mariani-Costantini R., Messerini L., Mori S., Cama A.,
RA Battista P.;
RT "Transcripts with splittings of exons 15 and 16 of the hMLH1 gene in
RT normal lymphocytes: implications in RNA-based mutation screening of
RT hereditary nonpolyposis colorectal cancer";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001359; AAB58936.1; -.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1850 MW; 996602B4FFF583D2 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 9 SLTL 12

RESULT 40
Q9TDQ2
ID Q9TDQ2 PRELIMINARY; PRT; 17 AA.
AC Q9TDQ2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit 5 (fragment).
GN ND5.
OS Macaca sylvanus (Barbary ape).

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OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9546;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=20028760; PubMed=10563020;
RA Bailey J.F., Henneberg M., Colson I.B., Ciarallo A., Hedges R.E.,
RA Sykes B.;
RT "Monkey business in Pompeii--unique find of a juvenile Barbary macaque
RT skeleton in Pompeii identified using osteology and ancient DNA
RT techniques.";
RL Mol. Biol. Evol. 16:1410-1414(1999).
RW EMBL; AF064450; AAF09258.1; -.
KW Mitochondrion.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 2002 MW; CE16F446963413D2 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
DB 14 SLTL 17

RESULT 41
ID Q9T379 PRELIMINARY; PRT; 17 AA.
AC Q9T379;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Macaca sylvanus (Barbary ape).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9546;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=20028760; PubMed=10563020;
RA Bailey J.F., Henneberg M., Colson I.B., Ciarallo A., Hedges R.E.M.,
RA Sykes B.;
RT "Monkey business in Pompeii - unique find of a juvenile Barbary
RT macaque skeleton in Pompeii identified using osteology and ancient DNA
RT techniques.";
RL Mol. Biol. Evol. 16:1410-1414(1999).
RW EMBL; AF064452; AAF09259.1; -.
DR EMBL; AF064451; AAF09258.1; -.
KW Mitochondrion.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1974 MW; CE16F45DE01D13D2 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
DB 14 SLTL 17

RESULT 42
Q16244
ID Q16244 PRELIMINARY; PRT; 18 AA.
AC Q16244;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE STS protein (Fragment).
GN STS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
RT "Characterization of the deletion breakpoints in a patient with
RT steroid sulfatase deficiency.";
RL Hum. Mutat. 4:76-78(1994).
RW EMBL; S74383; AAD14153.1; -.
FT NON TER 1 1
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 22.2%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
DB 2 PLPL 5

RESULT 43
Q8WN06
ID Q8WN06 PRELIMINARY; PRT; 18 AA.
AC Q8WN06;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Neuronal nicotinic receptor beta 4 subunit (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Valor L.M., Campos-Caro A., Carrasco-Serrano C., Ortiz J.A.,
RA Ballesta J.J., Criado M.;
RT "Transcription Factors NF-Y and Sp1 are Important Determinants of the
RT Promoter Activity of the Bovine and Human Neuronal Nicotinic Receptor
RT Beta4 Subunit Genes.";
RL J. Biol. Chem. 277:10000-10006(2002).
RW EMBL; AF453876; AAL57839.1; -.
DR Receptor.
KW NON TER 18 18
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1946 MW; 43BB1157148CEB76 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
DB 5 LPLV 8

RESULT 44
Q31687
ID Q31687 PRELIMINARY; PRT; 19 AA.
AC Q31687;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN ATP8.

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OS Artemia parthenogenetica.
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=6663;
RN [1]_TaxID=6663;
RP SEQUENCE FROM N.A.
RC STRAIN=La Mata;
RX MEDLINE=94223692; PubMed=8169960;
RA Perez M.I., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
RT "Speciation in the artemia genus: mitochondrial DNA analysis of
RT bisexual and parthenogenetic brine shrimps.";
RL J. Mol. Evol. 38:156-168(1994).
DR EMBL; X67263; CAA47685.1; -.
KW Mitochondrion.
FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLP 15
DB ||||
5 LPLP 8

RESULT 45
Q905F5 ID Q905F5 PRELIMINARY; PRT; 19 AA.
AC Q905F5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG311;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410450; AAL10267.1; -.
FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2221 MW; BE83B262BA711903 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDVE 8
DB ||||
2 TDVE 5

RESULT 46
Q9R9A5 ID Q9R9A5 PRELIMINARY; PRT; 20 AA.
AC Q9R9A5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Ammonia monooxygenase 1 subunit C (Fragment).
GN AMOCl.
OS Nitrospira sp. NpAV.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;

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OC Nitrosomonadaceae; Nitrospira.
OX NCBI_TaxID=58133;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NpAV;
RX MEDLINE=96001263; PubMed=7557469;
RA Klotz M.G., Norton J.M.;
RT "Sequence of an ammonia monooxygenase subunit A-encoding gene from
RT Nitrospira sp. NpAV.";
RL Gene 163:159-160(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NpAV;
RX MEDLINE=96275898; PubMed=8674986;
RA Norton J.M., Low J.M., Klotz M.G.;
RT "The gene encoding ammonia monooxygenase subunit A exists in three
RT nearly identical copies in Nitrospira sp. NpAV.";
RL FEMS Microbiol. Lett. 139:181-188(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NpAV;
RX MEDLINE=97306641; PubMed=9163908;
RA Klotz M.G., Alzerreca J., Norton J.M.;
RT "A gene encoding a membrane protein exists upstream of the amoA/amoB
RT genes in ammonia oxidizing bacteria: a third member of the amo
RT operon?";
RL FEMS Microbiol. Lett. 150:65-73(1997).
DR EMBL; AF032438; AAB86880.1; -.
KW Monooxygenase.
FT NON TER 1 1
FT NON TER 20 AA; 2266 MW; A745DC66ACC3E2A9 CRC64;
SQ SEQUENCE 20 AA; 2266 MW; A745DC66ACC3E2A9 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTDV 7
DB ||||
1 LTDV 4

RESULT 47
Q9R987 ID Q9R987 PRELIMINARY; PRT; 20 AA.
AC Q9R987;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Ammonia monooxygenase subunit C1 (Fragment).
GN AMOCl.
OS Nitrospira sp. Np39-19.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OX Nitrosomonadaceae; Nitrospira.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Np39-19;
RA Norton J.M., Alzerreca J.J., Klotz M.G.;
RT "Diversity of the genes encoding ammonia monooxygenase in autotrophic
RT ammonia-oxidizing bacteria.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Np39-19;
RA Shiozawa T.L., Norton J.M., Alzerreca J.J., Klotz M.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042170; AAC25054.1; -.
KW Monooxygenase.
FT NON TER 1 1
FT NON TER 20 AA; 2266 MW; A745DC66ACC3F2A9 CRC64;
SQ SEQUENCE 20 AA; 2266 MW; A745DC66ACC3F2A9 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTVL 7
|||||
Db 1 LTVL 4

RESULT 48

Q96T45 PRELIMINARY; PRT; 20 AA.
AC Q96T45;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MER receptor tyrosine kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517330; PubMed=11062461;
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfeissted-Sylla E., Vollrath D.;
RT "Mutations in MERK, the human orthologue of the RCS rat retinal
RT dystrophy gene, cause retinitis pigmentosa."
RL Nat. Genet. 26:270-271(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfeissted-Sylla E., Vollrath D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366903; AAK54121.1; --
KW Kinase; Receptor.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2232 MW; A853BEF7EECE2910 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
|||||
Db 5 PLPL 8

RESULT 49

Q9S900 PRELIMINARY; PRT; 20 AA.
AC Q9S900;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C7 peptide (Fragment).
OS Vigna sinensis (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3920;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RA Phytochemistry 31:731-735(1992).
RL HSP; P02248; IUBI
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2211 MW; BAA7DDE7501B6B9E CRC64;

Query Match 22.2%; Score 4; DB 10; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
|||||
Db 6 LTLT 9

RESULT 50

Q9QUW2 PRELIMINARY; PRT; 20 AA.
AC Q9QUW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 22 kDa INTRALYSOSOMAL lipid-transfer protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=97104296; PubMed=8948454;
RA Kuwana T., Mullock B.M., Luzzio J.P.;
RT "Identification of a lysosomal protein causing lipid transfer, using a
RT fluorescence assay designed to monitor membrane fusion between rat
RT liver endosomes and lysosomes."
RL Biochem. J. 308:937-946(1995).
DR HSP; P17900; IGI3.
SQ SEQUENCE 20 AA; 2211 MW; 3A160591EA5542C5 CRC64;

Query Match 22.2%; Score 4; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
|||||
Db 17 SLTL 20

RESULT 51

Q85636 PRELIMINARY; PRT; 20 AA.
AC Q85636;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Revertant mutant dl567rev patch region including partial LTR and gag
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86089316; PubMed=2416955;
RA Colicelli J., Goff S.P.;
RT "Isolation of a recombinant murine leukemia virus utilizing a new
RT primer tRNA."
RL J. Virol. 57:37-45(1986).
RN [2]
RP SEQUENCE OF 1-5 FROM N.A.
RX MEDLINE=88019205; PubMed=3660592;
RA Colicelli J., Goff S.P.;
RT "Identification of endogenous retroviral sequences as potential donors
RT for recombinational repair of mutant retroviruses: Positions of
RT crossover points."
RL Virology 160:518-522(1987).
DR EMBL; M12275; AAA46501.1; --
DR InterPro; IPR000840; Gag_MA.
DR Pfam; PF01140; Gag_MA; 1.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2214 MW; FB14F3F0FB11AC31 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
|||
Db 10 SLTL 13

RESULT 52

P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=613771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRamide."
RL Nature 305:328-330(1993).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 1 LPL 3

RESULT 53

P93233
ID P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN LE-ACS1B.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843;
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum)."
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
KW Lyase.
FT NON TER 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 3 PLV 5

RESULT 54

Q66205
ID Q66205 PRELIMINARY; PRT; 7 AA.
AC Q66205;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Membrane protein (1 is 3rd base in codon) (Fragment).
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FS772/70;
RX MEDLINE=88216185; PubMed=2835592;
RA Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
RT "Sequence of the Nucleoprotein Gene from a Virulent British Field
RT Isolate of Transmissible Gastroenteritis Virus and its Expression in
RT Saccharomyces Cerevisiae."
RL Mol. Microbiol. 2:89-99(1988).
DR EMBL; Y00542; CAA68606.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 1 EKL 3

RESULT 55

O42564
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells."
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
KW Ionic channel.
FT NON TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17


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Q8H9K1
ID Q8H9K1 PRELIMINARY; PRT; 8 AA.
AC Q8H9K1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Gp30.2 protein (Fragment).
GN 30.2.
OS Bacteriophage L210.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCBI_TaxID=192973;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolesinskiene G., Nivinskis R.;
RT "A pair of overlapping genes 30.3 and 30.3' of T4-related
RT bacteriophages.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458400; CAD30256.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
Db 6 LTD 8

RESULT 61
O31363
ID O31363 PRELIMINARY; PRT; 9 AA.
AC O31363;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Outer surface protein C (Fragment).
OS OSCP.
GN Borrelia gattinii.
OS Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OC NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97436044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93699; AAC45533.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1019 MW; 4864C1A731A44333 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db 5 TLT 7

RESULT 62
P83157
ID P83157 PRELIMINARY; PRT; 9 AA.
AC P83157;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).

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OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Iron; Metal-binding.
FT NON_TER
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 6 PLP 8

RESULT 63
Q16605
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330756; PubMed=3138230;
RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RT "Human glutathione S-transferases. The Ha multigene family encodes
RT products of different but overlapping substrate specificities.";
RL J. Biol. Chem. 263:12797-12800(1988).
DR EMBL; M21867; AAA52617.1; -.
DR EMBL; M21866; AAA35938.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;

Query Match 16.7%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLH 11
Db 6 KLH 8

RESULT 64
Q9TWV0
ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Antho-RPAMIDE=NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

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OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE
RA MEDLINE=93126143; PubMed=1480510;
RX Carlstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15
Db 5 PLP 7

RESULT 65
Q94VD8 ID Q94VD8 PRELIMINARY; PRT; 9 AA.
AC Q94VD8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus niloticus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407514; AAL10096.1; -.
KW Mitochondrion.
FT NON TER 9
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
Db 2 TLT 4

RESULT 66
Q94VC6 ID Q94VC6 PRELIMINARY; PRT; 9 AA.
AC Q94VC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus pilbarensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).

DR EMBL; AF407518; AAL10108.1; -.
KW Mitochondrion.
FT NON TER 9
SQ SEQUENCE 9 AA; 1064 MW; 874CASA36411A735 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3
Db 2 SLT 4

RESULT 67
Q94VE1 ID Q94VE1 PRELIMINARY; PRT; 9 AA.
AC Q94VE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus mertensi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62044;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407512; AAL10090.1; -.
KW Mitochondrion.
FT NON TER 9
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
Db 2 TLT 4

RESULT 68
Q98J8 ID Q98J8 PRELIMINARY; PRT; 9 AA.
AC Q98J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORYZATENSIN-BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oryzatensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q98J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 16.7%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 6 PLP 8

RESULT 69
Q61723 Q61723 PRELIMINARY; PRT; 9 AA.
AC Q61723;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE NF-kappa-B DNA-binding subunit (Fragment).
GN NFKB1 OR NF-KAPPA-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cbVJ; TISSUE=Spleen;
RX MEDLINE=90367113; PubMed=2203532;
RA Ghosh S., Gafford A.M., Riviere L.R., Tempst P., Nolan G.P.,
RA Baltimore D.;
RA "Cloning of the p50 DNA binding subunit of NF-kappa-B: Homology to rel
RT and dorsal.";
RL Cell 62:1019-1029(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cbVJ; TISSUE=Spleen;
RX MEDLINE=94156215; PubMed=8112620;
RA Huo L., Chung W.H., Rothstein T.L.;
RT "C-terminal sequence of the NF-kappa-B p50 precursor from primary
RT murine B-lymphocytes.";
RL Gene 139:287-288(1994).
DR EMBL; L13466; AAC37644.1; -.
DR MGD; MGI:97312; Nfkb1.
KW DNA-binding.
FT NON TER 1 1
FT CONFLICT 5 5 A -> P (IN REF. 1).
FT NON TER 9 9
SQ SEQUENCE 9 AA; 925 MW; 300821E72DC1B408 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12
Db 6 LHL 8

RESULT 70
Q85723 Q85723 PRELIMINARY; PRT; 9 AA.
AC Q85723;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE v-sis and p28-sis genes (Fragment).
OS Simian sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11817;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84106822; PubMed=6319011;
RA Devare S.G., Shatzman A., Robbins K.C., Rosenberg M., Aaronson S.A.;
RT "Expression of the PDGF-related transforming protein of simian sarcoma
RT virus in E. coli.";
RL Cell 36:43-49(1984).
DR EMBL; K01473; AAA46816.1; -.

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FT NON TER 9 9
SQ SEQUENCE 9 AA; 1048 MW; 9C53A866C361A731 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db 2 TLT 4

RESULT 71
Q935G1 Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1.01C.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham P., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 904 MW; 5FDC77776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 1 PLP 3

RESULT 72
Q9XBH3 Q9XBH3 PRELIMINARY; PRT; 10 AA.
AC Q9XBH3;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Celf-like protein (Fragment).
GN C5LF.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "Genome organisation is not conserved between Bacillus cereus and

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RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL; AJ000394; CAB40625.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC33339C9D6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
DB 8 VEK 10

RESULT 73
Q9R5T2 PRELIMINARY; PRT; 10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]_TaxID=436;
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1111 MW; 5091D4AAB2D77767 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
DB 2 HLP 4

RESULT 74
P83154 PRELIMINARY; PRT; 10 AA.
ID P83154;
AC P83154;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -1- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.

CC -1- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.
FT NON TER 10
SQ SEQUENCE 10 AA; 1144 MW; 2F9B662B5B172737 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
DB 2 LPL 4

RESULT 75
Q9TG86 PRELIMINARY; PRT; 10 AA.
ID Q9TG86;
AC Q9TG86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS COI.
OS Diploglossus bilobatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Anguimorpha; Anguillidae;
OC Diploglossus.
OX NCBI_TaxID=102183;
RN [1]_TaxID=102183;
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621;
RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
RA Papenfuss T.J.;
RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
RT in anquid lizards and related taxonomic families.";
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL; AF085608; AAD5154.1; -.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1255 MW; 5DEB80C7336411A7 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
DB 2 TLT 4

Search completed: November 25, 2003, 19:34:02
Job time : 35.8023 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLFLTDVEXLHLPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Ewe colostrinin pe
5	18	100.0	18	23	Colostrinin consti
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Neural cell regula
8	33.3	6	11	AA03868	Hypotensive peptid
9	6	33.3	6	21	Bioactive peptid

10	6	33.3	8	22	AA507194	Colostrinin peptid
11	6	33.3	9	11	AA03874	Hypotensive peptid
12	6	33.3	9	22	AAE07204	Modified colostrin
13	5	27.8	9	22	AA889809	HIV gp120 protein
14	5	27.8	9	22	AA889810	HIV gp120 protein
15	5	27.8	9	22	AA889811	HIV gp120 protein
16	5	27.8	9	22	AA889811	Human MHC class I
17	5	27.8	9	22	AA24855	Human MHC class I
18	5	27.8	9	22	AA24955	Human MHC class I
19	5	27.8	10	22	AA25004	Human MHC class I
20	5	27.8	10	22	AA25103	Human MHC class I
21	5	27.8	10	22	AA25203	Human MHC molecule
22	5	27.8	11	22	AA20470	Mouse CD166 peptid
23	5	27.8	11	24	AB03415	Human expressed pr
24	5	27.8	12	22	AA889415	HIV gp120 protein
25	5	27.8	12	22	AA889855	HIV gp120 protein
26	5	27.8	12	22	AA889856	HIV gp120 protein
27	5	27.8	12	22	AA889857	HIV gp120 protein
28	5	27.8	14	20	AA10295	Angiopoietin deriv
29	5	27.8	14	22	AA503935	Human gene 38 enco
30	5	27.8	15	18	AAW39008	Peptide resembling
31	5	27.8	15	18	AAW39898	Peptide resembling
32	5	27.8	15	22	AA889429	HIV gp120 protein
33	5	27.8	15	22	AA889430	HIV gp120 protein
34	5	27.8	15	22	AA889431	HIV gp120 protein
35	5	27.8	15	22	AA889619	HIV gp120 protein
36	5	27.8	15	22	AA889620	HIV gp120 protein
37	5	27.8	15	22	AA889621	HIV gp120 protein
38	5	27.8	15	22	AA889622	HIV gp120 protein
39	5	27.8	15	22	AA889623	HIV gp120 protein
40	5	27.8	15	22	AA890009	HIV gp120 protein
41	5	27.8	15	22	AA890010	HIV gp120 protein
42	5	27.8	15	22	AA890011	HIV gp120 protein
43	5	27.8	15	22	AA890012	HIV gp120 protein
44	5	27.8	15	22	AA890013	HIV gp120 protein
45	5	27.8	15	22	AA890014	HIV gp120 protein
46	5	27.8	15	22	AA890015	HIV gp120 protein
47	5	27.8	15	22	AA890016	HIV gp120 protein
48	5	27.8	15	22	AA890022	HIV gp120 protein
49	5	27.8	15	22	AA890023	HIV gp120 protein
50	5	27.8	15	22	AA890024	HIV gp120 protein
51	5	27.8	15	22	AA890025	HIV gp120 protein
52	5	27.8	15	22	AA890026	HIV gp120 protein
53	5	27.8	15	22	AA890027	HIV gp120 protein
54	5	27.8	15	22	AA890028	HIV gp120 protein
55	5	27.8	15	22	AA890029	HIV gp120 protein
56	5	27.8	15	22	AA890030	HIV gp120 protein
57	5	27.8	15	22	AA890031	HIV gp120 protein
58	5	27.8	15	22	AA890032	HIV gp120 protein
59	5	27.8	15	22	AA890033	HIV gp120 protein
60	5	27.8	15	22	AA890039	HIV gp120 protein
61	5	27.8	15	22	AA890040	HIV gp120 protein
62	5	27.8	15	22	AA890041	HIV gp120 protein
63	5	27.8	15	22	AA890042	HIV gp120 protein
64	5	27.8	15	22	AA890101	HIV gp120 protein
65	5	27.8	15	22	AA890102	HIV gp120 protein
66	5	27.8	15	22	AA890103	HIV gp120 protein
67	5	27.8	15	22	AA890104	HIV gp120 protein
68	5	27.8	15	22	AA890110	HIV gp120 protein
69	5	27.8	15	22	AA890111	HIV gp120 protein
70	5	27.8	15	22	AA890112	HIV gp120 protein
71	5	27.8	15	22	AA890113	HIV gp120 protein
72	5	27.8	15	22	AA890114	HIV gp120 protein
73	5	27.8	15	22	AA890115	HIV gp120 protein
74	5	27.8	15	22	AA890116	HIV gp120 protein
75	5	27.8	15	22	AA890118	HIV gp120 protein
76	5	27.8	15	22	AA890141	HIV gp120 protein
77	5	27.8	15	23	AB53239	Dentrobacter perm
78	5	27.8	16	23	AB53243	Bacterial peptide
79	5	27.8	17	20	AA07455	Mouse TS10q23.3 ge
80	5	27.8	18	20	AA04173	Human secreted pro
81	5	27.8	18	22	AA89447	HIV gp120 protein
82	5	27.8	18	22	AA89448	HIV gp120 protein

83 5 27.8 18 22 AAB89449 HIV gp120 protein
84 5 27.8 18 22 AAB89663 HIV gp120 protein
85 5 27.8 18 22 AAB89664 HIV gp120 protein
86 5 27.8 18 22 AAB89665 HIV gp120 protein
87 5 27.8 18 22 AAB89666 HIV gp120 protein
88 5 27.8 18 22 AAB89667 HIV gp120 protein
89 5 27.8 18 22 AAB89668 HIV gp120 protein
90 5 27.8 19 23 AAB89669 HIV gp120 protein
91 5 27.8 19 23 AAB89670 HIV gp120 protein
92 5 27.8 20 20 AAB89671 HIV gp120 protein
93 4 22.2 5 15 AAB89672 HIV gp120 protein
94 4 22.2 5 19 AAB89673 HIV gp120 protein
95 4 22.2 6 21 AAB89674 HIV gp120 protein
96 4 22.2 6 22 AAB89675 HIV gp120 protein
97 4 22.2 6 22 AAB89676 HIV gp120 protein
98 4 22.2 7 21 AAB89677 HIV gp120 protein
99 4 22.2 7 21 AAB89678 HIV gp120 protein
100 4 22.2 7 22 AAB89679 HIV gp120 protein

ALIGNMENTS

RESULT 1
AAB72268
ID AAB72268 standard; peptide; 18 AA.
XX
AC AAB72268;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 23.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO20011937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REG-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
WPI; 2001-202804/20.
XX
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
XX Claim 1; Page 34; 50pp; English.
XX
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrinum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTLTDEKHLPLPLVQ 18
Db 1 SLTLTDEKHLPLPLVQ 18
RESULT 2
AAB72521
ID AAB72521 standard; Peptide; 18 AA.
XX
AC AAB72521;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #22.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
WPI; 2001-218342/22.
XX
XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 26; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTLTDEKHLPLPLVQ 18
Db 1 SLTLTDEKHLPLPLVQ 18
RESULT 3
AAB72553
ID AAB72553 standard; Peptide; 18 AA.
XX
AC AAB72553;
XX
DT 09-MAY-2001 (first entry)
XX

```

DE Colostrinin peptide #22.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23..
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX
XX Sequence 18 AA;
XX
XX Query Match 100.0%; Score 18; DB 22; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-11;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SLTLTQVEKHLPLPLVQ 18
XX |||||
XX Db 1 SLTLTQVEKHLPLPLVQ 18
XX
XX RESULT 4
XX AAB59331
XX ID AAB59331 standard; Peptide; 18 AA.
XX
XX AC AAB59331;
XX
XX 21-MAR-2001 (first entry)
XX
XX Ewe colostrinin peptide fragment C-6.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO200075173-A2.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX PS Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
XX SQ Sequence 18 AA;
XX
XX Query Match 100.0%; Score 18; DB 22; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-11;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SLTLTQVEKHLPLPLVQ 18
XX |||||
XX Db 1 SLTLTQVEKHLPLPLVQ 18
XX
XX RESULT 5
XX AAE20250
XX ID AAE20250 standard; peptide; 18 AA.
XX
XX AC AAE20250;
XX
XX 18-JUN-2002 (first entry)
XX
XX Colostrinin constituent peptide #22.
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX transplantation; implantation; dermatological; vulnary.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 18
XX /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostrinin, its
XX constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress
XX level in a cell e.g. mammalian or human cell present in a cell culture,
XX tissue, organ, or organism; or for treating oxidative damage to the skin
XX of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTQVEKHLPLPLVQ 18
 |||||
 DB 1 SLTLTQVEKHLPLPLVQ 18
 |||||

RESULT 6

AA051057
 ID AA051057 standard; Peptide; 18 AA.

XX AC AA051057;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 139-156).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 139-156. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTQVEKHLPLPLVQ 18
 |||||
 DB 1 SLTLTQVEKHLPLPLVQ 18
 |||||

RESULT 7

AA014599

ID AA014599 standard; peptide; 18 AA.

XX AC AA014599;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 22.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in


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CC  the method of the invention.
XX
SQ  Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTDEKHLPLPLVQ 18
Db 1 SLTLTDEKHLPLPLVQ 18

RESULT 8
AAR03868
ID AAR03868 standard; Protein; 6 AA.
XX
AC AAR03868;
XX
DT 17-FEB-1993 (first entry)
XX
DE Hypotensive peptide (7).
XX
KW Hypotensor; salt.
XX
OS Synthetic.
XX
PN JP02062828-A.
XX
PD 02-MAR-1990.
XX
PF 26-AUG-1988; 88JP-0211696.
XX
PR 26-AUG-1988; 88JP-0211696.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI; 1990-111933/15.
XX
PT New peptide used as active ingredient of hypotensive agent -
PT which may be prepd. e.g. as tablets, capsules, powder, syrup,
PT injection prepn. etc.
XX
PS Claim; Page 7; 9pp; Japanese.
XX
CC The peptides given in AAR03862-76 and their salts can be used as
CC components of hypotensive agents.
CC The hypotensor may be in the form of tablets, capsules, powder,
CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of
CC the peptide.
XX
SQ Sequence 6 AA;

Query Match 33.3%; Score 6; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPLP 15
Db 1 LHLPLP 6

RESULT 9
AAV69541
ID AAV69541 standard; peptide; 6 AA.
XX
AC AAV69541;
XX
DT 19-APR-2000 (first entry)
XX
DE Bioactive peptide #7 from whey protein hydrolysate.
XX
KW Whey protein hydrolysate; bioactive peptide; non bitter flavour;

KW food product; digestible; hypotensive.
XX
OS Unidentified.
XX
PN WO9965326-A1.
XX
PD 23-DEC-1999.
XX
PF 14-JUN-1999; 99WO-NZ00084.
XX
PR 17-JUN-1998; 98NZ-0330710.
XX
PA (NZDA-) NEW ZEALAND DAIRY BOARD.
XX
PI Schlothauer R, Schollum LM, Singh AM, Reid JR;
XX
DR WPI; 2000-116705/10.
XX
PT Preparation of whey protein hydrolysate containing bioactive peptides
PT but does not have bitter flavor -
XX
PS Claim 19; Page 21; 32pp; English.
XX
CC Sequences AAY69535-Y69536 represent bioactive peptides which are
CC components of whey protein hydrolysate. The invention relates to the
CC preparation of whey protein hydrolysate containing such bioactive
CC peptides by treating a whey protein containing substrate with one or more
CC enzymes capable of hydrolysing whey proteins to produce the whey protein
CC hydrolysate containing bioactive peptides, and terminating the hydrolysis
CC before substantial production of unacceptable bitter flavours. The
CC invention also encompasses a non bitter product produced by partial
CC hydrolysis of a substrate containing whey proteins, where the product
CC comprises bioactive peptides and has a degree of hydrolysis of the whey
CC proteins of below 10%, a food product containing the non bitter product,
CC any one or a combination of two or more of the bioactive peptides of the
CC invention, and a method for reducing systolic blood pressure in a patient
CC which comprises administering the non bitter product to the patient. The
CC peptides, products and food products are useful in a method for the
CC reduction of systolic blood pressure. The whey protein products are free
CC from bitter flavours and contain bioactive peptides. The products of the
CC process have high digestibility and good organoleptic properties. The
CC products may have bland or slightly sweet taste and are free of soapy
CC and/or brothy flavours.
XX
SQ Sequence 6 AA;

Query Match 33.3%; Score 6; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPLP 15
Db 1 LHLPLP 6

RESULT 10
AAE07194
ID AAE07194 standard; peptide; 8 AA.
XX
AC AAE07194;
XX
DT 06-NOV-2001 (first entry)
XX
DE Colostrin peptide 10.
XX
KW Colostrin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
KW antiviral.
XX
OS Unidentified.

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XX WO200155199-A1.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-GB00329.
 XX PR 26-JAN-2000; 2000GB-0001825.
 XX PA (REGG-) REGEN THERAPEUTICS PLC.
 XX PI Georgiades JA;
 XX DR WPI; 2001-488775/53.
 XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX Claim 1; Page 15; 40pp; English.
 XX CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 10 related to the invention.
 CC Colostrinin peptide 10 corresponds to position 150-157 of beta-caesin.
 XX
 XX Sequence 8 AA;
 XX Query Match 33.3%; Score 6; DB 22; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 LPLPLV 17
 Db 1 LPLPLV 6
 RESULT 11
 AAR03874
 ID AAR03874 standard; Protein; 9 AA.
 AC AAR03874;
 XX 17-FEB-1993 (first entry)
 XX Hypotensive peptide (13).
 DE Hypotensor; salt.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 4..7
 FT /note= "claimed peptide"
 FT Misc-difference 1..2
 FT /note= "amino acids 1-2 may be serially deleted"

FT Misc-difference 1..4
 FT /note= "amino acids 1-4 may be deleted"
 FT Misc-difference 1..5
 FT /note= "amino acids 1-5 may be deleted"
 FT Misc-difference 1..6
 FT /note= "amino acids 1-6 may be deleted"
 XX JP02062828-A.
 XX 02-MAR-1990.
 XX 26-AUG-1988; 88JP-0211696.
 XX 26-AUG-1988; 88JP-0211696.
 XX (AJIN) AJINOMOTO KK.
 XX WPI; 1990-111933/15.
 XX New peptide used as active ingredient of hypotensive agent -
 PT which may be prepd. e.g. as tablets, capsules, powder, syrup,
 PT injection prepn. etc.
 XX Claim; Page 2; 9pp; Japanese.
 XX Amino acids (1-2) and (1-4 to 1-6) may be serially deleted.
 CC The peptides given in AAR03862-76 and their salts can be used as
 CC components of hypotensive agents.
 CC The hypotensor may be in the form of tablets, capsules, powder,
 CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of
 CC the peptide.
 XX Sequence 9 AA;
 XX Query Match 33.3%; Score 6; DB 11; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 LHLPLP 15
 Db 4 LHLPLP 9
 RESULT 12
 AAE07204
 ID AAE07204 standard; peptide; 9 AA.
 XX AAE07204;
 XX 06-NOV-2001 (first entry)
 XX Modified colostrinin cyclic peptide #10.
 XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Ser found at the C-terminal end"
 XX WO200155199-A1.
 XX 02-AUG-2001.
 XX 26-JAN-2001; 2001WO-GB00329.
 XX

PR 26-JAN-2000; 2000GB-0001825.

PA (REGS-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of
PT the immune system and the central nervous system comprises ten
PT amino-terminal amino acid sequence derived from peptides present in
PT colostrinin -

XX Example 2; Page 9; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g. dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxiliary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child.
CC The present sequence is modified colostrinin cyclic peptide #10 related
CC to the invention.

XX Sequence 9 AA;

Query Match 33.3%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPLV 17

DB 2 LPLPLV 7

RESULT 13

AAB89809

ID AAB89809 standard; Peptide; 9 AA.

XX AAB89809;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #302.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

XX WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 68; 114pp; English.

XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.

XX Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STRLT 5

DB 5 STRLT 9

RESULT 14

AAB89810

ID AAB89810 standard; Peptide; 9 AA.

XX AAB89810;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #903.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

XX WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 68; 114pp; English.

XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.

XX Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SLTLT 5
        |||||
Db      4 SLTLT 8

RESULT 15
AAB89811
ID AAB89811 standard; Peptide; 9 AA.
XX
XX
AC AAB89811;
XX
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #904.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
XX WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX DR WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 68; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX QY      1 SLTLT 5
        |||||
        3 SLTLT 7
Db

Query Match      27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
        3 SLTLT 7
Db

RESULT 16
AAM24655
ID AAM24655 standard; Peptide; 9 AA.
XX
XX AC AAM24655;
XX
XX DT 04-DEC-2001 (first entry)
XX
XX DE Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.
XX
XX CC 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
XX cyrostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
XX single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
XX chromosome 1q31-q32.
XX

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OS Homo sapiens.
XX WO200159115-A2.
XX
XX PD 16-AUG-2001.
XX
XX PF 09-FEB-2001; 2001WO-US04426.
XX
XX PR 09-FEB-2000; 2000US-0181261.
XX
XX PA (UROG-) UROGENESYS INC.
XX
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX Mitchell SC, Jakobovits A;
XX
XX DR WPI; 2001-514669/56.
XX
XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or
XX therapeutic agent in multiple cancers such as prostate, bladder and
XX bone cancer -
XX
XX PS Example 15; Page 77; 112pp; English.
XX
XX CC The polypeptide sequences represent the 83P5G4-related protein and
XX peptide fragments of the protein. 83P5G4 exhibits prostate specific
XX expression in normal adult tissue, but it is also aberrantly expressed in
XX many cancers including tumours of the prostate, testis, bladder, kidney,
XX brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
XX liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
XX peptide fragments and specific PCR primers are therefore useful for
XX diagnosing and treating cancer. A vector comprising a polynucleotide
XX which encodes a single chain monoclonal antibody, that immunospecifically
XX binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
XX polynucleotide having the 83P5G4 coding sequence, are both useful in the
XX preparation of a composition for treating a patient with a cancer that
XX expresses 83P5G4. The sequences can be used in diagnostic methods to
XX monitor the level of 83P5G4 gene products in serum, blood, urine and
XX tissue and to thereby detect the presence of cancerous cells.
XX
XX SQ      Sequence 9 AA;
        Query Match      27.8%; Score 5; DB 22; Length 9;
        Best Local Similarity 100.0%; Pred. No. 9.3e+05;
        Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LPLPL 16
        |||||
        2 LPLPL 6
Db

RESULT 17
AAM24955
ID AAM24955 standard; Peptide; 9 AA.
XX
XX AC AAM24955;
XX
XX DT 04-DEC-2001 (first entry)
XX
XX DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #32.
XX
XX CC 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
XX cyrostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
XX single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
XX chromosome 1q31-q32.
XX
XX OS Homo sapiens.
XX
XX PN WO200159115-A2.
XX
XX PD 16-AUG-2001.
XX
XX PF 09-FEB-2001; 2001WO-US04426.

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XX PR 09-FEB-2000; 2000US-0181261.
XX PA (UROG-) UROGENESYS INC.
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX PT Mitchell SC, Jakobovits A;
XX DR WPI; 2001-514669/56.
XX CC The polypeptide sequences represent the 83P5G4-related protein and
XX CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
XX CC expression in normal adult tissue, but it is also aberrantly expressed in
XX CC many cancers including tumours of the prostate, testis, bladder, kidney,
XX CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
XX CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
XX CC peptide fragments and specific PCR primers are therefore useful for
XX CC diagnosing and treating cancer. A vector comprising a polynucleotide
XX CC which encodes a single chain monoclonal antibody, that immunospecifically
XX CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
XX CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
XX CC preparation of a composition for treating a patient with a cancer that
XX CC expresses 83P5G4. The sequences can be used in diagnostic methods to
XX CC monitor the level of 83P5G4 gene products in serum, blood, urine and
XX CC tissue and to thereby detect the presence of cancerous cells.
XX SQ Sequence 9 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
DB |||||
5 LPLPL 9

RESULT 18
AAW25052
ID ARM25052 standard; Peptide; 9 AA.
XX AC
XX ANM25052;
XX DT 04-DEC-2001 (first entry)
XX DE Human MHC class I molecule HLA-B7 binding 83P5G4 peptide #29.
XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
XX KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
XX KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
XX KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
XX KW chromosome 1q31-q32.
XX OS Homo sapiens.
XX PN WO200159115-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US04426.
XX PR 09-FEB-2000; 2000US-0181261.
XX PA (UROG-) UROGENESYS INC.
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX PT Mitchell SC, Jakobovits A;

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XX DR WPI; 2001-514669/56.
XX CC An isolated 83P5G4-related protein useful as a diagnostic and/or
XX PT therapeutic agent in multiple cancers such as prostate, bladder and
XX PT bone cancer -
XX PS Example 15; Page 87; 112pp; English.
XX CC The polypeptide sequences represent the 83P5G4-related protein and
XX CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
XX CC expression in normal adult tissue, but it is also aberrantly expressed in
XX CC many cancers including tumours of the prostate, testis, bladder, kidney,
XX CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
XX CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
XX CC peptide fragments and specific PCR primers are therefore useful for
XX CC diagnosing and treating cancer. A vector comprising a polynucleotide
XX CC which encodes a single chain monoclonal antibody, that immunospecifically
XX CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
XX CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
XX CC preparation of a composition for treating a patient with a cancer that
XX CC expresses 83P5G4. The sequences can be used in diagnostic methods to
XX CC monitor the level of 83P5G4 gene products in serum, blood, urine and
XX CC tissue and to thereby detect the presence of cancerous cells.
XX SQ Sequence 9 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
DB |||||
5 LPLPL 9

RESULT 19
ARM25004
ID ANM25004 standard; Peptide; 10 AA.
XX AC
XX ANM25004;
XX DT 04-DEC-2001 (first entry)
XX DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #81.
XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
XX KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
XX KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
XX KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
XX KW chromosome 1q31-q32.
XX OS Homo sapiens.
XX PN WO200159115-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US04426.
XX PR 09-FEB-2000; 2000US-0181261.
XX PA (UROG-) UROGENESYS INC.
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX PT Mitchell SC, Jakobovits A;
XX DR WPI; 2001-514669/56.
XX CC An isolated 83P5G4-related protein useful as a diagnostic and/or
XX PT therapeutic agent in multiple cancers such as prostate, bladder and
XX PT bone cancer -

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PS Example 15; Page 86; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 20

AAM25103

ID AAM25103 standard; Peptide; 10 AA.

XX AC AAM25103;

XX DT 04-DEC-2001 (first entry)

XX DE Human MHC class I molecule HLA-B7 binding 83P5G4 peptide #80.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytosatic; gene therapy; antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.

XX OS Homo sapiens.

XX WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UOOG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PI Mitchell SC, Jakobovits A;

XX DR WPI; 2001-514669/56.

XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -

XX PS Example 15; Page 89; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,

CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 21

AAM25203

ID AAM25203 standard; Peptide; 10 AA.

XX AC AAM25203;

XX DT 04-DEC-2001 (first entry)

XX DE Human MHC molecule HLA-B35 binding 83P5G4 peptide #80.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytosatic; gene therapy; antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.

XX OS Homo sapiens.

XX WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UOOG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PI Mitchell SC, Jakobovits A;

XX DR WPI; 2001-514669/56.

XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -

XX PS Example 15; Page 91; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that

CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.

XX
SQ Sequence 10 AA;
Query Match 27.8%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 22
AAB20470
ID AAB20470 standard; Peptide; 11 AA.
XX
XX
XX AAB20470;
XX
DT 21-JUN-2001 (first entry)
XX
DE Mouse CD166 peptide isolated in database screening.
XX
XX CD166; ALCAM; mouse; PSK; seizure related protein; epilepsy;
KW neurological disorder; diagnosis; therapy.
XX
XX Mus sp.
XX
XX WO200125268-A1.
XX
XX
PD 12-APR-2001.
XX
XX
PF 04-OCT-2000; 2000WO-DK00556.
XX
XX
PR 04-OCT-1999; 99DK-0001420.
XX
XX (SCHR/) SCHROTZ-KING P.
PA (KING/) KING A.
PA (MANN/) MANN M.
PA (ANDE/) ANDERSEN J.
PA (KUES/) KUESTER B.
XX
XX Schrotz-King P, King A, Mann M, Andersen J, Kuester B;
PI WPI; 2001-290605/30.
XX
DR
XX
PT Novel human seizure related proteins useful for controlling epileptic
PT seizures and neurological disorders, and for identifying potential drug
PT targets for use in diagnosis and/or prognosis of neurological disorders

XX
PS Disclosure; Page 58; 150pp; English.
XX
CC The present sequence is that of a mouse CD166 (ALCAM) peptide
CC identified during a proteomics screening approach for membrane
CC receptors in the brain. 9 Proteins from an Rp-HPIC preparation
CC from the mouse E16 brain plasma membrane were analyzed by
CC nanoelectrospray tandem mass spectrometry. Peptide sequences were
CC found by searching NRDB or EST databases with peptide sequence tags.
CC Sample 8 was identified as CD166. Sample 7 was novel, and named
CC PSK-1. Human PSKs (see AAB2046-48) were subsequently identified.
CC These are novel transmembrane receptor or secreted proteins that
CC are potentially involved in the control or generation of seizures
CC such as epileptic seizures or other neurological disorders.
CC PSK-1, -2 and -3 polynucleotides and polypeptides can be used to
CC identify potential drug targets. They can also be used in the
CC diagnosis of seizure related conditions or other neurodegeneration
CC such as Alzheimer, Rasmussen's Encephalitis, Parkinson's disease,
CC multiple sclerosis, cerebrovascular disorders (stroke syndromes)
CC like ischaemia, Huntington's disease or schizophrenia (claimed),
CC and in the treatment of conditions caused by PSK upregulation,

CC deficiency or impaired function.
XX
SQ Sequence 11 AA;
Query Match 27.8%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLTDV 7
|||||
Db 6 TLTDV 10

RESULT 23
ABU03415
ID ABU03415 standard; Protein; 11 AA.
XX
XX
XX ABU03415;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #195.
XX
KW Translational profiling; expressed protein tag; EPT; kinase;
KW phosphatase; protease; protease inhibitor; transporter;
KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer;
KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX
PD 10-OCT-2002.
XX
XX
PF 28-MAR-2002; 2002WO-US09671.
XX
XX
PR 28-MAR-2001; 2001US-279495P.
PR 21-MAY-2001; 2001US-292544P.
PR 08-AUG-2001; 2001US-310801P.
PR 01-OCT-2001; 2001US-326370P.
PR 04-DEC-2001; 2001US-336780P.
PR 20-FEB-2002; 2002US-358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
PT or leukemia -
XX
XX Claim 10; SEQ ID No 195; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor.
CC The polypeptide is useful as an immunogenic composition for eliciting
CC in a mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to
CC this polypeptide, is useful for treating cancer. The polypeptide is
CC also useful for identifying compounds that binds to a naturally
CC processed class I or class II MHC-binding polypeptide. The polypeptides
CC and polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling.

CC Note: This sequence does not appear in the printed specification but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 11 AA;

Query Match 27.8%; Score 5; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLTDV 7
 |||||
 Db 6 TLTDV 10

RESULT 24
 AAB89415
 ID AAB89415 standard; Peptide; 12 AA.
 XX AC
 XX AAB89415;
 XX DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #508.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;
 XX DR WPI; 2001-244398/25.
 XX PT Novel polypeptides useful for treating HIV infection, have homology to
 XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PS Example 10; Page 69; 114pp; English.
 XX CC The present invention describes a number of peptides which are able to
 XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX CC useful in the treatment of HIV, as they prevent replication of the
 XX CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 26
 AAB89856
 ID AAB89856 standard; Peptide; 12 AA.
 XX AC AAB89856;
 XX DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #949.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;
 XX DR WPI; 2001-244398/25.
 XX PT Novel polypeptides useful for treating HIV infection, have homology to
 XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PS Example 9; Page 57; 114pp; English.
 XX CC The present invention describes a number of peptides which are able to
 XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX CC useful in the treatment of HIV, as they prevent replication of the
 XX CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 |||||
 Db 6 SLTLT 10

RESULT 25
 AAB89855
 ID AAB89855 standard; Peptide; 12 AA.
 XX AC AAB89855;
 XX PI Saxinger C;

DT 23-MAY-2001 (first entry)
 XX HIV gp120 protein binding peptide #948.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;
 XX DR WPI; 2001-244398/25.
 XX PT Novel polypeptides useful for treating HIV infection, have homology to
 XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PS Example 10; Page 69; 114pp; English.
 XX CC The present invention describes a number of peptides which are able to
 XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX CC useful in the treatment of HIV, as they prevent replication of the
 XX CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 26
 AAB89856
 ID AAB89856 standard; Peptide; 12 AA.
 XX AC AAB89856;
 XX DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #949.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;
 XX DR WPI; 2001-244398/25.
 XX PT Novel polypeptides useful for treating HIV infection, have homology to
 XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PS Example 10; Page 69; 114pp; English.
 XX CC The present invention describes a number of peptides which are able to
 XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX CC useful in the treatment of HIV, as they prevent replication of the
 XX CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 26
 AAB89856
 ID AAB89856 standard; Peptide; 12 AA.
 XX AC AAB89856;
 XX DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #949.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;


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DR WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions
XX
XX Example 10; Page 69; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 12 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLTLT 5
Db |||||
7 SLTLT 11
RESULT 27
AAB89857
ID AAB89857 standard; Peptide; 12 AA.
XX
AC AAB89857;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #950.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
PN WO2000116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
FR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions
XX
XX Example 10; Page 69; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 12 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLTLT 5
Db |||||
7 SLTLT 11

```

```

Db |||||
6 SLTLT 10
RESULT 28
AAY30295
ID AAY30295 standard; peptide; 14 AA.
XX
AC AAY30295;
XX
DT 23-NOV-1999 (first entry)
XX
DE Angiopoietin derived peptide #10.
XX
KW Angiogenesis; tumour; metastasis; wound healing; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; cancer; blood supply; imaging;
KW treatment; angiopoietin; Tie-1; Tie-2; TPCK Trypsin; protease;
XX receptor tyrosine kinase.
OS Synthetic.
XX
PN WO9940947-A2.
XX
PD 19-AUG-1999.
XX
PF 11-FEB-1999; 99WO-CA00101.
XX
PR 11-FEB-1998; 98US-0074420.
XX
PA (RESO-) RESOLUTION PHARM INC.
XX
PI Eshima D, Fauconnier T, Pollak A, Thornback J;
XX
DR WPI; 1999-527342/44.
XX
PT Angiogenesis targeting molecules, for, e.g. detecting and treating
PT cancer
XX
XX Example 16; Page 50; 70pp; English.
XX
XX Sequences AAY30286-Y30310 and AAY34151-Y34156 are peptides derived from
CC the angiopeptins through cleavage by the proteases TPCK Trypsin or
CC Staphylococcus aureus protease. The angiopeptins bind to the receptor
CC tyrosine kinase Tie-2 which is upregulated during angiogenesis.
CC Angiopoietin 1 (Ang 1) is ubiquitously expressed and interacts with
CC Tie-2 on endothelial cells and early haemopoietic cells. Angiopoietin 2
CC (Ang 2) is homologous to Ang 1 and competitively inhibits Ang 1
CC interaction with Tie-2. Angiogenesis is the process involved in creating
CC a blood supply to a tumour. The peptides are used in a compound that
CC binds to sites of angiogenesis. The compound consists of a chelator
CC moiety capable of complexing a radionuclide metal or a moiety capable of
CC binding to a halogen group, and an angiogenesis targeting molecule. The
CC peptides are incorporated in the angiogenesis targeting molecule. The
CC compounds are used for imaging and treating angiogenesis, and also to
CC detect, stage and treat tumours and metastases. Angiogenesis is also
CC required for wound healing and conditions such as diabetic retinopathy,
CC rheumatoid arthritis and psoriasis, therefore the compounds may also be
CC useful in the treatment of these conditions.
XX
XX Sequence 14 AA;
Qy 4 LTDVE 8
Db |||||
1 LTDVE 5
RESULT 29
AAE03935
ID AAE03935 standard; peptide; 14 AA.

```

```
XX AC AAE03935;
XX DT 09-AUG-2001 (first entry)
XX DE Human gene 38 encoded secreted protein fragment HBJFJ14, SEQ ID NO:98.
XX DX
XX EX
XX FX Human; secreted protein; proliferative disorder; cancer; tumour;
XX GW foetal abnormality; developmental abnormality; haematopoietic disorder;
XX KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX KW inflammation; allergy; neurological disorder; Alzheimer's disease;
XX KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX KW cardiovascular disorder; angogenic disorder; kidney disorder;
XX KW gastrointestinal disorder; pregnancy-related disorder;
XX KW endocrine disorder; infection; wound healing; vulnerary;
XX KW cell culture; chemotaxis; food additive; gene therapy;
XX KW binding partner identification.
XX OS Homo sapiens.
XX XX
XX PN WO200077022-A1.
XX PD
XX PP 21-DEC-2000.
XX PF 01-JUN-2000; 2000WO-US15136.
XX XX
XX PR 11-JUN-1999; 99US-0138629.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Rosen CA, Ruben SM, Komatsoulis GA;
XX XX
XX DR WPI; 2001-367020/38.
XX DR N-PSDB; AAD08382.
XX XX
XX PT Nucleic acids encoding 50 human secreted polypeptides, useful for
XX PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX PT disease, botulism, cancers and Scimitar syndrome -
XX XX
XX PS Claim 11; Page 546; 614pp; English.
XX XX
XX CC RAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
XX CC protein genes and AAE03898-AE03947 represent the proteins they encode.
XX CC AAE03948-AAD03996 represent human secreted protein fragments or variants.
XX CC The genes and their secreted proteins are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g., by protein or gene
XX CC therapy. Pathological conditions can be diagnosed by determining the
XX CC amount of the new protein in a sample or by determining the presence of
XX CC mutations in the new genes. Specific uses are described for each of the
XX CC 50 genes, based on the tissues in which they are most highly expressed,
XX CC and include developing products for the diagnosis or treatment of
XX CC proliferative disorders, cancer, tumours, foetal and developmental
XX CC abnormalities, haematopoietic disorders, diseases of the immune system,
XX CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX CC allergies, neurological disorders (e.g., Alzheimer's disease,
XX CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX CC cardiovascular disorders, angionecy-related disorders, endocrine
XX CC gastrointestinal disorders, pregnancy-related disorders, endocrine
XX CC disorders, and infections. The proteins can also be used to aid wound
XX CC healing and epithelial cell proliferation, to prevent skin aging due to
XX CC sunburn, to maintain organs before transplantation, for supporting cell
XX CC culture of primary tissues, to regenerate tissues, to identify their
XX CC cognate ligands or binding partners, and in chemotaxis, and can be used
XX CC as a food additive or preservative to modify storage properties.
XX CC Antibodies specific for a protein of the invention can be used in
XX CC alleviating symptoms associated with the disorders mentioned above, and
XX CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX CC immunosorbent assay (ELISA). The present sequence represents a human
XX CC secreted protein fragment of the invention.
XX XX
XX SQ Sequence 14 AA;
```

Query Match 27.8%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPL 14
|||||

Db 5 LHLPL 9

RESULT 30

AAW39008

ID AAW39008 standard; peptide; 15 AA.

XX AAW39008;

XX AC AAW39008;

XX DT 27-MAR-1998 (first entry)

XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:407.

XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

XX KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;

XX KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.

XX PN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

XX PI Sparks AB, Thorn JM;

XX DR WPI; 1997-424972/39.

XX PT Src homology region 3 binding peptide - used to activate Src
XX PT tyrosine kinase(s) and to stimulate immune response by increasing
XX PT production of certain lymphokine(s), e.g. interleukin-1

XX PS Claim 22; Page 93; 131pp; English.

XX CC The present sequence represents a peptide which resembles a Src homology
XX CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX CC (a) peptides which bind the SH3 domain of Cortactin, (b) peptides which
XX CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX CC domain of Abl; (d) peptides which bind the SH3 domain of PLC gamma; (e)
XX CC peptides which bind the SH3 domain of p53bp2; (f) peptides which bind
XX CC the SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX CC binding peptides can be used in the method to identify inhibitors of
XX CC their binding to their respective SH3 domains, which could be used to
XX CC modulate the pharmacological activity of proteins or polypeptide
XX CC containing the SH3 domain. The peptides can also be used to activate
XX CC Src or Src-related protein tyrosine kinases, to stimulate the immune
XX CC response by increasing the production of certain lymphokines, e.g.
XX CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX CC Src related proteins.

SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
 |||||
 Db 3 LPLPL 7

RESULT 31
 AAW38988
 ID AAW38988 standard; peptide; 15 AA.
 XX
 AC AAW38988;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:395.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 PN WO9730074-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US02298.
 XX
 PR 16-FEB-1996; 96US-0602999.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX
 DR WPI; 1997-424972/39.
 XX
 CC Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 PS Claim 22; Page 92; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

QY 12 LPLPL 16
 |||||
 Db 10 LPLPL 14

Query Match 27.8%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32
 AAB89429
 ID AAB89429 standard; Peptide; 15 AA.
 XX
 AC AAB89429;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #522.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-US23505.
 XX
 PR 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 CC Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX
 PS Example 9; Page 58; 114pp; English.
 XX
 CC The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.

QY 1 SLTIL 5
 |||||
 Db 9 SLTIL 13

RESULT 33
 AAB89430
 ID AAB89430 standard; Peptide; 15 AA.
 XX
 AC AAB89430;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #523.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-US23505.
 XX

Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
PR 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db 8 SLTLT 12
XX
XX RESULT 34
XX AAB89431
XX ID AAB89431 standard; Peptide; 15 AA.
XX
XX AC AAB89431;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #524.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db 8 SLTLT 12
XX
XX RESULT 34
XX AAB89431
XX ID AAB89431 standard; Peptide; 15 AA.
XX
XX AC AAB89431;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #524.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db 11 SLTLT 15
XX
XX RESULT 36
XX AAB89620
XX ID AAB89620 standard; Peptide; 15 AA.
XX
XX AC AAB89620;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #713.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX
```



```

Query Match      27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 42
AAB90011
ID AAB90011 standard; Peptide; 15 AA.
XX AC
XX AC
XX AC
DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1104.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match      27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 43
AAB90012
ID AAB90012 standard; Peptide; 15 AA.
XX AC
XX AC
XX AC
DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1105.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

Query Match      27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 44
AAB90013
ID AAB90013 standard; Peptide; 15 AA.
XX AC
XX AC
XX AC
DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1106.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match      27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 45
AAB90014
ID AAB90014 standard; Peptide; 15 AA.
XX AC
XX AC
XX AC
DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1107.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

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XX Synthetic.
OS WO200116182-A2.
XX PN 08-MAR-2001.
XX PD 25-AUG-2000; 2000WO-US23505.
XX PF 27-AUG-1999; 99US-0151270.
XX PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA Saxinger C;
XX PI WPI; 2001-244398/25.
XX DR Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions -
XX PS Example 10; Page 73; 114pp; English.
XX PS The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match      27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 46
AAB90015
ID AAB90015 standard; Peptide; 15 AA.
XX AC
XX AC
XX AC
DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1108.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match      27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 47
AAB90016
ID AAB90016 standard; Peptide; 15 AA.
XX AC
XX AC
XX AC
DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1109.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

```

PS Example 10; Page 73; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 45
AAB90014
ID AAB90014 standard; Peptide; 15 AA.
XX
AC AAB90014;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1107.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 73; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 46
AAB90015

ID AAB90015 standard; Peptide; 15 AA.
XX
AC AAB90015;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1108.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 73; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 47
AAB90016
ID AAB90016 standard; Peptide; 15 AA.
XX
AC AAB90016;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1109.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 73; 114pp; English.

XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5

Db 8 SLTTLT 12

RESULT 48

AAB90022

ID AAB90022 standard; Peptide; 15 AA.

XX AC AAB90022;

DT 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #1115.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Synthetic.

XX WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US23505.

XX PR 27-AUG-1999; 99US-0151270.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 73; 114pp; English.

XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5

Db 8 SLTTLT 12

RESULT 49

AAB90023

ID AAB90023 standard; Peptide; 15 AA.

XX AC AAB90023;

DT 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #1116.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Synthetic.

XX WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US23505.

XX PR 27-AUG-1999; 99US-0151270.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 73; 114pp; English.

XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 2e+02; Length 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5

Db 8 SLTTLT 12

RESULT 50

AAB90024

ID AAB90024 standard; Peptide; 15 AA.

XX AC AAB90024;

DT 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #1117.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

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OS Synthetic.
XX WO200116182-A2.
XX
XX
XX 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX Db |||||
XX 8 SLTTLT 12
XX
XX RESULT 51
XX AAB90025
XX ID AAB90025 standard; Peptide; 15 AA.
XX
XX AC AAB90025;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #1118.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX Db |||||
XX 8 SLTTLT 12
XX
XX RESULT 51
XX AAB90025
XX ID AAB90025 standard; Peptide; 15 AA.
XX
XX AC AAB90025;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #1118.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX Db |||||
XX 8 SLTTLT 12
XX
XX RESULT 53
XX AAB90027
XX ID AAB90027 standard; Peptide; 15 AA.

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XX AC AAB90027;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1120.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PS Example 10; Page 73; 114pp; English.
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SLTTLT 5
XX DB |||||
XX 8 SLTTLT 12
XX RESULT 54
XX AAB90028
XX ID AAB90028 standard; Peptide; 15 AA.
XX AC AAB90028;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1121.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PS Example 10; Page 73; 114pp; English.
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SLTTLT 5
XX DB |||||
XX 8 SLTTLT 12
XX RESULT 54
XX AAB90028
XX ID AAB90028 standard; Peptide; 15 AA.
XX AC AAB90028;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1121.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PS Example 10; Page 73; 114pp; English.
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SLTTLT 5
XX DB |||||
XX 8 SLTTLT 12
XX RESULT 55
XX AAB90029
XX ID AAB90029 standard; Peptide; 15 AA.
XX AC AAB90029;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1122.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PS Example 10; Page 73; 114pp; English.
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SLTTLT 5
XX DB |||||
XX 8 SLTTLT 12

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XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 56
AAB90030
ID AAB90030 standard; Peptide; 15 AA.
XX AC
XX AAB90030;
XX 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1123.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 57
AAB90031
ID AAB90031 standard; Peptide; 15 AA.
XX AC
XX AAB90031;
XX 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1124.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.

XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 58
AAB90032
ID AAB90032 standard; Peptide; 15 AA.
XX AC AAB90032;
XX 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1125.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 74; 114pp; English.

PI Saxinger C;
 XX WPI; 2001-244398/25.
 XX Novel polypeptides useful for treating HIV infection, have homology to
 XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PT
 XX Example 10; Page 74; 114pp; English.
 XX
 XX The present invention describes a number of peptides which are able to
 XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX useful in the treatment of HIV, as they prevent replication of the
 XX virus. The present sequence is an example of a peptide of the invention.
 XX
 XX Sequence 15 AA;
 SQ Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLT 5
 DB 8 SLTLT 12
 |||||
 |||||

RESULT 62
 AAB90041
 ID AAB90041 standard; Peptide; 15 AA.
 AC AAB90041;
 XX
 XX 23-MAY-2001 (first entry)
 XX HIV gp120 protein binding peptide #1134.
 XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX replication; CCR5; CXCR4; CD4; STRL33.
 XX Synthetic.
 XX WO200116182-A2.
 XX 08-MAR-2001.
 XX 25-AUG-2000; 2000WO-US23505.
 XX 27-AUG-1999; 99US-0151270.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Saxinger C;
 XX WPI; 2001-244398/25.
 XX Novel polypeptides useful for treating HIV infection, have homology to
 XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PT
 XX Example 10; Page 74; 114pp; English.
 XX
 XX The present invention describes a number of peptides which are able to
 XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX useful in the treatment of HIV, as they prevent replication of the
 XX virus. The present sequence is an example of a peptide of the invention.
 XX
 XX Sequence 15 AA;
 SQ Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLT 5
 DB 8 SLTLT 12
 |||||
 |||||

RESULT 64
 AAB90101
 ID AAB90101 standard; Peptide; 15 AA.
 AC AAB90101;
 XX
 XX 23-MAY-2001 (first entry)
 XX HIV gp120 protein binding peptide #1194.
 XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX replication; CCR5; CXCR4; CD4; STRL33.
 XX Synthetic.
 XX
 XX Sequence 15 AA;
 SQ Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 DB 8 SLTLT 12
 |||||
 |||||

RESULT 63
 AAB90042
 ID AAB90042 standard; Peptide; 15 AA.
 XX
 XX AAB90042;
 XX
 XX 23-MAY-2001 (first entry)
 XX HIV gp120 protein binding peptide #1135.
 XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX replication; CCR5; CXCR4; CD4; STRL33.
 XX Synthetic.
 XX WO200116182-A2.
 XX 08-MAR-2001.
 XX 25-AUG-2000; 2000WO-US23505.
 XX 27-AUG-1999; 99US-0151270.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Saxinger C;
 XX WPI; 2001-244398/25.
 XX Novel polypeptides useful for treating HIV infection, have homology to
 XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 XX PT and binds to HIV gp120 under physiological conditions -
 XX PT
 XX Example 10; Page 74; 114pp; English.
 XX
 XX The present invention describes a number of peptides which are able to
 XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
 XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 XX useful in the treatment of HIV, as they prevent replication of the
 XX virus. The present sequence is an example of a peptide of the invention.
 XX
 XX Sequence 15 AA;
 SQ Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLT 5
 DB 8 SLTLT 12
 |||||
 |||||

RESULT 64
 AAB90101
 ID AAB90101 standard; Peptide; 15 AA.
 XX
 XX AAB90101;
 XX
 XX 23-MAY-2001 (first entry)
 XX HIV gp120 protein binding peptide #1194.
 XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 XX replication; CCR5; CXCR4; CD4; STRL33.
 XX Synthetic.
 XX
 XX Sequence 15 AA;
 SQ Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US233505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PS (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
Db 8 SLTTLT 12
XX
RESULT 65
AAB90102
ID AAB90102 standard; Peptide; 15 AA.
XX
AC AAB90102;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1195.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US233505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PS (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
Db 8 SLTTLT 12
XX
RESULT 66
AAB90103
ID AAB90103 standard; Peptide; 15 AA.
XX
AC AAB90103;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1196.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US233505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PS (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
Db 8 SLTTLT 12
XX
RESULT 67
AAB90104
ID AAB90104 standard; Peptide; 15 AA.
XX
AC AAB90104;

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XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1197.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 75; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX Db |||||
XX 8 SLTTLT 12
XX
XX RESULT 69
XX AAB90111
XX ID AAB90111 standard; Peptide; 15 AA.
XX AC AAB90111;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1204.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES..
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 75; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX Db |||||
XX 8 SLTTLT 12
XX
XX RESULT 68
XX AAB90110
XX ID AAB90110 standard; Peptide; 15 AA.
XX AC AAB90110;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1203.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;

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QY 1 SLTTLT 5
 DB 8 SLTTLT 12

RESULT 70
 ID AAB90112 standard; Peptide; 15 AA.
 XX AC AAB90112;
 DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #1205.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;
 XX WPI; 2001-244398/25.
 XX PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
 XX PS Example 10; Page 75; 114pp; English.
 XX CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.

QY Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 DB 8 SLTTLT 12

RESULT 71
 ID AAB90113 standard; Peptide; 15 AA.
 XX AC AAB90113;
 DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #1206.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.

QY Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 DB 8 SLTTLT 12

RESULT 72
 ID AAB90114 standard; Peptide; 15 AA.
 XX AC AAB90114;
 DT 23-MAY-2001 (first entry)
 XX DE HIV gp120 protein binding peptide #1207.
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX OS Synthetic.
 XX PN WO200116182-A2.
 XX PD 08-MAR-2001.
 XX PF 25-AUG-2000; 2000WO-US23505.
 XX PR 27-AUG-1999; 99US-0151270.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Saxinger C;
 XX WPI; 2001-244398/25.
 XX PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
 XX PS Example 10; Page 75; 114pp; English.
 XX CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.

QY Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 DB 8 SLTTLT 12

CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTLT 5
DB 8 SLTLT 12
RESULT 73
AAB90115
ID AAB90115 standard; Peptide; 15 AA.
XX AAB90115;
XX 23-MAY-2001 (first entry)
DT HIV gp120 protein binding peptide #1208.
DE Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Saxinger C;
PI WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 76; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTLT 5
DB 8 SLTLT 12
RESULT 74
AAB90116
ID AAB90116 standard; Peptide; 15 AA.
XX AAB90116;
XX Saxinger C;
XX 23-MAY-2001 (first entry)
DT HIV gp120 protein binding peptide #1211.
DE Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Saxinger C;
PI Saxinger C;

DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1209.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Saxinger C;
PI WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 76; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTLT 5
DB 8 SLTLT 12
RESULT 75
AAB90118
ID AAB90118 standard; Peptide; 15 AA.
XX AAB90118;
XX 23-MAY-2001 (first entry)
DT HIV gp120 protein binding peptide #1211.
DE Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Saxinger C;
PI Saxinger C;

DR WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 76; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
Db |||||
8 SLTTLT 12

Search completed: November 25, 2003, 19:27:10
Job time : 46.9419 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8837 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDEKHLPLPLVQ 18

Scoring table: OILGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	18	100.0	18	15	US-10-281-652-23
2	6	33.3	14	15	US-10-148-936-8
3	5	27.8	9	10	US-09-780-053-148
4	5	27.8	9	10	US-09-780-053-448
5	5	27.8	9	10	US-09-780-053-545
6	5	27.8	9	15	US-10-084-813-916
7	5	27.8	9	15	US-10-084-813-917
8	5	27.8	9	15	US-10-084-813-918
9	5	27.8	10	10	US-09-780-053-497
10	5	27.8	10	10	US-09-780-053-596
11	5	27.8	10	10	US-09-780-053-696
12	5	27.8	12	12	US-10-286-457-346
13	5	27.8	12	15	US-10-084-813-537
14	5	27.8	12	15	US-10-084-813-962
15	5	27.8	12	15	US-10-084-813-963

16	5	27.8	12	15	US-10-084-813-964
17	5	27.8	15	9	US-09-829-855-223
18	5	27.8	15	12	US-10-161-791-385
19	5	27.8	15	12	US-10-161-791-407
20	5	27.8	15	15	US-10-084-813-29
21	5	27.8	15	15	US-10-084-813-521
22	5	27.8	15	15	US-10-084-813-522
23	5	27.8	15	15	US-10-084-813-523
24	5	27.8	15	15	US-10-084-813-726
25	5	27.8	15	15	US-10-084-813-727
26	5	27.8	15	15	US-10-084-813-728
27	5	27.8	15	15	US-10-084-813-729
28	5	27.8	15	15	US-10-084-813-730
29	5	27.8	15	15	US-10-084-813-1115
30	5	27.8	15	15	US-10-084-813-1116
31	5	27.8	15	15	US-10-084-813-1117
32	5	27.8	15	15	US-10-084-813-1118
33	5	27.8	15	15	US-10-084-813-1119
34	5	27.8	15	15	US-10-084-813-1120
35	5	27.8	15	15	US-10-084-813-1121
36	5	27.8	15	15	US-10-084-813-1122
37	5	27.8	15	15	US-10-084-813-1128
38	5	27.8	15	15	US-10-084-813-1129
39	5	27.8	15	15	US-10-084-813-1130
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45	5	27.8	15	15	US-10-084-813-1136
46	5	27.8	15	15	US-10-084-813-1137
47	5	27.8	15	15	US-10-084-813-1138
48	5	27.8	15	15	US-10-084-813-1139
49	5	27.8	15	15	US-10-084-813-1145
50	5	27.8	15	15	US-10-084-813-1146
51	5	27.8	15	15	US-10-084-813-1147
52	5	27.8	15	15	US-10-084-813-1148
53	5	27.8	15	15	US-10-084-813-1207
54	5	27.8	15	15	US-10-084-813-1208
55	5	27.8	15	15	US-10-084-813-1209
56	5	27.8	15	15	US-10-084-813-1210
57	5	27.8	15	15	US-10-084-813-1216
58	5	27.8	15	15	US-10-084-813-1217
59	5	27.8	15	15	US-10-084-813-1218
60	5	27.8	15	15	US-10-084-813-1219
61	5	27.8	15	15	US-10-084-813-1220
62	5	27.8	15	15	US-10-084-813-1221
63	5	27.8	15	15	US-10-084-813-1222
64	5	27.8	15	15	US-10-084-813-1224
65	5	27.8	16	9	US-09-829-855-227
66	5	27.8	17	12	US-10-299-003-14
67	5	27.8	18	15	US-10-084-813-552
68	5	27.8	18	15	US-10-084-813-553
69	5	27.8	18	15	US-10-084-813-554
70	5	27.8	18	15	US-10-084-813-770
71	5	27.8	18	15	US-10-084-813-771
72	5	27.8	18	15	US-10-084-813-772
73	5	27.8	18	15	US-10-084-813-773
74	5	27.8	18	15	US-10-084-813-774
75	5	27.8	19	9	US-09-829-855-225
76	5	27.8	20	11	US-09-983-802-664
77	5	27.8	20	12	US-10-340-288-5
78	4	22.2	4	9	US-09-804-866-12
79	4	22.2	5	9	US-09-804-866-13
80	4	22.2	7	9	US-09-739-254-132
81	4	22.2	7	9	US-09-904-615-132
82	4	22.2	7	12	US-10-055-088-132
83	4	22.2	7	15	US-10-054-988-132
84	4	22.2	8	9	US-09-358-423-23
85	4	22.2	8	9	US-09-358-423-24
86	4	22.2	8	12	US-10-224-125-32
87	4	22.2	8	14	US-10-047-881-23
88	4	22.2	9	10	US-10-047-881-24
89	4	22.2	9	10	US-09-780-053-566

Sequence 964, App
Sequence 223, App
Sequence 385, App
Sequence 407, App
Sequence 29, App
Sequence 521, App
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Sequence 523, App
Sequence 726, App
Sequence 727, App
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Sequence 729, App
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Sequence 1116, App
Sequence 1117, App
Sequence 1118, App
Sequence 1119, App
Sequence 1120, App
Sequence 1121, App
Sequence 1128, App
Sequence 1129, App
Sequence 1130, App
Sequence 1131, App
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Sequence 773, App
Sequence 774, App
Sequence 225, App
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Sequence 12, Appl
Sequence 13, Appl
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 23, Appl
Sequence 24, Appl
Sequence 32, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 566, App

89 4 22.2 9 10 US-09-894-018-312 Sequence 312, App
90 4 22.2 9 10 US-09-821-831-68 Sequence 68, Appl
91 4 22.2 9 10 US-09-919-048-84 Sequence 84, Appl
92 4 22.2 9 10 US-09-919-048-126 Sequence 126, App
93 4 22.2 9 10 US-09-919-048-170 Sequence 170, App
94 4 22.2 9 10 US-09-017-743C-16 Sequence 16, Appl
95 4 22.2 9 10 US-09-909-460-91 Sequence 91, Appl
96 4 22.2 9 12 US-10-155-883B-53 Sequence 53, Appl
97 4 22.2 9 12 US-09-793-451-122 Sequence 122, App
98 4 22.2 9 12 US-09-793-451-131 Sequence 131, App
99 4 22.2 9 12 US-09-793-451-142 Sequence 142, App
100 4 22.2 9 12 US-09-793-451-236 Sequence 236, App

ALIGNMENTS

RESULT 1
US-10-281-652-23
; Sequence 23, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-23

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTDEKHLPLPLVQ 18
Db 1 SLTLTDEKHLPLPLVQ 18

RESULT 2
US-10-148-936-8
; Sequence 8, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA9963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-8

Query Match 33.3%; Score 6; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPLV 17
Db 5 LPLPLV 10

RESULT 3
US-09-780-053-148
; Sequence 148, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-148

Query Match 27.8%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
Db 2 LPLPL 6

RESULT 4
US-09-780-053-448
; Sequence 448, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09

```
;
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-448
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Query Match          27.8%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 LPLPL 16
Db      5 LPLPL 9
```

```
RESULT 5
US-09-780-053-545
; Sequence 545, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-545
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```
Query Match          27.8%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 LPLPL 16
Db      5 LPLPL 9
```

```
RESULT 6
US-10-084-813-916
; Sequence 916, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 916
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-084-813-916
```

```
;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-916
```

```
Query Match          27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SLTTL 5
Db      5 SLTTL 9
```

```
RESULT 7
US-10-084-813-917
; Sequence 917, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 917
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-917
```

```
Query Match          27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SLTTL 5
Db      4 SLTTL 8
```

```
RESULT 8
US-10-084-813-918
; Sequence 918, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 918
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-918
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Query Match 27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTIT 5
|||||
Db 3 SLTIT 7

RESULT 9
US-09-780-053-497
; Sequence 497, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-497

Query Match 27.8%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 10
US-09-780-053-596
; Sequence 596, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-596

Query Match 27.8%; Score 5; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 11
US-09-780-053-696
; Sequence 696, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-696

Query Match 27.8%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 12
US-10-286-457-346
; Sequence 346, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, b
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-346

Query Match 27.8%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHLP 13
|||||

Db 6 KLHLP 10

RESULT 13

US-10-084-813-537
; Sequence 537, Application US/10084813
; Publication No. US20030068615A1

GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 537
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-537

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 6 SLTLT 10

RESULT 14

US-10-084-813-962
; Sequence 962, Application US/10084813
; Publication No. US20030068615A1

GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 962
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-962

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 8 SLTLT 12

RESULT 15

US-10-084-813-963

; Sequence 963, Application US/10084813
; Publication No. US20030068615A1

GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 963
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-963

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 7 SLTLT 11

RESULT 16

US-10-084-813-964
; Sequence 964, Application US/10084813
; Publication No. US20030068615A1

GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 964
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-964

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 6 SLTLT 10

RESULT 17

US-09-829-855-223
; Sequence 223, Application US/09829855
; Patent No. US20020065609A1

GENERAL INFORMATION:

; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations

; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Denitrobacter permanens
US-09-829-855-223

Query Match 27.8%; Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 13 PLPLV 17
Db 4 PLPLV 8

RESULT 18
US-10-161-791-385
; Sequence 385, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-385

Query Match 27.8%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 12 LPLPL 16
Db 10 LPLPL 14

RESULT 19
US-10-161-791-407
; Sequence 407, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-407

Query Match 27.8%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 12 LPLPL 16
Db 3 LPLPL 7

RESULT 20
US-10-084-813-29
; Sequence 29, Application US/10084813
; Publication No. US20030068615A1

```
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-29

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 21
US-10-084-813-521
; Sequence 521, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 521
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-521

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 9 SLTLT 13

RESULT 22
US-10-084-813-522
; Sequence 522, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
```

```
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 522
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-522

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 23
US-10-084-813-523
; Sequence 523, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 523
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-523

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 7 SLTLT 11

RESULT 24
US-10-084-813-726
; Sequence 726, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
```

; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 726
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-726

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 11 SLTTLT 15

RESULT 25
US-10-084-813-727
; Sequence 727, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 727
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-727

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 10 SLTTLT 14

RESULT 26
US-10-084-813-728
; Sequence 728, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 728
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-730

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-728

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 9 SLTTLT 13

RESULT 27
US-10-084-813-729
; Sequence 729, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 729
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-729

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 28
US-10-084-813-730
; Sequence 730, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 730
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-730

Query Match 27.8%; Score 5; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 |||||
 Db 7 SLTTLT 11

RESULT 29
 US-10-084-813-1115
 ; Sequence 1115, Application US/10084813
 ; Publication No. US20030068615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAXINGER, CARL
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
 ; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
 ; FILE REFERENCE: 215875
 ; CURRENT APPLICATION NUMBER: US/10/084,813
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 60/151,270
 ; PRIOR FILING DATE: 1999-08-27
 ; NUMBER OF SEQ ID NOS: 1242
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1115
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
 US-10-084-813-1115

Query Match 27.8%; Score 5; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 |||||
 Db 8 SLTTLT 12

RESULT 30
 US-10-084-813-1116
 ; Sequence 1116, Application US/10084813
 ; Publication No. US20030068615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAXINGER, CARL
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
 ; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
 ; FILE REFERENCE: 215875
 ; CURRENT APPLICATION NUMBER: US/10/084,813
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 60/151,270
 ; PRIOR FILING DATE: 1999-08-27
 ; NUMBER OF SEQ ID NOS: 1242
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1116
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
 US-10-084-813-1116

Query Match 27.8%; Score 5; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 |||||
 Db 8 SLTTLT 12

RESULT 31
 US-10-084-813-1117
 ; Sequence 1117, Application US/10084813
 ; Publication No. US20030068615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAXINGER, CARL
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
 ; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
 ; FILE REFERENCE: 215875
 ; CURRENT APPLICATION NUMBER: US/10/084,813
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 60/151,270
 ; PRIOR FILING DATE: 1999-08-27
 ; NUMBER OF SEQ ID NOS: 1242
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1117
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
 US-10-084-813-1117

Query Match 27.8%; Score 5; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 |||||
 Db 8 SLTTLT 12

RESULT 32
 US-10-084-813-1118
 ; Sequence 1118, Application US/10084813
 ; Publication No. US20030068615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAXINGER, CARL
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
 ; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
 ; FILE REFERENCE: 215875
 ; CURRENT APPLICATION NUMBER: US/10/084,813
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 60/151,270
 ; PRIOR FILING DATE: 1999-08-27
 ; NUMBER OF SEQ ID NOS: 1242
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1118
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
 US-10-084-813-1118

Query Match 27.8%; Score 5; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 |||||
 Db 8 SLTTLT 12

```
RESULT 33
US-10-084-813-1119
; Sequence 1119, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1119
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 34
US-10-084-813-1120
; Sequence 1120, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1120
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1120
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 35
US-10-084-813-1121
; Sequence 1121, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1121
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12
```

```
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1121
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 36
US-10-084-813-1128
; Sequence 1128, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1128
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1128
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 37
US-10-084-813-1129
; Sequence 1129, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1129
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12
```

; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1129

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 38

US-10-084-813-1130
; Sequence 1130, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1130
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1130

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 39

US-10-084-813-1131
; Sequence 1131, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1131

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 40

US-10-084-813-1132
; Sequence 1132, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1132

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 41

US-10-084-813-1133
; Sequence 1133, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1133
; LENGTH: 15
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1133

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||

RESULT 42
US-10-084-813-1134
; Sequence 1134, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1134
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1134

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||

RESULT 43
US-10-084-813-1135
; Sequence 1135, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1135
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1135

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||

RESULT 44
US-10-084-813-1136
; Sequence 1136, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1136
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1136

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||

RESULT 45
US-10-084-813-1137
; Sequence 1137, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1137
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1137

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||
```

```
Db      8 S L T L T 12
|||||
RESULT 46
US-10-084-813-1138
; Sequence 1138, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1138
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1138
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 S L T L T 5
Db      8 S L T L T 12
|||||
RESULT 47
US-10-084-813-1139
; Sequence 1139, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1139
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1139
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 S L T L T 5
Db      8 S L T L T 12
|||||
RESULT 48
US-10-084-813-1140
; Sequence 1140, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1140
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1140
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 S L T L T 5
Db      8 S L T L T 12
|||||
RESULT 49
US-10-084-813-1146
; Sequence 1146, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1146
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1146
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 S L T L T 5
Db      8 S L T L T 12
|||||
RESULT 50
US-10-084-813-1147
; Sequence 1147, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
```

```
US-10-084-813-1145
; Sequence 1145, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1145
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1145
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 S L T L T 5
Db      8 S L T L T 12
|||||
RESULT 49
US-10-084-813-1146
; Sequence 1146, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1146
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1146
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 S L T L T 5
Db      8 S L T L T 12
|||||
RESULT 50
US-10-084-813-1147
; Sequence 1147, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
```


; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1147

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 51
US-10-084-813-1148
; Sequence 1148, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1148
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1148

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 52
US-10-084-813-1207
; Sequence 1207, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1207
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1207

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 53
US-10-084-813-1208
; Sequence 1208, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1208
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1208

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 54
US-10-084-813-1209
; Sequence 1209, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1209
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1209

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 55
US-10-084-813-1210
; Sequence 1210, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1210
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1210

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 56
US-10-084-813-1216
; Sequence 1216, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1216

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 57
US-10-084-813-1217
; Sequence 1217, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1217
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1217

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 58
US-10-084-813-1218
; Sequence 1218, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1218
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1218

Query Match      27.8%; Score 5; DB 15; Length 15;
```

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
|||||
Db 8 SLTTLT 12

RESULT 59
US-10-084-813-1219
; Sequence 1219, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1219
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1219

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
|||||
Db 8 SLTTLT 12

RESULT 60
US-10-084-813-1220
; Sequence 1220, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1220
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1220

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
|||||

Db 8 SLTTLT 12

RESULT 61
US-10-084-813-1221
; Sequence 1221, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1221
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1221

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
|||||
Db 8 SLTTLT 12

RESULT 62
US-10-084-813-1222
; Sequence 1222, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1222
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1222

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
|||||
Db 8 SLTTLT 12

RESULT 63
US-10-084-813-1224

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; Sequence 1224, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1224
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1224

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
DB 8 SLTLT 12

RESULT 64
US-09-829-855-227
; Sequence 227, Application US/09829855
; Patent No. US20020065609A1
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Benzene mineralizing clone SB-1
US-09-829-855-227

Query Match      27.8%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17
DB 4 PLPLV 8

RESULT 65
US-10-299-003-14
; Sequence 14, Application US/10299003
; Publication No. US2003013924A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar

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; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavcigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; OTHER INFORMATION: Mus musculus
US-10-299-003-14

Query Match      27.8%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPL 14
DB 3 LHLPL 7

RESULT 66
US-10-084-813-552
; Sequence 552, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 552
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-552

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
DB 12 SLTLT 16

RESULT 67
US-10-084-813-553
; Sequence 553, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 553
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-553

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; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 553
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-553

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 11 SLTLT 15

RESULT 68
US-10-084-813-554
; Sequence 554, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 554
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-554

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 10 SLTLT 14

RESULT 69
US-10-084-813-770
; Sequence 770, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
```

```
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 770
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-770

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 14 SLTLT 18

RESULT 70
US-10-084-813-771
; Sequence 771, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 771
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-771

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 13 SLTLT 17

RESULT 71
US-10-084-813-772
; Sequence 772, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
```

```
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-772

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 12 SLTTLT 16

RESULT 72
US-10-084-813-773
/ Sequence 773, Application US/10084813
/ Publication No. US20030068615A1
/ GENERAL INFORMATION:
/ APPLICANT: SAXINGER, CARL
/ TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
/ FILE REFERENCE: 215875
/ CURRENT FILING DATE: 2002-02-27
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/151,270
/ PRIOR FILING DATE: 1999-08-27
/ NUMBER OF SEQ ID NOS: 1242
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 773
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-773

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 11 SLTTLT 15

RESULT 73
US-10-084-813-774
/ Sequence 774, Application US/10084813
/ Publication No. US20030068615A1
/ GENERAL INFORMATION:
/ APPLICANT: SAXINGER, CARL
/ TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
/ FILE REFERENCE: 215875
/ CURRENT FILING DATE: 2002-02-27
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/151,270
/ PRIOR FILING DATE: 1999-08-27
/ NUMBER OF SEQ ID NOS: 1242
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 774
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
```

US-10-084-813-774

```
Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SLTTLT 5
Db 10 SLTTLT 14
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RESULT 74

```
US-09-829-855-225
/ Sequence 225, Application US/09829855
/ Patent No. US20020065609A1
/ GENERAL INFORMATION:
/ APPLICANT: Matthew, Ashby N.
/ TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
/ FILE REFERENCE: ASHEY-1
/ CURRENT APPLICATION NUMBER: US/09/829,855
/ CURRENT FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: US 60/196063
/ PRIOR FILING DATE: 2000-04-10
/ PRIOR APPLICATION NUMBER: US 60/196258
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 244
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 225
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Desulfobulbus sp. BG25
US-09-829-855-225
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Query Match      27.8%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 13 PLPLV 17
Db 4 PLPLV 8
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RESULT 75

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US-09-983-802-664
/ Sequence 664, Application US/09983802
/ Publication No. US20030022185A1
/ GENERAL INFORMATION:
/ APPLICANT: Fischer et al.
/ TITLE OF INVENTION: 123 Human Secreted Proteins
/ FILE REFERENCE: PZ010P1
/ CURRENT APPLICATION NUMBER: US/09/983,802
/ CURRENT FILING DATE: 2001-10-25
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
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/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-664

Query Match      27.8%; Score 5; DB 11; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 LPLPL 16
Db      1 LPLPL 5

Search completed: November 25, 2003, 20:37:00
Job time : 28.8837 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-23
Perfect score: 18
Sequence: 1 SLRLTDEKHLPLPLVQ 18

Scoring table: OLIIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
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- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	4	US-09-641-803-23
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3	5	27.8	15	3	US-08-602-999A-407
4	5	27.8	15	4	US-09-500-124-385
5	5	27.8	15	4	US-09-500-124-407
6	5	27.8	17	4	US-09-140-749-14
7	5	27.8	20	4	US-09-227-357-664
8	4	22.2	5	3	US-09-202-832-6
9	4	22.2	6	1	US-08-212-433A-32
10	4	22.2	6	3	US-08-716-256-32
11	4	22.2	6	4	US-09-211-877-1
12	4	22.2	6	5	PCT-US95-03239-32
13	4	22.2	7	1	US-08-081-539-113
14	4	22.2	7	1	US-08-466-647-113
15	4	22.2	7	4	US-09-904-615-132
16	4	22.2	8	1	US-08-320-373-78
17	4	22.2	9	1	US-08-454-207A-44
18	4	22.2	9	1	US-08-787-547-91
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20	4	22.2	9	3	US-09-510-738A-84
21	4	22.2	9	3	US-09-510-738A-126
22	4	22.2	9	3	US-08-197-484-38
23	4	22.2	9	4	US-08-766-596A-9
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66	4	22.2	14	1	US-08-440-391-11
67	4	22.2	14	1	US-08-476-537-82
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92	4	22.2	16	1	US-07-942-245-154
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94	4	22.2	16	2	US-08-647-960-18
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96	4	22.2	16	3	US-08-602-999A-234
97	4	22.2	16	4	US-09-180-100-25
98	4	22.2	16	4	US-08-182-967-28
99	4	22.2	16	4	US-09-500-124-234
100	4	22.2	17	1	US-07-798-776-16

ALIGNMENTS

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RESULT 1
US-09-641-803-23
; Sequence 23, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-23
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Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLDVKKHLPLVQ 18
Db 1 SLTLDVKKHLPLVQ 18

RESULT 2
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
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; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385
Query Match 27.8%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
Db 10 LPLPL 14

RESULT 3
US-08-602-999A-407
; Sequence 407, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-407
Query Match 27.8%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 12 LPLPL 16
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Db 3 LPLPL 7

RESULT 4
US-09-500-124-385
; Sequence 385, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-385

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
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Db 10 LPLPL 14

RESULT 5
US-09-500-124-407
; Sequence 407, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-407

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
| | | | |
Db 3 LPLPL 7

RESULT 6
US-09-140-749-14
; Sequence 14, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtligian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0

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; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-14

Query Match      27.8%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred.No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LHLPL 14
        |||||
Db      3 LHLPL 7

RESULT 7
US-09-227-357-664
; Sequence 664, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
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; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-664

Query Match      27.8%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred.No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 LPLPL 16
        |||||
Db      1 LPLPL 5

RESULT 8
US-09-202-832-6
; Sequence 6, Application US/09202832
; Patent No. 6194190
; GENERAL INFORMATION:
; APPLICANT: IZU, Yukiko
; APPLICANT: TANAKA, Tetsuki
; APPLICANT: MIYAGI, Masaru
; APPLICANT: TANIGAWA, Tetsuo
; APPLICANT: TOMONO, Jun
; APPLICANT: TSUNASAWA, Susumu
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
; FILE REFERENCE: 1422-368P
; CURRENT APPLICATION NUMBER: US/09/202,832
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa = N-acetyl-glycine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: Peptide
US-09-202-832-6

Query Match      22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 DVEK 9
        |||||
Db      2 DVEK 5
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RESULT 9
US-08-212-433A-32
; Sequence 32, Application US/08212433A
; Patent No. 5538897
; GENERAL INFORMATION:
; APPLICANT: Yates, III, John R.
; APPLICANT: Eng, James K.
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
; TITLE OF INVENTION: DATABASES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,433A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Hughes, Richard L.
; REGISTRATION NUMBER: 31,264
; REFERENCE/DOCKET NUMBER: 16336-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-433A-32

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 10
US-08-716-256-32
; Sequence 32, Application US/08716256
; Patent No. 6017693
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,256
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-256-32

Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 11
US-09-211-877-1
; Sequence 1, Application US/09211877
; Patent No. 8458766
; GENERAL INFORMATION:
; APPLICANT: Fenical, William
; APPLICANT: Jensen, Paul R.
; APPLICANT: Rowley, David C.
; TITLE OF INVENTION: Halovir, An Antiviral Marine Natural Product, and
; FILE REFERENCE: P-UD 3148
; CURRENT APPLICATION NUMBER: US/09/211,877
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Scytalidium CNL240
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Aib;
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: leucinol
US-09-211-877-1

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLVQ 18
Db 2 PLVQ 5

RESULT 12
PCT-US95-03239-32
; Sequence 32, Application PC/TUS9503239
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
```

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; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-03239-32

Query Match 22.2%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 13
US-08-081-539-113
; Sequence 113, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,539
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-647-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 14
US-08-466-647-113
; Sequence 113, Application US/08466647
; Patent No. 5543141
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,539
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-647-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-081-539-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 14
US-08-466-647-113
; Sequence 113, Application US/08466647
; Patent No. 5543141
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,539
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-647-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 13 PLPL 16
||||
Db 3 PLPL 6

RESULT 15

US-09-904-615-132
; Sequence 132: Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-615-132

Query Match 22.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 LTLT 5
||||
Db 3 LTLT 6

RESULT 16

US-08-320-373-78
; Sequence 78, Application US/08320373
; Patent No. 5559025
; GENERAL INFORMATION:
; APPLICANT: Ahorn, Horst
; APPLICANT: Maurer-Poggy, Ingrid
; APPLICANT: Sommergruber, Wolfgang
; APPLICANT: Zophel, Andreas
; APPLICANT: Blaas, Dieter
; APPLICANT: Kuchler, Ernst
; APPLICANT: Liebig, Hans-Dieter
; APPLICANT: Skern, Timothy
; TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
; TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates
; TITLE OF INVENTION: Having an Inhibitory Effect
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/08/320,373
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/971,619
; FILING DATE: 06-NOV-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-320-373-78

Query Match 22.2%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 14 LPLV 17
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Db 4 LPLV 7

RESULT 17

US-08-454-207A-44
; Sequence 44, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0183
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-454-207A-44

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 9 KLHL 12
||||

Db 4 KLHL 7

RESULT 18

US-08-787-547-91

; Sequence 91, Application US/08787547

; Patent No. 5783567

; GENERAL INFORMATION:

; APPLICANT: Hedley, Mary Lynne

; APPLICANT: Curley, Joanne M.

; APPLICANT: Langer, Robert S.

; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY

; TITLE OF INVENTION: OF NUCLEIC ACID

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08787,547

; FILING DATE: 22-JAN-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 08191/003001

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 91:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-787-547-91

Query Match 22.2%; Score 4; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12

Db 1 KLHL 4

RESULT 19

US-08-630-645-9

; Sequence 9, Application US/08630645

; Patent No. 5948763

; GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED

; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,645

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-630-645-9

Query Match 22.2%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db 5 PLPL 8

RESULT 20

US-09-510-738A-84

; Sequence 84, Application US/09510738A

; Patent No. 6268165

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP-A

; CURRENT APPLICATION NUMBER: US/09/510,738A

; CURRENT FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 188

; SEQ ID NO 84

; LENGTH: 9

; TYPE: PPT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 264-272 of the hepsin protein

US-09-510-738A-84

Query Match 22.2%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db 3 PLPL 6

RESULT 21

US-09-510-738A-126
; Sequence 126, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 265-273 of the hepsin protein
US-09-510-738A-126

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db ||||
2 PLPL 5

RESULT 22
US-09-510-738A-170
; Sequence 170, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 170
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 264-272 of the hepsin protein
US-09-510-738A-170

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db ||||
3 PLPL 6

RESULT 23
US-08-197-484-38
; Sequence 38, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY

; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-38

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
Db ||||
1 KLHL 4

RESULT 24
US-08-766-596A-9
; Sequence 9, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-9

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 13 PLPL 16
Db 5 PLPL 8

RESULT 25
US-09-861-966-84
Sequence 84, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-A/Div
CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 84
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 264-272 of the hepsin protein

US-09-861-966-84

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 26

US-09-861-966-126
Sequence 126, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-A/Div
CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 126
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 265-273 of the hepsin protein

US-09-861-966-126

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 13 PLPL 16
Db 2 PLPL 5

RESULT 27
US-09-861-966-170
Sequence 170, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-A/Div
CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 170
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 264-272 of the hepsin protein

US-09-861-966-170

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 28
US-09-311-784A-174
Sequence 174, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Ciesnut, Robert W.
APPLICANT: Epimmune Inc.

```

; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV pol 489 (peptide 927.46)
US-09-311-784A-174

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
      ||||
Db      1 KLHL 4

RESULT 29
US-09-369-247-157
; Sequence 157, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024p1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-157

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 EKLH 11
      ||||
Db      3 EKLH 6

RESULT 30
PCT-US95-02121-38
; Sequence 38, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-38

Query Match      22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
      ||||
Db      1 KLHL 4

RESULT 31
PCT-US96-10220-9
; Sequence 9, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326

```

```
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-10220-9

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 5 PLPL 8

RESULT 32
5223606-10
; Patent No. 5223606
; APPLICANT: BLAUDIN DE THE, HUGHES, MARCHIO, AGNES, TIOLLAIS,
; PIERRE, DEJEAN, ANNE
; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/134,130
; FILING DATE: 17-DEC-1987
; PRIOR APPLICATION DATA:
; SEQ ID NO: 10:
; LENGTH: 9
5223606-10

Query Match 22.2%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLVQ 18
Db 6 PLVQ 9

RESULT 33
US-08-159-339A-351
; Sequence 351, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 351:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-351

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
Db 6 KLHL 9

RESULT 34
US-08-159-339A-352
; Sequence 352, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
```

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 352:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-159-339A-352

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12
Db 6 KLHL 9

RESULT 35

US-08-159-339A-353
Sequence 353, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.

APPLICANT: Sette, Alessandro

APPLICANT: Celis, Esben

TITLE OF INVENTION: HLA Binding peptides and Their Uses

NUMBER OF SEQUENCES: 1254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX:

INFORMATION FOR SEQ ID NO: 353:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-159-339A-353

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12
Db 6 KLHL 9

RESULT 36

US-08-908-643C-17

Sequence 17, Application US/08908643C

Patent No. 6120995

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

Pearlman, Joshua M.

Barber, Michael T.

Schultz, Stephanie

Parkinson, Scott J.

TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO
COLORECTAL CANCER CELLS AND METHODS OF
USING THE SAME

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,643C

FILING DATE: 07-Aug-1997

CLASSIFICATION: N/A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mark Deluca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUU-2209

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-08-908-643C-17

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LHLP 13
Db 10 LHLP 13

```
Db      4  HLPL 7

RESULT 37
US-08-637-759B-220
; Sequence 220, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS: 501
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-220

Query Match      22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11  HLPL 14
Db      5  HLPL 8

RESULT 38
US-08-637-759B-220
; Sequence 220, Application US/08637759B
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-220

Query Match      22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11  HLPL 14
Db      5  HLPL 8

RESULT 39
US-09-201-945-220
; Sequence 220, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-871-355A-220

Query Match      22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11  HLPL 14
Db      5  HLPL 8
```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 873-8794
 TELEFAX: (404) 873-8795
 INFORMATION FOR SEQ ID NO: 220:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 US-09-201-945-220

Query Match 22.2%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 HLPL 14
 Db 5 HLPL 8

RESULT 40

US-07-756-250-3
 Sequence 3, Application US/07756250
 Patent No. 5268275

GENERAL INFORMATION:
 APPLICANT: Wu, Sheue-Mei
 APPLICANT: Staiford, Darrel W.
 TITLE OF INVENTION: Vitamin K-Dependent Carboxylase
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
 ADDRESSEE: Gibson
 STREET: Post Office Drawer 34009
 CITY: Charlotte
 STATE: No. 5268275th Carolina
 COUNTRY: U.S.A.
 ZIP: 28234

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/756,250
 FILING DATE: 19910909
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/697,427
 FILING DATE: 08-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Sibley, Kenneth D.
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5470-34
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-881-3140
 TELEFAX: 919-881-3175
 TELEX: 575102

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-756-250-3

Query Match 22.2%; Score 4; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 PLVQ 18

Db 7 PLVQ 10

RESULT 41

US-08-178-554-1
 Sequence 1, Application US/08178554
 Patent No. 5446019

GENERAL INFORMATION:
 APPLICANT: ELY, SUSAN
 APPLICANT: TIPPETT, JANET MARY
 TITLE OF INVENTION: BACTERIAL STRAIN
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3918

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/178,554
 FILING DATE: 06-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9300124.6
 FILING DATE: 06-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 206082/SEE 37367/US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-178-554-1

Query Match 22.2%; Score 4; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 Db 3 SLTL 6

RESULT 42

US-08-036-555B-164
 Sequence 164, Application US/08036555B
 Patent No. 5530109

GENERAL INFORMATION:
 APPLICANT: Goodearl, Andrew; Stroobant, Paul;
 APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
 APPLICANT: Chen, Maio Su; Hiles, Ian
 TITLE OF INVENTION: Glial Mitogenic Factors, Their
 TITLE OF INVENTION: Preparation and Use
 NUMBER OF SEQUENCES: 184
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York

```

; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-036-555B-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 43
US-08-469-569-164
; Sequence 164, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Mao Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM

```

```

; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-569-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 44
US-08-249-322A-164
; Sequence 164, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Mao Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teal, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-249-322A-164

```

```

Query Match          22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 DVEK 9
Db      9 DVEK 12

```

```

RESULT 45
US-08-469-526A-164
; Sequence 164, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Maio Su
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-526A-164

```

```

Query Match          22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 DVEK 9
Db      9 DVEK 12

```

```

RESULT 46
US-08-734-591A-164
; Sequence 164, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A

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FILING DATE: 22-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,335
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-591A-164

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
DB 9 DVEK 12

RESULT 47
US-08-469-660-164
Sequence 164, Application US/08469660
Patent No. 5876973
GENERAL INFORMATION:
APPLICANT: Gwynne, David I.; Marchionni, Mark;
APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIP: 02111-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,660

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,396
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/984,085
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/927,337
FILING DATE: 10-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/017004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-660-164

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
DB 9 DVEK 12

RESULT 48
US-09-371-710-41
Sequence 41, Application US/09371710A
Patent No. 6146868
GENERAL INFORMATION:
APPLICANT: Kozel, Thomas R.
APPLICANT: Bloomer, Sherri L.
APPLICANT: Savoy, Anne C.
TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
FILE REFERENCE: D6245
CURRENT APPLICATION NUMBER: US/09/371,710A
CURRENT FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: associated amino acid sequence of PCR primer 45-mer
US-09-371-710-41

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
DB 3 KLHL 6

RESULT 49
US-08-470-335-164

; Sequence 164, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470.335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-335-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 6 DVEK 9
Db 9 DVEK 12

RESULT 50
US-08-602-999A-253
; Sequence 253, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602.999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-253

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 12 LPLP 15
Db 6 LPLP 9

RESULT 51
US-08-735-021-164
; Sequence 164, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in 1 is unknown.
US-08-735-021-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 6 DVEK 9
Db 9 DVEK 12

RESULT 52
US-08-734-664A-164

Qy 6 DVEK 9

```

1  RESULT 54
2  US-09-648-386-41
3  ; Sequence 41, Application US/09648386
4  ; Patent No. 6284508
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Kozel, Thomas R.
7  ; APPLICANT: Bloomer, Sherri L.
8  ; APPLICANT: Savoy, Anne C.
9  ; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
10 ; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
11 ; FILE REFERENCE: D6245D
12 ; CURRENT APPLICATION NUMBER: US/09/648,386
13 ; CURRENT FILING DATE: 2000-08-25
14 ; PRIOR APPLICATION NUMBER: US 09/371,710
15 ; PRIOR FILING DATE: 1999-08-09
16 ; NUMBER OF SEQ ID NOS: 50
17 ; SEQ ID NO 41
18 ; LENGTH: 12
19 ; TYPE: PRT
20 ; ORGANISM: Artificial sequence
21 ; FEATURE:

```

OTHER INFORMATION: associated amino acid sequence of PCR primer 45-mer
US-09-648-386-41

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12
Db 3 KLHL 6

RESULT 55

US-09-500-124-253
Sequence 253, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-253

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLP 15
Db 6 LPLP 9

RESULT 56

US-08-467-602-164

Sequence 164, Application US/08467602C
Patent No. 644642
GENERAL INFORMATION:
APPLICANT: Sklar, Robert
APPLICANT: Marchionni, Mark
APPLICANT: Gwynne, David I.
TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 04585/028003
CURRENT APPLICATION NUMBER: US/08/467,602C
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/209,204
EARLIER FILING DATE: 1994-03-08
EARLIER APPLICATION NUMBER: 08/059,022
EARLIER FILING DATE: 1993-05-06
NUMBER OF SEQ ID NOS: 420
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 164
LENGTH: 12
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-467-602-164

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9
Db 9 DVEK 12

RESULT 57

PCT-US94-05083C-160
Sequence 160, Application PC/TUS9405083C
GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: METHODS FOR ALTERING
TITLE OF INVENTION: MUSCLE CONDITION
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
MEDIUM TYPE: kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05083C
FILING DATE: 06-MAY-94
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-May-93
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/028W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is
; OTHER INFORMATION: unknown.
PCT-US94-05083C-160

Query Match 22.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
|||
Db 9 DVEK 12

RESULT 58
PCT-US95-06846A-164
; Sequence 164, Application PC/TUS9506846A
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Mao Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Felife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06846A
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5250.5

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
PCT-US95-06846A-164

Query Match 22.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
|||
Db 9 DVEK 12

RESULT 59
US-08-291-601-3
; Sequence 3, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,601
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9401M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-291-601-3

Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTLL 5
|||
Db 8 LTLL 11

RESULT 60
US-08-602-999A-92
; Sequence 92, Application US/08602999A

Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-92

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 13 PLPL 16
Db 5 PLPL 8

RESULT 61
US-09-177-249-248
; Sequence 248, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01

; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 248
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-248
Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 SLTL 4
Db 9 SLTL 12
RESULT 62
US-08-278-865-92
; Sequence 92, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: STC SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCJELLELAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite #00
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413 3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-92

Query Match 22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 13 PLPL 16
Db 5 PLPL 8

RESULT 63

US-09-500-124-92
; Sequence 92, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-92

Query Match 22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 5 PLPL 8

RESULT 64
US-07-956-700B-82
; Sequence 82, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-07-956-700B-82

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPL 13
Db 5 LHLPL 8

RESULT 65
US-08-258-851-6
; Sequence 6, Application US/08258851
; Patent No. 5585244
; GENERAL INFORMATION:
; APPLICANT: Elizabeth A. Allegretto
; APPLICANT: J. Wesley Pike
; TITLE OF INVENTION: DETECTION OF RETINOID
; TITLE OF INVENTION: RECEPTOR SUBTYPE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,851
; FILING DATE: 10 June 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

```
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
US-08-258-851-6

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLVQ 18
Db 10 PLVQ 13

RESULT 66
US-08-440-391-11
; Sequence 11, Application US/08440391
; Patent No. 5656725
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-440-391-11

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
Db 11 LPLV 14

RESULT 67
US-08-476-537-82
; Sequence 82, Application US/08476537
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; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-82

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLP 13
Db 5 LHLP 8

RESULT 68
US-08-485-607-82
; Sequence 82, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
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;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/956,700
;; FILING DATE: 10/21/92
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Thomas E. No. 5792627thrup
;; REGISTRATION NUMBER: 33,268
;; REFERENCE/DOCKET NUMBER: ARCD:058
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 1-312-744-0090
;; TELEFAX: 1-312-755-4489
;; INFORMATION FOR SEQ ID NO: 82:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: Amino acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Peptide
US-08-485-607-82

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 10 LHLP 13
|||
Db 5 LHLP 8

RESULT 69
US-08-908-597A-11
;; Sequence 11, Application US/08908597A
;; Patent No. 5863795
;; GENERAL INFORMATION:
;; APPLICANT: CHITTENDEN, Thomas D.; and
;; APPLICANT: LUTZ, Robert J.
;; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
;; TITLE OF INVENTION: MODULATE APOPTOSIS
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hale and Dorr
;; STREET: 1455 Pennsylvania Avenue, N.W.
;; CITY: Washington
;; STATE: D.C.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/908,597A
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/440,391
;; FILING DATE: 12-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WIXON, HENRY N.
;; REGISTRATION NUMBER: 32,073
;; REFERENCE/DOCKET NUMBER: 104322.147
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-942-8400
;; TELEFAX: 202-942-8484
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-908-597A-11

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 14 LPLV 17
|||
Db 11 LPLV 14

RESULT 70
US-08-764-640-34
;; Sequence 34, Application US/08764640
;; Patent No. 5869451
;; Patent No. 5869451 5837683
;; GENERAL INFORMATION:
;; APPLICANT: Dower, William J.
;; APPLICANT: Barrett, Ronald W.
;; APPLICANT: Cwirlla, Steven E.
;; APPLICANT: Gates, Christian
;; APPLICANT: Schatz, Peter J.
;; APPLICANT: Balasubramanian, Palaniappan
;; APPLICANT: Wagstrom, Christopher R.
;; APPLICANT: Hendren, Richard W.
;; APPLICANT: Depince, Randolph B.
;; APPLICANT: Podduturi, Surekha
;; APPLICANT: Yin, Qun
;; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;; TITLE OF INVENTION: RECEPTOR
;; NUMBER OF SEQUENCES: 244
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Glaxo Wellcome
;; STREET: Five Moore Drive, P.O. Box 13398
;; CITY: Research Triangle Park
;; STATE: NC
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/764,640
;; FILING DATE: 11-DEC-1996
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hrubiec, Robert T.
;; REGISTRATION NUMBER: 36,392
;; REFERENCE/DOCKET NUMBER: PK3281
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-248-1000
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-764-640-34

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 LTLT 5
|||
Db 5 LTLT 8

RESULT 71
US-08-475-879-82
;; Sequence 82, Application US/08475879
;; Patent No. 5972644

Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrupp
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-475-879-82

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLP 13
Db 5 LHLP 8
|||||

RESULT 72
US-08-973-225-34
; Sequence 34, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC

COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubic, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-973-225-34

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTLT 5
Db 5 LTLT 8
|||||

RESULT 73
US-09-244-298A-34
; Sequence 34, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,298A
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubic, Robert T.
; REGISTRATION NUMBER: 36,392

; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-34

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
|||
Db 5 LTLT 8
|||

RESULT 74
US-09-236-385A-11
; Sequence 11, Application US/09236385A
; Patent No. 6221615
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS

; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,385A
; FILING DATE: 25-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073

; (C) ATTORNEY DOCKET NO. 104322.147CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-236-385A-11

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
|||
Db 11 LPLV 14
|||

RESULT 75
US-09-516-704-34

; Sequence 34, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Gates, Christian
; Schatz, Peter J.
; Balasubramanian, Palaniappan
; Wagstrom, Christopher R.
; Hendren, Richard W.
; Deprince, Randolph B.
; Podduturi, Surekha
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/516,704
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-516-704-34

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
|||
Db 5 LTLT 8
|||

Search completed: November 25, 2003, 20:30:00
Job time : 15.5465 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.80233 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SMWQPP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR_76:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	42.9	7	S71299	ICL2 protein - Par
2	3	42.9	7	PT0283	Ig heavy chain CRD
3	3	42.9	10	PT0322	Ig heavy chain CRD
4	3	42.9	11	YHRT	morphogenetic neur
5	3	42.9	11	YHHU	morphogenetic neur
6	3	42.9	11	YHBO	morphogenetic neur
7	3	42.9	11	YHXAE	morphogenetic neur
8	3	42.9	11	YHJPHY	morphogenetic neur
9	3	42.9	12	PN0046	ATP synthase D cha
10	3	42.9	13	G61458	Ig lambda chain V-
11	3	42.9	15	B39109	hypothetical 1.5K
12	3	42.9	15	A60221	apolipoprotein A-I
13	3	42.9	17	S10786	enamelin, 26K - bo
14	3	42.9	19	PC1323	endopeptidase Clp
15	3	42.9	19	S59486	cell wall protein,
16	3	42.9	19	A37968	neural surface pro
17	3	42.9	20	S28779	octopamine recepto
18	2	28.6	4	PT0661	T-cell receptor be
19	2	28.6	5	A32516	cholecystokinin-5
20	2	28.6	5	B37988	acid proteinase li
21	2	28.6	5	PT0580	T-cell receptor be
22	2	28.6	6	A31263	dihydrofolate redu
23	2	28.6	6	A61068	locustakinin - mig
24	2	28.6	6	S71349	beta-crystallin B2
25	2	28.6	7	A61081	tryptophyllin, bas
26	2	28.6	7	PC1316	large granule L3 c
27	2	28.6	7	I46868	alpha-myosin heavy
28	2	28.6	7	A39690	neural cell adhesi
29	2	28.6	7	A58718	carnocin UI49 - Ca

30	2	28.6	7	PN0649	pullulanase (EC 3.
31	2	28.6	8	S10596	adipokinetic hormo
32	2	28.6	8	PQ0012	cholecystokinin -
33	2	28.6	8	A43001	cholecystokinin -
34	2	28.6	8	B24749	neuropeptide B - b
35	2	28.6	8	S43971	tumor-associated a
36	2	28.6	8	B39745	endoglycosylcerami
37	2	28.6	8	S16324	hypothetical prote
38	2	28.6	8	S21288	lectin - potato (f
39	2	28.6	8	PT0030	inulinase (EC 3.2.
40	2	28.6	8	JS0315	leucokinin V - Mad
41	2	28.6	8	JS0316	leucokinin VI - Ma
42	2	28.6	8	JS0317	leucokinin VII - M
43	2	28.6	8	JS0318	leucokinin VIII -
44	2	28.6	8	E47193	neuropeptide calla
45	2	28.6	8	A14683	aspartate transami
46	2	28.6	8	PT0368	Ig gamma chain C r
47	2	28.6	8	S10783	enamelin f - bovin
48	2	28.6	8	PT0559	T-cell receptor be
49	2	28.6	8	A38887	T-cell receptor ga
50	2	28.6	8	C39690	neural cell adhesi
51	2	28.6	8	A61102	parathyroid hormon
52	2	28.6	9	A24244	adipokinetic hormo
53	2	28.6	9	A61357	phyllocaerulein -
54	2	28.6	9	A61358	bradykinin-like pe
55	2	28.6	9	A61057	Thr-6 bradykinin -
56	2	28.6	9	A26744	bradykinin-like pe
57	2	28.6	9	A61363	bradykinin - commo
58	2	28.6	9	A60579	bradykinin-like pe
59	2	28.6	9	B60246	ornitho-kinin - ch
60	2	28.6	9	B41983	orf downstream to b
61	2	28.6	9	S55696	phosphoenolpyruvat
62	2	28.6	9	D57444	neuropeptide Grb-A
63	2	28.6	9	A61620	locustamyotropin I
64	2	28.6	9	S65433	bradykinin - horn
65	2	28.6	9	S77984	cytochrome-c oxida
66	2	28.6	9	PT0299	Ig heavy chain CRD
67	2	28.6	9	S26508	collagen alpha 2(V
68	2	28.6	9	I58350	gene c-mpl protein
69	2	28.6	9	B30572	T-cell receptor be
70	2	28.6	9	A43065	hydroxyproline-3-b
71	2	28.6	10	XAV16B	angiotensin-conver
72	2	28.6	10	XASNPC	angiotensin-conver
73	2	28.6	10	RHAQ1	gonadoliberin I -
74	2	28.6	10	SPPGNK	thyromedlin K - pig
75	2	28.6	10	JC1367	thyroliberin poten
76	2	28.6	10	A61337	caerulein - frog (
77	2	28.6	10	A13687	caerulein-like pep
78	2	28.6	10	PC2171	triacylglycerol li
79	2	28.6	10	S39030	lysyl-bradykinin -
80	2	28.6	10	S18396	probable glucosae-6
81	2	28.6	10	C35389	urease (EC 3.5.1.5
82	2	28.6	10	A59272	peptide-N4-(N-acet
83	2	28.6	10	B59272	peptide-N4-(N-acet
84	2	28.6	10	H28027	protein P11 - curl
85	2	28.6	10	A36454	trypsin-modulating
86	2	28.6	10	B37196	bradykinin-potenti
87	2	28.6	10	H37196	bradykinin-potenti
88	2	28.6	10	S26506	collagen alpha 1(V
89	2	28.6	10	S10785	enamelin, 22K - bo
90	2	28.6	10	B38887	T-cell receptor ga
91	2	28.6	10	S65387	cytochrome-c oxida
92	2	28.6	10	C30572	T-cell receptor be
93	2	28.6	10	PH0923	T-cell receptor be
94	2	28.6	10	B61218	alpha-gliadin 6Ha
95	2	28.6	10	S53789	neuropeptide Pec-H
96	2	28.6	11	XAV1BH	bradykinin-potenti
97	2	28.6	11	XASNEA	bradykinin-potenti
98	2	28.6	11	EOOCC	eledoisin - curled
99	2	28.6	11	BOCC	eledoisin - musky
100	2	28.6	11	D60409	kassinin-like pept

ALIGNMENTS

RESULT 1

S71299
ICL2 protein - Paramesitium tetraurelia (fragment)

C:Species: Paramesitium tetraurelia
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C:Accession: S71299
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A:Title: Characterization of centrin genes in Paramesitium.
A:Reference number: S71298; MUID:96248429; PMID:8665928
A:Accession: S71299
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGC5

Query Match 42.9%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 2

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0283
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0283
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 5 QPP 7

RESULT 3

PT0322
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0322
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0322
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
|||
Db 6 SWM 8

RESULT 4

YHRT
morphogenetic neuropeptide - rat

C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from C
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical str
C:Comment: This peptide was first isolated from nerve cells of hydra and was called
een found in mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutar
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 1 QPP 3

RESULT 5

YHHU
morphogenetic neuropeptide - human

C:Species: Homo sapiens (man)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from C
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: B01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical str
C:Comment: This peptide was first isolated from nerve cells of hydra and was called
malian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neur
P:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #s

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 1 QPP 3

RESULT 6

YHBO
morphogenetic neuropeptide - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: C01427; A01427
R;Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1991

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterate
A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427
A;Molecule type: protein
A;Residues: 1-11 <SCH>

R;Bir, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator

C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 1 QPP 3

RESULT 7

YHAE
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)
N;Alternate names: head activator
C;Species: Anthopleura elegantissima
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900

A;Accession: A93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>

R;Bir, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator

C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 1 QPP 3

RESULT 8

YHJFY
morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900

A;Accession: B93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>

R;Bir, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator

C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 1 QPP 3

RESULT 9

PN0046
ATP synthase D chain, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0046

R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne
A;Reference number: PN0041

A;Accession: PN0046
A;Molecule type: protein
A;Residues: 1-12 <KAR>

A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blo
C;Keywords: brain; mitochondrion

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6
Db 6 QPP 8

RESULT 10

G61458
Ig lambda chain V-II region (AZI) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C;Accession: G61458; PLO159

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-a
A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Accession: G61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>

C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glyco
C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 6 QPP 8

RESULT 11
 B39109
 hypothetical 1.5K protein - hepatitis C virus
 N:Alternate names: hypothetical protein 2
 C:Species: hepatitis C virus
 C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
 C:Accession: B39109; JQ1585
 R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
 A:Reference number: A39109; MUID:91156678; PMID:1705704
 A:Accession: B39109
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-15 <HAN>
 A:Cross-references: GB:MS8406
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A:Title: Cloning and sequencing of the structural region and expression of putative core
 A:Reference number: JQ1584; MUID:92300349; PMID:1318944
 A:Accession: JQ1585
 A:Molecule type: genomic RNA
 A:Residues: 1-15 <KUM>
 A:Experimental source: strain U.K.

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 5 QPP 7

RESULT 12
 A60221
 apolipoprotein A-I - common carp (fragment)
 C:Species: Cyprinus carpio (common carp)
 C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
 C:Accession: A60221
 R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
 J. Neurochem. 55, 1237-1243, 1990
 A:Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve reg
 A:Reference number: A60221; MUID:90376100; PMID:2118944
 A:Accession: A60221
 A:Molecule type: protein
 A:Residues: 1-15 <HAR>
 A>Note: protein from plasma and from optic nerve yielded the same sequence
 C:Keywords: lipid binding; lipoprotein

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 2 QPP 4

RESULT 13
 S10786
 enamelin, 26K - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C:Accession: S10786
 R:Strawich, E.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is
 A:Reference number: S10780; MUID:90336641; PMID:2379503
 A:Accession: S10786
 A:Molecule type: protein
 A:Residues: 1-17 <STR>
 C:Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 14
 PC1323
 endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chloroi
 C:Species: chloroplast Nicotiana glauca (curled-leaved tobacco)
 C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-2000
 C:Accession: PC1323
 R:Fejes, E.; Engler, D.; Maliga, P.
 Theor. Appl. Genet. 79, 28-32, 1990
 A:Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana so
 A:Reference number: PC1321
 A:Accession: PC1323
 A:Molecule type: DNA
 A:Residues: 1-19 <FEJ>
 C:Genetics:
 A:Genome: chloroplast
 C:Function:
 A>Description: ATP-driven cleavage of proteins to small peptides
 A>Note: magnesium required
 C:Superfamily: endopeptidase Clp chain P
 C:Keywords: ATP; chloroplast; hydrolase; serine proteinase
 F3/Active site: His #status predicted

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6
 |||
 Db 3 QPP 5

RESULT 15
 S59486
 cell wall protein, 22K - kidney bean (fragment)
 C:Species: Phaseolus vulgaris (kidney bean)
 C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S59486
 R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to diff.
 A:Reference number: S59481; MUID:96011753; PMID:7548825
 A:Accession: S59486
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <WOJ>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 16
A37968
neural surface protein Bravo - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997
C;Accession: A37968; A36345
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
J. Cell Biol. 112, 1049, 1991
A;Reference number: A37968; MUID:91154309; PMID:1999455
A;Contents: erratum
A;Accession: A37968
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
J. Cell Biol. 111, 3087-3096, 1990
A;Title: Topologically restricted appearance in the developing chick retinotectal system
A;Reference number: A36345; MUID:91100421; PMID:2269667
A;Accession: A36345
A;Molecule type: protein
A;Residues: 1-7, 9-19 <DE2>

Query Match 42.9%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
DB 15 QPP 17

RESULT 17
S28779
Octopamine receptor - common eastern firefly (fragment)
C;Species: Photinus pyralis (common eastern firefly)
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 23-Feb-1997
C;Accession: S28779
R;Nathanson, J.A.; Kantham, L.; Hunnicutt, E.J.
FEBS Lett. 259, 117-120, 1989
A;Title: Isolation and N-terminal amino acid sequence of an octopamine ligand binding pr
A;Reference number: S28779; MUID:90092510; PMID:2513233
A;Accession: S28779
A;Molecule type: protein
A;Residues: 1-20 <NAT>
C;Keywords: G protein-coupled receptor; membrane protein; neurotransmitter receptor

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
DB 18 MHQ 20

RESULT 18
PT0661
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0661
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0661
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
DB 2 SW 3

RESULT 19
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
A;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
||
DB 2 WM 3

RESULT 20
B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C;Species: Physarum polycephalum
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C;Accession: B37988
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki
J. Biol. Chem. 265, 19898-19903, 1990
A;Title: Purification and characterization of a novel intracellular acid proteinase f
A;Reference number: A37988; MUID:91060608; PMID:2246266
A;Accession: B37988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MUR>

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
DB 3 PP 4

RESULT 21
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580

A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 3 SW 4

RESULT 22

A31263
 C;Species: Plasmodium falciparum
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C;Accession: A31263

R;Peterson, D.S.; Walliker, D.; Wellem, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A;Reference number: A34217; PMID:89057886; PMID:2904149

A;Accession: A31263

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-6 <PPT>

C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 2 SW 3

RESULT 23

A61068
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
 C;Accession: A61068
 R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
 Regul. Pept. 37, 49-57, 1992

A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri

A;Reference number: A61068; PMID:92262851; PMID:1585017

A;Accession: A61068

A;Molecule type: protein

A;Residues: 1-6 <SCH>

C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide

F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 4 SW 5

RESULT 24

S71349
 beta-crystallin B2 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999
 C;Accession: S71349
 R;Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers, J.
 Eur. J. Biochem. 239, 23-32, 1996

A;Title: The cooperation between two silencers creates an enhancer element that cont;

A;Reference number: S71349; PMID:96305362; PMID:8706714

A;Accession: S71349

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-6 <DIR>

A;Cross-references: EMBL:X83671

A;Experimental source: strain Wistar; lens epithelial cells

C;Genetics:

A;Gene: CRYBB2

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
 ||
 Db 5 HQ 6

RESULT 25

A61081
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C;Accession: A61081
 R;Montecucchi, P.C.; Vincenti, M.; Lazarini, A.M.; Rusconi, L.; Erspamer, V.
 Int. J. Pept. Protein Res. 33, 391-395, 1989

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-cont.

A;Reference number: A61081

A;Accession: A61081

A;Molecule type: protein

A;Residues: 1-7 <WON>

C;Comment: The biological activity of this peptide was not determined.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hydroxyproline; skin

F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 4 SW 5

RESULT 26

PC1316
 large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
 C;Species: Tachyplesus tridentatus
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: PC1316
 R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.;
 J. Biochem. 114, 307-316, 1993

A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus trid

A;Reference number: PC1309; PMID:94110249; PMID:8282718

A;Accession: PC1316

A;Molecule type: protein

A;Residues: 1-7 <SHI>

C;Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 3 QP 4

RESULT 27

I46868
 alpha-myosin heavy chain - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: I46868
 R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
 A>Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular
 A:Reference number: I46868; MUID:84221901; PMID:6328491
 A:Accession: I46868
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <FRT>
 A:Cross-references: GB:X01698; NID:G165538; PIDN:AAA1415.1; PID:G165539

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
 ||
 Db 3 MH 4

RESULT 28
 A39690
 neural cell adhesion molecule, cardiac splice form -, -, - - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C:Accession: A39690
 R:Reyes, A.A.; Small, S.J.; Akeson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m
 A:Reference number: A39690; MUID:91141516; PMID:1996115
 A:Accession: A39690
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-7 <REY>
 A:Cross-references: GB:M63970
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 1 QP 2

RESULT 29
 A58718
 carnocin UI49 - Carnobacterium sp. (fragment)
 C:Species: Carnobacterium sp.
 C>Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 C:Accession: A58718
 R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
 Appl. Environ. Microbiol. 58, 1417-1422, 1992
 A>Title: Purification and characterization of a new bacteriocin isolated from a Carnobac
 A:Reference number: A58718; MUID:92321768; PMID:1622206
 A:Accession: A58718
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <STO>
 C:Keywords: antibiotic; lanthionine

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 5 QP 6

RESULT 30
 PN0649
 pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
 C:Species: Bacillus sp.
 C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
 C:Accession: PN0649
 R:Kim, C.H.; Choi, H.I.; Lee, D.S.
 Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
 A>Title: Purification and biochemical properties of an alkaline pullulanase from alka
 A:Reference number: PN0649; MUID:94080025; PMID:7764261
 A:Accession: PN0649
 A:Molecule type: protein
 A:Residues: 1-7 <KIM>
 C:Comment: This enzyme is used together with glucoamylase to improve the efficiency of
 nent in high maltose syrups.
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 5 SW 6

RESULT 31
 S10596
 adipokinetic hormone - pond skimmer
 C:Species: Libellula auripennis
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
 C:Accession: S10596
 R:Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A>Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating
 A:Reference number: S10596; MUID:90359055; PMID:2390213
 A:Accession: S10596
 A:Molecule type: protein
 A:Residues: 1-8 <BIO>
 C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
 F;8/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 7 SW 8

RESULT 32
 PQ0012
 cholecystokinin - southeastern quoll
 N:Alternate names: CCK
 C:Species: Dasyurus viverrinus (southeastern quoll)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
 C:Accession: PQ0012
 R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
 Peptides 9, 429-431, 1988
 A>Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
 A:Reference number: PQ0012; MUID:88234141; PMID:3375140
 A:Accession: PQ0012
 A:Molecule type: protein
 A:Residues: 1-8 <FAN>
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
 F;2/Binding site: sulfate (Tyr) (covalent) #status predicted

F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 WM 3
||
5 WM 6

RESULT 33

A43001
cholecystokinin - tamar wallaby
N;Alternate names: CCK
C;Species: Macropus eugenii (tamar wallaby)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C;Accession: A43001; PQ0012
Peptides 9, 429-431, 1998
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: A43001
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 WM 3
||
5 WM 6

RESULT 34

B24749
neuropeptide B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C;Accession: B24749
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two
A;Reference number: A94074; MUID:86067985; PMID:3865193
A;Accession: B24749
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 QP 6
||
4 QP 5

RESULT 35

S43971
tumor-associated antigen MUT1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: S43971
R;Hendelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A;Reference number: S43971; MUID:94217811; PMID:8164742
A;Accession: S43971
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAN>
C;Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 QP 6
||
7 QP 8

RESULT 36

B39745
endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)
C;Species: Rhodococcus sp.
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 31-Dec-1993
C;Accession: B39745
R;Ito, M.; Ikegami, Y.; Yanagata, T.
J. Biol. Chem. 266, 7919-7926, 1991.
A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases.
Die using these activator proteins.

A;Reference number: A39745; MUID:91210321; PMID:1850427
A;Accession: B39745
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <ITO>
C;Keywords: glycosidase; hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 6 PP 7
||
2 PP 3

RESULT 37

S16324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991.
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked
A;Reference number: S16323; MUID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
A;Cross-references: EMBL:X58821; NID:G16327; PIDN:CAA41624.1; PID:G579259

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 6 PP 7
||
7 PP 8

RESULT 38

S21288
lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A;Title: Chitin-binding proteins in potato (*Solanum tuberosum* L.) tuber. Characterization
 A;Reference number: S21288; PMID:92272683; PMID:1590771
 A;Accession: S21288
 A;Molecule type: protein
 A;Residues: 1-8 <MIL>
 A;Experimental source: var. Ulster Sceptre
 C;Function:
 A;Description: may be involved in defence mechanism of the plant
 C;Keywords: hydroxyproline, lectin

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 ||
 Db 7 PP 8

RESULT 39
 PT0030
 inulinase (EC 3.2.1.7) - *Aspergillus ficuum* (fragment)
 N;Alternate names: inulase
 C;Species: *Aspergillus ficuum*
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
 C;Accession: PT0030
 R;Etalib, M.; Baratti, J.C.
 Agric. Biol. Chem. 54, 61-68, 1990
 A;Title: Molecular and kinetic properties of *Aspergillus ficuum* inulinases.
 A;Reference number: PT0030; PMID:90344234; PMID:1368526
 A;Accession: PT0030
 A;Molecule type: protein
 A;Residues: 1-8 <ETT>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 5 QP 6

RESULT 40
 JS0315
 Leucokinin V - Madeira cockroach
 C;Species: *Leucophaea maderae* (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0315
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropin
 A;Reference number: JS0315
 A;Accession: JS0315
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 6 SW 7

RESULT 41
 JS0317
 Leucokinin VII - Madeira cockroach
 C;Species: *Leucophaea maderae* (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0317
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 31-34, 1987
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the
 A;Reference number: JS0317
 A;Accession: JS0317
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 6 SW 7

RESULT 43
 JS0318
 Leucokinin VIII - Madeira cockroach
 C;Species: *Leucophaea maderae* (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0318
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 31-34, 1987
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the
 A;Reference number: JS0317
 A;Accession: JS0318
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 6 SW 7

JS0316
 Leucokinin VI - Madeira cockroach
 C;Species: *Leucophaea maderae* (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0316
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropin
 A;Reference number: JS0315
 A;Accession: JS0316
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
 F;8/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 6 SW 7

RESULT 42
 JS0317
 Leucokinin VII - Madeira cockroach
 C;Species: *Leucophaea maderae* (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0317
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 31-34, 1987
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the
 A;Reference number: JS0317
 A;Accession: JS0317
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 6 SW 7

Qy 1 SW 2
||
6 SW 7

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
||
Db 2 HQ 3

RESULT 44

E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C:Accession: E47393
R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequen
A:Reference number: A47393; MUID:93211980; PMID:8460157
A:Accession: E47393
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Experimental source: whole flies
A>Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 2 PP 3

RESULT 45

A14683
aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Gallus gallus (chicken)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C:Accession: A14683
R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.
FEBS Lett. 108, 98-102, 1979
A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
A:Reference number: A14683; MUID:80092116; PMID:520566
A:Accession: A14683
A:Molecule type: protein
A:Residues: 1-8 <WIL>
C:Keywords: aminotransferase; mitochondrion

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
||
Db 6 QP 7

RESULT 46

PT0368
IG gamma chain C region (gamma-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
C:Accession: PT0368
R:Milili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.
Mol. Immunol. 28, 753-761, 1991
A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
A:Reference number: PT0368; MUID:91312348; PMID:1906981
A:Accession: PT0368
A:Molecule type: mRNA
A:Residues: 1-8 <MIL>
A:Experimental source: fetal liver
C:Keywords: immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 8;

Qy 4 HQ 5
||
Db 2 HQ 3

RESULT 47

S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 4 PP 5

RESULT 48

PT0559
T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0559
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0559
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 4 PP 5

RESULT 49

A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamm
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: A38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WHE>
C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 2 SW 3

Db

RESULT 50

C39690

neural cell adhesion molecule, cardiac splice form -, -, + - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C;Accession: C39690
 R;Reyes, A.A.; Small, S.J.; Akeson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
 A;Reference number: A39690; MUID:91141516; PMID:11996115
 A;Accession: C39690
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: mRNA
 A;Residues: 1-8 <REV>
 A;Cross-references: GB:M63970
 C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 1 QP 2

Db

RESULT 51

A61102

parathyroid hormone-like protein, humoral hypercalcemia of malignancy - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C;Accession: A61102
 R;Weir, E.C.; Burtis, W.J.; Morris, C.A.; Brady, T.G.; Inosogna, K.L.
 Endocrinology 123, 2744-2751, 1988
 A;Title: Isolation of 16,000-Dalton parathyroid hormone-like proteins from two animal tu
 A;Reference number: A61102; MUID:89064600; PMID:3197642
 A;Accession: A61102
 A;Molecule type: protein
 A;Residues: 1-9 <WEI>
 A;Experimental source: apocrine cell adenocarcinoma
 C;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology
 C;Keywords: hormone; humoral hypercalcemia

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
 ||
 6 HQ 7

Db

RESULT 52

A24244

adipokinetic hormone - bollworm
 N;Alternate names: Hez-AKH
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
 C;Accession: A24244
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic
 A;Reference number: A24244; MUID:86186794; PMID:3964263

A;Accession: A24244
 A;Molecule type: protein
 A;Residues: 1-9 <JAF>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglute
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 7 SW 8

Db

RESULT 53

A61357

Phyllocaerulein - Sauvage's leaf frog
 C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
 C;Accession: A61357
 R;Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, V.
 Br. J. Pharmacol. 37, 198-206, 1969
 A;Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like r
 A;Reference number: A61357; MUID:70005484; PMID:5824931

A;Accession: A61357
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <ANA>
 C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotei
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Binding site: sulfat (Tyr) (covalent) #status experimental
 F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
 ||
 6 WM 7

Db

RESULT 54

A61358

bradykinin-like peptide I - Japanese pond frog
 C;Species: Rana nigromaculata (Japanese pond frog)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
 C;Accession: A61358
 R;Nakajima, T.
 Chem. Pharm. Bull. 16, 769-770, 1968
 A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the sk
 A;Reference number: A61358; MUID:68412013; PMID:5677638

A;Accession: A61358
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <NAK>
 C;Superfamily: unassigned animal peptides

C;Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 ||
 2 PP 3

Db

RESULT 55

A61057
 Thr-6 bradykinin - scoliid wasp (Colpa interrupta)
 C:Species: Colpa interrupta
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Aug-2000
 C:Accession: A61057
 R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
 Comp. Biochem. Physiol. C 96, 157-162, 1990
 A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap
 A:Reference number: A61057; MUID:91130217; PMID:1980872
 A:Accession: A61057
 A:Molecule type: protein
 A:Residues: 1-9 <PIE>
 C:Superfamily: unassigned animal peptides
 C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7
 ||
 Db 2 pp 3

RESULT 56
 A26744
 bradykinin-like peptide - garden dagger wasp
 N:Alternate names: Thr-6-bradykinin
 C:Species: Megascollia flavifrons (garden dagger wasp)
 C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000
 C:Accession: A26744
 R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
 Toxicon 25, 527-535, 1987
 A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
 A:Reference number: A94322; MUID:87293024; PMID:3617088
 A:Accession: A26744
 A:Molecule type: protein
 A:Residues: 1-9 <YAS>
 C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7
 ||
 Db 2 pp 3

RESULT 57
 A61363
 bradykinin - common frog
 C:Species: Rana temporaria (common frog)
 C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C:Accession: A61363
 R:Anastasi, A.; Brspamer, V.; Bertaccini, G.
 Comp. Biochem. Physiol. A 14, 43-52, 1965
 A:Title: Occurrence of bradykinin in the skin of Rana temporaria.
 A:Reference number: A61363
 A:Accession: A61363
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <ANA>
 C:Superfamily: unassigned animal peptides
 C:Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7
 ||
 Db 2 pp 3

RESULT 58
 A60579
 bradykinin-like peptide - slider turtle
 C:Species: Pseudemys scripta (slider)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: A60579
 R:Conlon, J.M.; Hicks, J.W.; Smith, D.D.
 Endocrinology 126, 985-991, 1990
 A:Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from
 A:Reference number: A60579; MUID:90126625; PMID:2298179
 A:Accession: A60579
 A:Molecule type: protein
 A:Residues: 1-9 <CON>
 C:Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammal
 C:Superfamily: unassigned animal peptides
 C:Keywords: plasma

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7
 ||
 Db 2 pp 3

RESULT 59
 B60246
 ornitho-kinin - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Aug-2000
 C:Accession: B60246
 R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
 Adv. Exp. Med. Biol. 247A, 359-367, 1989
 A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemi
 A:Reference number: A60246; MUID:90102072; PMID:2603803
 A:Accession: B60246
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <KIM>
 C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 pp 7
 ||
 Db 2 pp 3

RESULT 60
 B41983
 orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
 C:Species: Azotobacter vinelandii
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: B41983
 R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
 A:Title: Unification of the ferritin family of proteins.
 A:Reference number: A41983; MUID:92196129; PMID:1549605
 A:Accession: B41983
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid; protein
 A:Residues: 1-9 <GRO>
 A:Cross-references: GB:M83692; NID:9142297; PIDN:AAA22122.1; PID:9142299
 A>Note: sequence extracted from NCBI backbone (NCBIF:88442)

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 3 PP 4

RESULT 61
S55696
Phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55696
R;Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Trypanosoma brucei
A;Reference number: S55696; MUID:95284106; PMID:7766679
A;Accession: S55696
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <HUN>

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OP 6
||
Db 1 OP 2

RESULT 62
D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket Gryllus bimaculatus
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 8 SW 9

RESULT 63
A61620
locustamytotropin III - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C;Accession: A61620
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A;Title: Isolation, identification and synthesis of locustamytotropin III and IV, two additional members of the locustamytotropin family
A;Reference number: A61620
A;Accession: A61620
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Keywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OP 6
||
Db 3 OP 4

RESULT 64
S65433
bradykinin - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65433
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the diptere Haematobia irritans
A;Reference number: S65431; MUID:96215437; PMID:8647080
A;Accession: S65433
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <WID>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 2 PP 3

RESULT 65
S77984
cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77984
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77984
A;Molecule type: protein
A;Residues: 1-9 <ARN>
A;Experimental source: heart
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OP 6
||
Db 3 OP 4

RESULT 66
PT0299
Ig heavy chain CDR3 region (clone 5-103B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0299
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0299
A;Molecule type: DNA
A;Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 3 SW 4

RESULT 67

S26508
collagen alpha 2(VI) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Dec-1998
C;Accession: S26508
R;Jander, R.; Rautenberg, J.; Glanville, R.W.
Eur. J. Biochem. 133, 39-46, 1983
A;Title: Further characterization of the three polypeptide chains of bovine and human sh
A;Reference number: S26506; MUID:83209648; PMID:6852033
C;Accession: S26508
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <JAN>
C;Keywords: hydroxyproline
F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 6 PP 7

RESULT 68

I58350
gene c-mpl protein - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 28-Feb-1997
C;Accession: I58350
R;Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995
A;Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep
A;Reference number: I58350; MUID:95166571; PMID:7862460
C;Accession: I58350
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-9 <RES>
A;Cross-references: GB:S76841; NID:G912992
C;Genetics:
A;Gene: c-mpl

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 3 SW 4

RESULT 69

B30572
T-cell receptor beta chain C region (CRTE29) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C;Accession: B30572
R;Williams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of ut:
A;Reference number: A30563; MUID:89110038; PMID:2563271

A;Accession: B30572
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-9 <WIL>
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 8 PP 9

RESULT 70

A43065
hydroxyproline-3-bradykinin - frog (Heleophryne purcelli)
C;Species: Heleophryne purcelli
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A43065
R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.
Experientia 35, 1133, 1979
A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the Sou
A;Reference number: A43065; MUID:80024576; PMID:488255
C;Accession: A43065
A;Molecule type: protein
A;Residues: 1-9 <NAK>
C;Keywords: bradykinin; hydroxyproline; skin
F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 2 PP 3

RESULT 71

XA1168
angiotensin-converting enzyme inhibitor V-6-II - jararaca
C;Species: Bothrops jararaca (jararaca)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C;Accession: A01255
R;Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocyl, O.
Biochemistry 10, 4033-4039, 1971
A;Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararac
A;Reference number: A90356; MUID:72118526; PMID:4334402
C;Accession: A01255
A;Molecule type: protein
A;Residues: 1-10 <OND>
A;Note: the structure of the peptide was confirmed by synthesis
C;Comment: this peptide also potentiates bradykinin by inhibiting the kinases that i
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 9 PP 10

RESULT 72

XASNPC
angiotensin-converting enzyme inhibitor - aspic viper

C;Species: Vipera aspis (aspic viper)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
 C;Accession: A60377
 R;Komori, Y.; Sugihara, H.
 Int. J. Biochem. 22, 767-771, 1990
 A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
 A;Reference number: A60377; MUID:90382616; PMID:2169439
 A;Accession: A60377
 A;Molecule type: protein
 A;Residues: 1-10 <KOW>
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 ||
 Db 9 PP 10

RESULT 73

RHAQ1
 gonadoliberin I - American alligator
 N;Alternate names: gonadotropin-releasing hormone I
 C;Species: Alligator mississippiensis (American alligator)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
 C;Accession: A60066
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
 Regul. Pept. 33, 105-116, 1991
 A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of
 A;Reference number: A60066; MUID:91352338; PMID:1882082
 A;Accession: A60066
 A;Molecule type: protein
 A;Residues: 1-10 <LOW>
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 8 QP 9

RESULT 74

SPPGNK
 neuromedin K - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996
 C;Accession: A01560
 R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 114, 533-540, 1983
 A;Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.
 A;Reference number: A01560; MUID:83282812; PMID:6576785
 A;Accession: A01560
 A;Molecule type: protein
 A;Residues: 1-10 <KAN>
 A;Note: the structure of the peptide was confirmed by synthesis
 C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu
 C;Superfamily: neurokinin B precursor
 C;Keywords: amidated carboxyl end; hormone; spinal cord
 F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
 ||
 Db 2 MH 3

RESULT 75

JC1367
 thyroliberin potentiating neuropeptide - bovine
 N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiati
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1997
 C;Accession: JC1367
 R;Bulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.
 Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992
 A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovin
 A;Reference number: JC1367; MUID:93111999; PMID:1472021
 A;Accession: JC1367
 A;Molecule type: protein
 A;Residues: 1-10 <BUL>
 A;Experimental source: hypothalamus
 C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precurs
 C;Function:
 A;Description: potentiates thyroliberin-induced thyrotropin secretion
 C;Superfamily: thyroliberin precursor
 C;Keywords: hypothalamus; neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
 ||
 Db 4 WM 5

Search completed: November 25, 2003, 19:36:09
 Job time : 4.80233 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.48256 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWHQPP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	11	1	MORN HUMAN
2	3	42.9	20	1	OAR PHOPV
3	2	28.6	4	1	OCF3 OCTMI
4	2	28.6	6	1	EIO1_LITRU
5	2	28.6	6	1	LCK1_LOCMI
6	2	28.6	7	1	LANC_CARUI
7	2	28.6	7	1	TPFY_PACDA
8	2	28.6	7	1	UF04_MOUSE
9	2	28.6	8	1	AKH_LIBAU
10	2	28.6	8	1	ALL5_CALVO
11	2	28.6	8	1	CKKN_WACEU
12	2	28.6	8	1	LCK1_LEUMA
13	2	28.6	8	1	LCK2_LEUMA
14	2	28.6	8	1	LCK3_LEUMA
15	2	28.6	8	1	LCK4_LEUMA
16	2	28.6	8	1	LCK5_LEUMA
17	2	28.6	8	1	LCK6_LEUMA
18	2	28.6	8	1	LCK7_LEUMA
19	2	28.6	8	1	LCK8_LEUMA
20	2	28.6	8	1	NPB_BOVIN
21	2	28.6	8	1	PPK2_PERAM
22	2	28.6	9	1	ALI0_CARMA
23	2	28.6	9	1	COXE_THUOB
24	2	28.6	9	1	FAR3_PENMO
25	2	28.6	9	1	FAR4_PENMO
26	2	28.6	9	1	FRF1_SARBU
27	2	28.6	9	1	KNL3_BOMVA
28	2	28.6	9	1	LMT3_LOCOMI
29	2	28.6	9	1	RT33_BOVIN
30	2	28.6	9	1	YBFR_AZOVI
31	2	28.6	10	1	AH3_PRUSE
32	2	28.6	10	1	BPP2_BOTIN
33	2	28.6	10	1	BPP2_BOTJA

34	2	28.6	10	1	BPP8_BOTIN
35	2	28.6	10	1	BPP_VIPAS
36	2	28.6	10	1	BRK_ONCMY
37	2	28.6	10	1	CAER_LITXA
38	2	28.6	10	1	COXM_RAT
39	2	28.6	10	1	FAR6_PANRE
40	2	28.6	10	1	GON1_ALLMI
41	2	28.6	10	1	TKNK_PIG
42	2	28.6	10	1	TMOF_AEDAE
43	2	28.6	10	1	UPA2_HUMAN
44	2	28.6	10	1	UPA5_HUMAN
45	2	28.6	10	1	URE3_MORMO
46	2	28.6	11	1	ASL1_BACSE
47	2	28.6	11	1	BPP3_BOTIN
48	2	28.6	11	1	BPP4_BOTIN
49	2	28.6	11	1	BPPB_AGRHA
50	2	28.6	11	1	BPP_AGRHP
51	2	28.6	11	1	BRK_MEGFL
52	2	28.6	11	1	CA31_LITCI
53	2	28.6	11	1	CEP1_ACHFU
54	2	28.6	11	1	LADD_ONCMY
55	2	28.6	11	1	TKN1_PSEGU
56	2	28.6	11	1	TKN1_UPERU
57	2	28.6	11	1	TKN2_PSEGU
58	2	28.6	11	1	TKN3_PSEGU
59	2	28.6	11	1	TKN4_PSEGU
60	2	28.6	11	1	TKN5_PSEGU
61	2	28.6	11	1	TKNA_ONCMY
62	2	28.6	11	1	TKN_ELENO
63	2	28.6	12	1	FAR7_PENMO
64	2	28.6	12	1	FAR1_CALVO
65	2	28.6	12	1	FIF1_SARBU
66	2	28.6	12	1	HS9A_RAT
67	2	28.6	12	1	TKN2_KASMA
68	2	28.6	13	1	ACT7_SOYBN
69	2	28.6	13	1	AH4_PRUSE
70	2	28.6	13	1	BPP1_BOTJA
71	2	28.6	13	1	BRK_FARID
72	2	28.6	13	1	EL22_LITRU
73	2	28.6	13	1	EP65_HUMAN
74	2	28.6	13	1	LMT4_LOCM1
75	2	28.6	13	1	NP1_MICOC
76	2	28.6	13	1	TV13_PHYRO
77	2	28.6	14	1	MARI_ALTSP
78	2	28.6	14	1	MAST_VESBA
79	2	28.6	14	1	PH1_PRUSE
80	2	28.6	14	1	TAT_HV1W2
81	2	28.6	14	1	TAT_HV1Z8
82	2	28.6	15	1	AF1L_MALPA
83	2	28.6	15	1	AH2_PRUSE
84	2	28.6	15	1	CH1L_PEA
85	2	28.6	15	1	CXA2_CONAL
86	2	28.6	15	1	FXB7_PINPS
87	2	28.6	15	1	IRBP_CRISP
88	2	28.6	15	1	MK1_PALPR
89	2	28.6	15	1	NUO8_SOLITU
90	2	28.6	15	1	PH3_PRUSE
91	2	28.6	15	1	PRP_MYCBO
92	2	28.6	15	1	RES_PHYPA
93	2	28.6	15	1	SODM_STRGR
94	2	28.6	15	1	UC06_MAIZE
95	2	28.6	15	1	UC19_MAIZE
96	2	28.6	15	1	UE15_HORVU
97	2	28.6	15	1	UN01_PINPS
98	2	28.6	15	1	UP01_METAN
99	2	28.6	15	1	URE2_MORMO
100	2	28.6	16	1	AF1S_MALPA

ALIGNMENTS

RESULT 1

```

MORN HUMAN
ID MORN HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RN SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7230191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuroepitide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RN SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RN SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuroepitide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RN FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NHL5-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXA.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C3258878 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 1 QPP 3

RESULT 2
ID_OAR_PHOPY STANDARD; PRT; 20 AA.
AC P14803;
DT 01-APR-1990 (Rel. 14, Created)

Query Match 42.9%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
DB 18 MHQ 20

RESULT 3
ID_OCP3_OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus)
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
DB 18 MHQ 20

Query Match 42.9%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
DB 18 MHQ 20

```

```

DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Octopamine receptor (Octopamine binding protein) (Fragment).
OC Photinus pyralis (North American firefly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Cantharoidea; Lampyridae; Coleoptera; Polyphaga; Elateriformia;
OX NCBI_TaxID=7054;
RN [1]
RN SEQUENCE.
RC TISSUE=Light organ;
RX MEDLINE=90092510; PubMed=2513233;
RA Nathanson J.A., Kantham L., Hunnicutt E.J.;
RT "Isolation and N-terminal amino acid sequence of an octopamine ligand
RT binding protein.";
RL FEBS Lett. 259:117-120(1989).
CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A
CC NEUROTRANSMITTER, NEUROHORMONE, AND NEUROMODULATOR IN
CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR PIR; S28779; S28779.
DR InterPro; IPR00276; GPCR Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
KW G-protein coupled receptor.
FT UNSURE 2 2
FT UNSURE 9 9
FT UNSURE 19 19
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11BB8D4AB CRC64;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2 28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 SW 3
QY 1 SW 2
Db 4 SW 5

RESULT 4

E101 LITRU
ID E101 LITRU STANDARD; PRT; 6 AA.
AC P82036;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
ON NCBI_TaxID=104895;
RX [1]
RP SEQUENCE
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:639-645 (1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
Db 5 WM 6

RESULT 5

LOK1 LOCMI
ID LOK1 LOCMI STANDARD; PRT; 6 AA.
AC P41431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
ON NCBI_TaxID=7004;
RX [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57 (1992).
CC -|- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -|- SUBCELLULAR LOCATION: Secreted.
DR PIR; A61068.
KW Neuropeptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 654 MW; 6863565A5B9CDB000 CRC64;

RESULT 6

LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
ON NCBI_TaxID=35782;
RX [1]
RP SEQUENCE.

RA MEDLINE=92321768; PubMed=1622206;
RX Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.P.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422 (1992).
CC -|- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 5 QP 6

RESULT 7

TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE tryptophyllin-1 (pdt-1).
OS Pachymedusa dactylophora (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
ON NCBI_TaxID=75988;
RX [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactylophora tryptophyllin-1 (pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -|- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=809.2; METHOD=WALDI.
DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3 3
FT MOD RES 7 7
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 pp 7
Db 2 pp 3
RESULT 8
UF04_MOUSE
ID _UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
CC NON TER 7
FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 pp 7
Db 3 pp 4
RESULT 9
AKH_LIBAU
ID _AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
concentrating hormone family isolated and sequenced from a
dragonfly.";
RT Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT

CC -!- MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
FT MOD RES 8 8
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SW 2
Db 7 SW 8
RESULT 10
ALLS_CALVO
ID _ALLS_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD RES 3 3
FT MOD RES 8 8
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 883 MW; 7D9879CAB8477768 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 pp 7
Db 2 pp 3
RESULT 11
CCKN_MACEU
ID _CCKN_MACEU STANDARD; PRT; 8 AA.

AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M.eugenii, and D.viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD RES 2 2 SULFATION.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 WM 3
DB 5 WM 6
RESULT 12
LCK1 LEUMA
ID LCK1 LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroptins";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 893 MW; DC6365B449C76A CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 WM 3
DB 5 WM 6
RESULT 13
LCK2 LEUMA
ID LCK2 LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroptins";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SW 2
DB 6 SW 7
RESULT 14
LCK3 LEUMA
ID LCK3 LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroptins";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
6 SW 7

Db

RESULT 15

LCK4 LEUMA
ID LCK4 LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropeptides."
RL Comp. Biochem. Physiol. 84C:271-276 (1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
6 SW 7

Db

RESULT 16

LCK5 LEUMA
ID LCK5 LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30 (1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
6 SW 7

Db

RESULT 17

LCK6 LEUMA
ID LCK6 LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30 (1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
6 SW 7

Db

RESULT 18

LCK7 LEUMA
ID LCK7 LEUMA STANDARD; PRT; 8 AA.
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:31-34 (1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.


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DR PIR; JS0317; JS0317.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 866 MW; DC365A5B9CD76A CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
   ||
Db 6 SW 7

RESULT 19
LCK8 LEUMA
ID LCK8 LEUMA STANDARD; PRT; 8 AA.
AC P1990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Blaberidae; Leucophaea.
OC NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0318; JS0318.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
   ||
Db 6 SW 7

RESULT 20
NPB BOVIN
ID NPB BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";

DR Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C76D9C729 CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
   ||
Db 4 QP 5

RESULT 21
PPK2 PERAM
ID PPK2 PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokiniin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OC NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97333923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokiniins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokiniin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokiniin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
   ||
Db 2 PP 3

RESULT 22
AL10 CARMA
ID AL10 CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=96121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
FT SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
DB 3 QP 4
RESULT 23
COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103 (1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
FT SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
DB 3 QP 4

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RESULT 24
ID FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
FT SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
DB 2 QP 3
RESULT 25
ID FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
FT SEQUENCE 9 AA; 1121 MW; DA0E07340685A776 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
   ||
Db 2 QP 3

RESULT 26
FRF1_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
[1]
RN SEQUENCE, AMIDATION, AND FUNCTION.
RP TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D81D69CAB6C5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
   ||
Db 1 QP 2

RESULT 27
KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
[1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
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SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
   ||
Db 2 PP 3

RESULT 28
LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
[1]
RN SEQUENCE, AND SYNTHESIS.
RP TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kocharsky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
   ||
Db 3 QP 4

RESULT 29
RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
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RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 5 QP 6

RESULT 30
YBFR_AZOVI
ID YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=921196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).

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DR EMBL; M83692; AAA22122.1; --
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 3 PP 4

RESULT 31
AH3_PRUSE
ID AH3_PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OX eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC Glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT. THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 3 PP 4

RESULT 32
BPP2_BOTIN
ID BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 9 PP 10

RESULT 33
BPP2_BOTJA
ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;

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DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; A01255; XAVI6B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C77411773 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PP 7
 Db 9 PP 10

RESULT 34
 BPP8_BOTIN
 ID BPP8_BOTIN STANDARD; PRT; 10 AA.
 AC P30426;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Gigglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; H37196; H37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761FD8 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PP 7

DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; A01255; XAVI6B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C77411773 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PP 7
 Db 9 PP 10

RESULT 35
 BPP_VIPAS
 ID BPP_VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PP 7
 Db 9 PP 10

RESULT 36
 BRK_ONCMY
 ID BRK_ONCMY STANDARD; PRT; 10 AA.
 AC Q9PRZ1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lysyl-bradykinin-like.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=94039817; PubMed=8224232;
 RA Conlon J.M., Olson K.R.;
 RT "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma.";
 RL FEBS Lett. 334:75-78(1993).
 CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
 DR PIR; S39030; S39030.
 KW Bradykinin; Vasodilator.
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 DB 3 PP 4

RESULT 37
 CAER_LITXA STANDARD; PRT; 10 AA.
 AC P56264;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caerulein.
 OS Litoria xanthomera (Orange-thighed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OC NCBI_TaxID=79697;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97374000; PubMed=9230483;
 RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
 RA Ramsay S.L.;
 RT "New caerin antibacterial peptides from the skin glands of the
 RT Australian tree frog *Litoria xanthomera*.";
 RL J. Pept. Sci. 3:181-185 (1997).
 CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1290 MW; 99DEF3837861BBSA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
 DB 7 WM 8

RESULT 38
 COXM_RAT STANDARD; PRT; 10 AA.
 AC P80431;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIB, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 DE COX7B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;

"Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 amino-terminal sequences suggest identity of the fetal heart and the
 adult liver isoform."
 Eur. J. Biochem. 230:235-241 (1995).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC PIR: S65387; S65387.
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
 DB 2 HQ 3

RESULT 39
 FAR6_PANRE STANDARD; PRT; 10 AA.
 AC P82650;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRP-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OC NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRFamide-related
 RT peptides (fARPs) from free-living nematode, *Panagrellus redivivus*."
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 DB 5 QP 6

RESULT 40
 GON1_ALLMI STANDARD; PRT; 10 AA.
 AC P37041; P20407;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
 DE (Luliberin I).
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OC NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1892082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.B., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 8 QP 9

RESULT 41
TKNK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).
GN TAC3 OR NKNB.
OS Sus scrofa (Pig), and
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES=R. ridibunda; TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01560; SPPGNK.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAA1 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
DB 2 MH 3

RESULT 42
TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 5 PP 6

RESULT 43
UPA2_HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;

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RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
 DR SWISS-2DPAGE; P30088; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 6 6
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db 5 PP 6

RESULT 44
 UPAS_HUMAN STANDARD; PRT; 10 AA.
 ID UPAS_HUMAN STANDARD; PRT; 10 AA.
 AC P30091;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_SEQUENCE
 RP SEQUENCE
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30091; HUMAN.
 FT NON_TER 1 1
 FT VARIANT 9 9 G -> Y.
 FT NON_TER 10 10 /FTID=VAR_000002.
 SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 Db 3 QP 4

RESULT 45
 URE3_MORMO STANDARD; PRT; 10 AA.
 ID URE3_MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 UREA.
 GN Morganella morganii (Proteus morganii).
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]_SEQUENCE
 RP SEQUENCE
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences.";
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON_TER 10 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db 5 PP 6

RESULT 46
 ASL1_BACSE STANDARD; PRT; 11 AA.
 ID ASL1_BACSE STANDARD; PRT; 11 AA.
 AC P83146;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OS Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]_SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from Bacteroides stercoris HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQ 5
 Db 10 HQ 11

RESULT 47


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BPP3 BOTIN
ID _BPP3 BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 4 PP 5

RESULT 48
BPP4 BOTIN
ID _BPP4 BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBF13C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 4 PP 5

RESULT 49
BPPB AGKHA
ID _BPPB AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 4 PP 5

RESULT 50
BPP AGKHP
ID _BPP AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.

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KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PP 7
DB 4 PP 5

RESULT 51
BRK MEGFL
ID BRK MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scoliidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]_
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from the venom of Megascolia flavifrons."
RT solitary wasp Megascolia flavifrons."
RL Toxicon 25:527-535(1987).
RN [2]_
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons."
RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; B26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PP 7
DB 2 PP 3

RESULT 52
CA31_LITCI
ID CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;

[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montana tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro; IPR001651; Gastrin.
KW PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 1 1
FT MOD RES 4 4 SULFATION.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 8 WM 9

RESULT 53
CBP1_ACHFU
ID CBP1_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]_
RP SEQUENCE.
RC STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica."
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
CC MOVEMENT OF ACHATINA.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 4 SW 5

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RESULT 54
LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jørgensen J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -|- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
CC -|- COFACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
CC -|- SUBUNIT: MULTIMERIC.
KW Lectin; Calcium.
FT NOV PER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 PP 7
Db 9 PP 10

RESULT 55
TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simeaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Myobatrachinae; Pseudophryne.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QP 6
Db 1 QP 2

RESULT 57
TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.

FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CBIAB7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QP 6
Db 1 QP 2

RESULT 56
TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Eudean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QP 6
Db 1 QP 2

KW	Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW	Pyrrolidone carboxylic acid.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 11 11 AMIDATION.
SQ	SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;	
Best Local Similarity 100.0%; Pred.No. 2.8e+03; Indels 0; Gaps 0;	
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	5 QP 6
DB	1 QP 2
RESULT 59	
TKN4_PSEGU	STANDARD; PRT; 11 AA.
ID_TKN4_PSEGU	AC P429B9;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Substance P-like peptide I (PG-SPI).
OS	Pseudophryne guentheri (Guenther's toadlet).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC	Myobatrachinae; Pseudophryne.
NCBI_TaxID=30349;	[1]
RN	SEQUENCE.
RP	TISSUE=Skin secretion;
RC	MEDLINE=90287814; PubMed=2356157;
RX	SA Snamco M., Severini C., de Biase D., Barra D., Bossa F.,
RA	Roberts J.D., Melchiorri P., Erspamer V.;
RT	"Six novel tachykinin- and bombesin-related peptides from the skin of
RT	the Australian frog Pseudophryne guntheri.";
EL	Peptides 11:299-304(1990).
CC	-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC	EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC	SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC	MUSCLES.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Skin..
CC	-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR	PIR; E60409; E60409.
DR	InterPro; IPR003580; Protachykinin.
DR	InterPro; IPR002040; Tachykinin.
DR	Pfam; PF02202; Tachykinin; 1.
DR	SMART; SM00203; TK; 1
DR	PROSITE; PS00267; TACHYKININ; 1.
KW	Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW	Pyrrolidone carboxylic acid.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 11 11 AMIDATION.
SQ	SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;	
Best Local Similarity 100.0%; Pred.No. 2.8e+03;	
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	5 QP 6
DB	1 QP 2
RESULT 60	
TKNS_FSEGU	STANDARD; PRT; 11 AA.
ID_TKNS_FSEGU	AC P42990;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Substance P-like peptide II (PG-SPII).

OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Siamaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; F60409; F60409.
 DR InterPro; IPR003580; Protachykinin.
 DR Pfam; PF02202; Tachykinin.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION
 FT SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
 SQ
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 DB 1 QP 2

RESULT 61
 TKNA ONCMY
 ID TKNA ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; S23308; S23308.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; tachykinin; 1.

DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Siamaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; A01561; EOCC.
 DR PIR; B01561; EOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachykinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 FT SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;
 SQ
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 DB 1 QP 2

RESULT 63
 FARY PENMO
 ID FARY PENMO STANDARD; PRT; 12 AA.
 AC P83322;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FRFamide-like neuropeptide FLP7 (GYRKPFFNGSIF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.

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OX  NCBI_TaxID=6687;
RN  [1]
RP  SEQUENCE, AND MASS SPECTROMETRY.
RC  TISSUE=Eyestalk;
RX  MEDLINE=21956277; PubMed=11959015;
RA  Sithigornkul P., Pupuem J., Krungkarn C., Longyant S.,
RA  Chaivuthangkura P., Sithigornkul W., Petsom A.;
RT  "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RL  of the giant tiger prawn Penaeus monodon.";
RL  Comp. Biochem. Physiol. 131B:325-337(2002).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC  FAMILY.
CC  Neuropeptide; Amidation.
KW  MOD_RES 12 12
FT  MOD_RES 12 12
SQ  SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 PP 7
DB  5 PP 6

RESULT 64
FARI CALVO STANDARD; PRT; 12 AA.
AC  P41869;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  CallimyrFamide 1.
OS  Calliphora vomitoria (Blue blowfly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC  Calliphoridae; Calliphora.
OX  NCBI_TaxID=27454;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Thoracic ganglion;
RX  MEDLINE=92196111; PubMed=1549595;
RA  Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA  Rehfeld J.F., Thorpe A.;
RT  "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT  neuropeptides (designated callimyrFamides) from the blowfly
RT  Calliphora vomitoria.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC  FAMILY.
DR  PIR; E44787; E44787.
KW  Neuropeptide; Amidation.
FT  MOD_RES 12 12
SQ  SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 QP 6
DB  4 QP 5

RESULT 65
FIFI_SARBU STANDARD; PRT; 12 AA.
AC  P83349;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)

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DE  Neb-FIRamide 1.
OS  Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC  Sarcophagidae; Sarcophaga.
OX  NCBI_TaxID=7385;
RN  [1]
RP  SEQUENCE, AMIDATION, AND FUNCTION.
RC  TISSUE=CNS;
RX  MEDLINE=22342733; PubMed=12438685;
RA  Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA  Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT  "Identification in Drosophila melanogaster of the invertebrate G
RT  protein-coupled FMRamide receptor.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC  -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC  junctions.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC  FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD_RES 12 12
SQ  SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 PP 7
DB  2 PP 3

RESULT 66
HS9A_RAT STANDARD; PRT; 12 AA.
AC  P82955;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Heat shock protein HSP 90-alpha (Fragment).
GN  HSPCA.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=Sprague-Dawley; TISSUE=Liver;
RX  MEDLINE=21589773; PubMed=11732320;
RA  Langer T., Fasold H.;
RT  "Isolation and quantification of the heat shock protein 90 alpha and
RT  beta isoforms from rat liver.";
RL  Proteolipoma 218:54-56(2001).
CC  -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC  (BY SIMILARITY).
CC  -!- SUBUNIT: Homodimer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR  InterPro; IPR001404; Hsp90.
KW  PROSITE; PS00298; HSP90; PARTIAL.
FT  MOD_RES 4 4
FT  MOD_RES 4 4
FT  MOD_RES 6 6
FT  MOD_RES 12 12
SQ  SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 QP 6
DB      9 QP 10

RESULT 67
TKN2_KASMA
ID_TKN2_KASMA STANDARD; PRT; 12 AA.
AC P06614;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambatin.
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07436; S07436.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PP 7
DB      2 PP 3

RESULT 68
ACT7_SOYEN
ID_ACT7_SOYEN STANDARD; PRT; 13 AA.
AC F15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SACT.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Mesgher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5',
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PP 7
DB      2 PP 3

RESULT 69
AH4_PRUSE
ID_AH4_PRUSE STANDARD; PRT; 13 AA.
AC P29262;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II' (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II') (AH II') (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1417 MW; F7CC4FA321B9D051 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNIKUOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17120; CAA34980.1; --
CC PIR; S15755; S15755.
CC InterPro; IPR004001; Actin.
CC DR PROSITE; PS00406; ACTINS_1; PARTIAL.
CC DR PROSITE; PS00432; ACTINS_2; PARTIAL.
CC DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QP 6
DB      8 QP 9

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Qy      6 PP 7
      ||
Db      3 PP 4

RESULT 70
BPPI_BOTJA
ID  BPPI_BOTJA  STANDARD;      PRT;      13 AA.
AC  P01020; P30421;
DT  21-JUL-1996 (Rel. 01, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Bradykinin-potentiating peptide S3.1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
OS  Bothrops jararaca (Jararaca), and
OS  Bothrops insularis (Island jararaca) (Queimada jararaca).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC  Viperidae; Crotalinae; Bothrops.
OX  NCBI_TaxID=8724, 8723;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=B.jararaca; TISSUE=Venom;
RX  MEDLINE=72118526; PubMed=4334402;
RA  Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA  Kocy O.;
RT  "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT  jararaca. Isolation, elucidation of structure, and synthesis.";
RL  Biochemistry 10:4033-4039(1971).
RN  [2]
RP  SEQUENCE.
RC  SPECIES=B.insularis; TISSUE=Venom;
RX  MEDLINE=90351557; PubMed=2386615;
RA  Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT  "Primary structure and biological activity of bradykinin potentiating
RT  peptides from Bothrops insularis snake venom.";
RL  J. Protein Chem. 9:221-227(1990).
CC  -!- FUNCTION: This peptide both inhibits the activity of the
CC  angiotensin-converting enzyme and enhances the action of
CC  bradykinin by inhibiting the kinases that inactivate it.
CC  It acts as an indirect hypotensive agent.
DR  PIR; A01253; XAV19B.
KW  Hypotensive agent; Pyrrolidone carboxylic acid.
FT  MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ  SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PP 7
      ||
Db     12 PP 13

RESULT 71
BRK_PAPID
ID  BRK_PAPID  STANDARD;      PRT;      13 AA.
AC  P42717;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Waspkinin.
OS  Parapolybia indica.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC  Vespidae; Polistinae; Parapolybia.
OX  NCBI_TaxID=31921;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Venom;
RA  Toki T.; Yasuhara T., Nakajima T.;

"Isolation and sequential analysis of peptides on the venom sac of
Parapolybia indica.";
RL  Eisei Dobutsu 39:105-111(1988).
CC  -!- FUNCTION: Induces smooth muscle contraction.
CC  -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC  -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW  Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT  MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ  SEQUENCE 13 AA; 1573 MW; 2673CE3D83ECC867 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PP 7
      ||
Db      5 PP 6

RESULT 72
E122_LITRU
ID  E122_LITRU  STANDARD;      PRT;      13 AA.
AC  P82098;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Electrin 2.2.
OS  Litoria rubella (Desert tree frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC  Pelodyadinae; Litoria.
OX  NCBI_TaxID=104895;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Skin secretion;
RA  Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT  "Peptides from the skin glands of the Australian buzzing tree frog
RT  Litoria electrica. Comparison with the skin peptides from Litoria
RT  rubella.";
RL  Aust. J. Chem. 52:639-645(1999).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
KW  Amphibian defense peptide; Amidation.
FT  MOD RES 13 13 AMIDATION.
SQ  SEQUENCE 13 AA; 1598 MW; C1808EF3B357322 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QP 6
      ||
Db      9 QP 10

RESULT 73
EP65_HUMAN
ID  EP65_HUMAN  STANDARD;      PRT;      13 AA.
AC  P54963;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Erythrocyte 65 kDa protein (P65) (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX  MEDLINE=90004678; PubMed=2507249;
RA  Hart G.W., Haliwanger R.S., Holt G.D., Kelly W.G.;
RT  "Nucleoplasmic and cytoplasmic glycoproteins.";
RL  Ciba Found. Symp. 145:102-118(1989).
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CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
DR GO: 0005737; C:cytoplasm; NAS.
KW Glycoprotein.
FT NON_TER 1 1 O-LINKED (GLCNAC).
FT CARBOHYD 2 2
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; DOB873344C61A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 6 QP 7

RESULT 74
LMT4 LOCMI STANDARD; PRT; 13 AA.
AC P41430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 4 (LOM-MT-4).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RT de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
CC STIMULATOR THAN LOM-MT I, II AND III.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; B61620; B61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
Db 3 HQ 4

RESULT 75
MPI MICOC STANDARD; PRT; 13 AA.
AC P81532;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MPI protein (Fragments).
OS Microplitis ocellatae (Braconid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Microgasterinae; Microplitis.
OX NCBI_TaxID=99573;
RN [1]

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```

RP SEQUENCE.
RC TISSUE=larva;
RA Takahashi M., Quicke D.L.J.;
RL Submitted (OCT-1998) to the SWISS-PROT data bank.
CC -!- TISSUE SPECIFICITY: SALIVARY GLANDS.
CC -!- DEVELOPMENTAL STAGE: LARVAL.
FT NON_CONS 10 11
SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 7 PP 8

Search completed: November 25, 2003, 19:28:23
Job time : 3.55399 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 13.1453 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWMHQPP 7

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3	42.9	9	10	P82429
2	3	42.9	9	16	Q935G1
3	3	42.9	11	2	Q47569
4	3	42.9	11	13	Q8UUP1
5	3	42.9	13	5	Q9U5U2
6	3	42.9	13	12	Q67604
7	3	42.9	15	10	Q9S8N8
8	3	42.9	16	11	Q9JHB6
9	3	42.9	17	3	Q06800
10	3	42.9	17	4	Q14001
11	3	42.9	18	11	Q9JIE9
12	3	42.9	19	13	Q9PRT0
13	3	42.9	19	13	Q9PRN4
14	3	42.9	20	16	Q8RGY4
15	2	28.6	7	2	P72081
16	2	28.6	7	6	Q28742

17	2	28.6	7	8	P92214	P92214 amblyopyrum
18	2	28.6	7	8	P92393	P92393 hordeum vul
19	2	28.6	7	8	P92403	P92403 lophopyrum
20	2	28.6	7	8	P92427	P92427 peridictyon
21	2	28.6	7	8	P92430	P92430 aegilops ta
22	2	28.6	7	8	P92221	P92221 bromus iner
23	2	28.6	7	8	P92425	P92425 pseudoroegn
24	2	28.6	7	8	P92381	P92381 hordeum bra
25	2	28.6	7	8	P92387	P92387 henrardia p
26	2	28.6	7	8	P92210	P92210 agropyron c
27	2	28.6	7	8	P92440	P92440 thinopyrum
28	2	28.6	7	8	P92218	P92218 australopyr
29	2	28.6	7	8	P92390	P92390 heteranthel
30	2	28.6	7	8	P92372	P92372 haynaldia v
31	2	28.6	7	8	P92442	P92442 taeniatheru
32	2	28.6	7	8	P92226	P92226 crithopsis
33	2	28.6	7	8	P92385	P92385 hordeum mar
34	2	28.6	7	8	P92421	P92421 psathyrosta
35	2	28.6	8	4	Q16468	Q16468 homo sapien
36	2	28.6	8	5	P82685	P82685 periplaneta
37	2	28.6	8	5	P82686	P82686 periplaneta
38	2	28.6	8	5	P82687	P82687 periplaneta
39	2	28.6	8	5	P82688	P82688 periplaneta
40	2	28.6	8	5	P82689	P82689 periplaneta
41	2	28.6	8	6	Q9GMH3	Q9GMH3 lagenorhync
42	2	28.6	8	6	Q28866	Q28866 megaptera n
43	2	28.6	8	12	Q9J205	Q9J205 hepatitis c
44	2	28.6	8	12	Q64971	Q64971 alfalfa mos
45	2	28.6	9	2	Q53914	Q53914 streptomyce
46	2	28.6	9	2	Q43960	Q43960 azotobacter
47	2	28.6	9	2	Q93193	Q93193 pseudomonas
48	2	28.6	9	4	Q9UKJ6	Q9UKJ6 homo sapien
49	2	28.6	9	4	Q9UCS8	Q9UCS8 homo sapien
50	2	28.6	9	4	Q15891	Q15891 homo sapien
51	2	28.6	9	4	Q16386	Q16386 homo sapien
52	2	28.6	9	5	Q9TWV0	Q9TWV0 anthopleura
53	2	28.6	9	6	Q9GJV2	Q9GJV2 lagenorhync
54	2	28.6	9	6	Q9T777	Q9T777 bos taurus
55	2	28.6	9	6	Q9GJV3	Q9GJV3 lagenorhync
56	2	28.6	9	6	Q9GJV1	Q9GJV1 lagenorhync
57	2	28.6	9	8	Q8WFT4	Q8WFT4 diadema ant
58	2	28.6	9	10	P82440	P82440 nicotiana t
59	2	28.6	9	11	Q08979	Q08979 mus musculus
60	2	28.6	9	12	Q90350	Q90350 hepatitis g
61	2	28.6	9	12	Q71069	Q71069 canine dist
62	2	28.6	9	12	Q92766	Q92766 canine dist
63	2	28.6	9	12	Q71066	Q71066 canine dist
64	2	28.6	9	13	Q9PRJ4	Q9PRJ4 lepisosteus
65	2	28.6	9	13	Q8AYL5	Q8AYL5 carassius a
66	2	28.6	10	2	Q8AUM7	Q8AUM7 carassius a
67	2	28.6	10	2	Q9R5T2	Q9R5T2 acetobacter
68	2	28.6	10	2	P83062	P83062 bacillus ce
69	2	28.6	10	4	Q14096	Q14096 homo sapien
70	2	28.6	10	4	Q15342	Q15342 homo sapien
71	2	28.6	10	4	Q9UCR0	Q9UCR0 homo sapien
72	2	28.6	10	4	Q9UE86	Q9UE86 homo sapien
73	2	28.6	10	8	Q8WFT5	Q8WFT5 diadema ant
74	2	28.6	10	8	Q8WFT6	Q8WFT6 diadema ant
75	2	28.6	10	8	Q8SHA8	Q8SHA8 rhampholeon
76	2	28.6	10	8	Q8LLJ0	Q8LLJ0 cryza sativ
77	2	28.6	10	10	Q99213	Q99213 aegilops sq
78	2	28.6	10	10	P81898	P81898 prunus dulc
79	2	28.6	10	10	P81899	P81899 prunus dulc
80	2	28.6	10	11	Q91WZ3	Q91WZ3 rattus sp.
81	2	28.6	10	11	Q9QVFO	Q9QVFO mus sp. pro
82	2	28.6	10	11	Q9QVK7	Q9QVK7 mus sp. nep
83	2	28.6	10	11	Q8VHM9	Q8VHM9 mus musculus
84	2	28.6	10	11	Q9QVE9	Q9QVE9 mus sp. pro
85	2	28.6	10	11	Q8CJEO	Q8CJEO rattus norv
86	2	28.6	10	12	Q9Q0W9	Q9Q0W9 polyomaviru
87	2	28.6	10	12	Q8JTV0	Q8JTV0 polyomaviru
88	2	28.6	10	12	Q9Q0W1	Q9Q0W1 polyomaviru
89	2	28.6	10	12	Q8JTV6	Q8JTV6 polyomaviru

90 O90348 hepatitis g
 91 Q9Q0V9 polyomaviru
 92 Q8JVB4 polyomaviru
 93 Q9Q0W7 polyomaviru
 94 Q8JVB6 polyomaviru
 95 Q9Q0V7 polyomaviru
 96 Q8JVB2 polyomaviru
 97 Q8JVB7 polyomaviru
 98 P90391 tomato yell
 99 Q8JVB4 polyomaviru
 100 Q8JVB7 polyomaviru

ID P82429 PRELIMINARY; PRT; 9 AA.
 AC P82429;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 44 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0-0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 986 MW; C22CCACADG6C77776 CRC64;

ALIGNMENTS

RESULT 1
 P82429
 ID P82429 PRELIMINARY; PRT; 9 AA.
 AC P82429;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 44 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0-0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 986 MW; C22CCACADG6C77776 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
 Db 2 Qpp 4

RESULT 2
 Q935G1
 ID Q935G1 PRELIMINARY; PRT; 9 AA.
 AC Q935G1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative membrane protein (Fragment).
 GN HCM1.O1C.
 OS Salmonella typhi.
 OG Plasmid pHCM1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Raque A., Rien T.T., Holroyd S., Jørgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 DR EMBL; ALS13383; CAB09867.1; -.
 KW Plasmid; Complete proteome.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 904 MW; 5FCDCT7776D86767 CRC64;

Query Match 42.9%; Score 3; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
 Db 5 Qpp 7

RESULT 3
 Q47569
 ID Q47569 PRELIMINARY; PRT; 11 AA.
 AC Q47569;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
 DE Hypothetical 1.3 kDa protein (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=94162733; PubMed=7764507;
 RA Yamada M., Yanai S., Talkuder A.;
 RT "Analysis of products of the Escherichia coli genomic genes and
 RT regulation of their expressions: an applicable procedure for genomic
 RT analysis of other microorganisms.";
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
 DR EMBL; D21156; BAA04692.1; -.
 KW Hypothetical protein.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1322 MW; C0B8E40E37672732 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
 Db 1 MHQ 3

RESULT 4
 Q8UUP1
 ID Q8UUP1 PRELIMINARY; PRT; 11 AA.
 AC Q8UUP1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Beta-TrCP protein (Fragment).
 GN BETA-TRCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Carnevali P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis";
RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
DR ENBL; AJ428930; CAD21927.1; -.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 9 QPP 11

RESULT 5
Q9USJ2
ID Q9USJ2 PRELIMINARY; PRT; 13 AA.
AC Q9USJ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GPI-phospholipase C (Fragment).
GN GPI-PLC.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILTAR1;
RA Webb H.D., Gaud A.F., Carrington M.;
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally related genes or to genes showing the same developmentally regulated expression";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ250727; CAB60093.1; -.
DR InterPro: IPR003633; Varsurf_glyc_PPLC.
DR Pfam: PF03490; Varsurf_PPLC; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 11 SWM 13

RESULT 6
Q67604
ID Q67604 PRELIMINARY; PRT; 13 AA.
AC Q67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BCL.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;

RT "Diversity among geminiviruses associated with vegetables from Valle del Fuerte, Sinaloa, Mexico";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR ENBL; L27273; AAA47820.1; -.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1376 MW; D471DB4D634E76C2 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 7 QPP 9

RESULT 7
Q9S8N8
ID Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis";
RL Electrophoresis 14:1060-1066 (1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 4 QPP 6

RESULT 8
Q9JHB6
ID Q9JHB6 PRELIMINARY; PRT; 16 AA.
AC Q9JHB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Meprin 1 beta (Fragment).
GN MEP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96147211; PubMed=8567689;
RA Dietrich J.M., Jiang W., Bond J.S.;
RT "A novel meprin beta' mRNA in mouse embryonal and human colon carcinoma cells";
RL J. Biol. Chem. 271:2271-2278 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Jiang W., Kumar J.M., Bond J.S.;
RT "Structure of the mouse metalloprotease meprin beta gene (Meplb): alternative splicing in cancer cells";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF160982; AAF80401.1; -;
 DR MGI; MGI:96964; Mep1b.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1979 MW; EB9785A3F6189622 CRC64;
 Query Match 42.9%; Score 3; DB 11; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOP 6
 DB 5 HOP 7

RESULT 9

Q06800 PRELIMINARY; PRT; 17 AA.
 AC Q06800;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE N1780.
 GN N1780.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96287653; PubMed=8686380;
 RA Nasr F., Becam A.M., Herbert C.J.;
 RT "The sequence of 36.8 kb from the left arm of chromosome XIV reveals
 RT 24 complete open reading frames: 18 correspond to new genes, one of
 RT which encodes a protein similar to the human myotonic dystrophy
 RT kinase.";
 RL Yeast 12:169-175(1996).
 DR EMBL; X92517; CAA63292.1; -;
 SQ SEQUENCE 17 AA; 2139 MW; BD7E9AFAADF754AF CRC64;

Query Match 42.9%; Score 3; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
 DB 1 MHQ 3

RESULT 10

Q14001 PRELIMINARY; PRT; 17 AA.
 AC Q14001;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Cyclic nucleotide phosphodiesterase (Fragment).
 GN CGIPDEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97079687; PubMed=8921398;
 RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
 RT "Molecular cloning and chromosomal assignment of the human homologue
 RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
 RT in fat metabolism located at 11p15.1.";
 RL Genomics 37:211-218(1996).
 DR EMBL; X95522; CAA64776.1; -;
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 DB 15 QPP 17

RESULT 11

Q9JIE9 PRELIMINARY; PRT; 18 AA.
 AC Q9JIE9;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Protein arginine N-methyltransferase 1 (Fragment).
 GN MRMT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20307889; PubMed=10848611;
 RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;
 RT "Arginine N-methyltransferase 1 is required for early postimplantation
 RT mouse development, but cells deficient in the enzyme are viable.";
 RL Mol. Cell. Biol. 20:4859-4869(2000).
 DR EMBL; AF32718; AAF37294.1; -;
 KW Methyltransferase; Transferase.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1931 MW; 392B2C312C4A8372 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 DB 13 QPP 15

RESULT 12

Q9PRT0 PRELIMINARY; PRT; 19 AA.
 AC Q9PRT0;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE 23A7 antigen (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95332492; PubMed=7608337;
 RA Denburg J.L., Caldwell R.T., Warner J.M.;
 RT "Developmental changes in epitope accessibility as an indicator of
 RT multiple states of an immunoglobulin-like neural cell adhesion
 RT molecule.";
 RL J. Comp. Neurol. 354:533-550(1995).

SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EBD03 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

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Db          15 QPP 17
||||
RESULT 13
Q9PRN4      PRELIMINARY;      PRT;      19 AA.
AC Q9PRN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match      42.9%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 QPP 7
||||
Db          14 QPP 16

RESULT 14
Q8RGY4      PRELIMINARY;      PRT;      20 AA.
AC Q8RGY4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein FN0141.
GN FN0141.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasteva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Ponstein M., Kyrpides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; A2010528; AAL94347.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 20 AA; 2542 MW; 15BD7516B34C2A14 CRC64;

Query Match      42.9%; Score 3; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 QPP 7
||||
Db          12 QPP 14

RESULT 15
P72081      PRELIMINARY;      PRT;      7 AA.
AC P72081;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CEFF.
OS Nocardia lactandurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactandurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RT O-carbamoyltransferase for cephamycin biosynthesis.";
RL Gene 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 MH 4
||||
Db          2 MH 3

RESULT 16
Q28742      PRELIMINARY;      PRT;      7 AA.
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Heu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match      28.6%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 MH 4
||||
Db          3 MH 4

RESULT 17
P92214      PRELIMINARY;      PRT;      7 AA.
AC P92214;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)

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DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein 11 (Fragment).
 GN RPS11.
 OS Amblyopyrum muticum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Amblyopyrum.
 OX NCBI_TaxID=4595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H5572; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77756; CAB01346.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

 Query Match 28.6%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 PP 7
 Db 1 PP 2

 RESULT 18
 P92393
 ID P92393 PRELIMINARY; PRT; 7 AA.
 AC P92393;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein 11 (Fragment).
 GN RPS11.
 OS Hordeum vulgare (Barley).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H3139; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77764; CAB01370.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

 Query Match 28.6%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 PP 7
 Db 1 PP 2

 RESULT 19
 P92403
 ID P92403 PRELIMINARY; PRT; 7 AA.
 AC P92403;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein 11 (Fragment).
 GN RPS11.
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Lophopyrum.
 OX NCBI_TaxID=4588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6692; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77743; CAB01307.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

 Query Match 28.6%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 PP 7
 Db 1 PP 2

 RESULT 20
 P92427
 ID P92427 PRELIMINARY; PRT; 7 AA.
 AC P92427;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN RPS11.
 OS Peridictyon sanctum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Peridictyon.
 OX NCBI_TaxID=37683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H5575; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77749; CAB01325.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

 Query Match 28.6%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 PP 7
 Db 1 PP 2

 RESULT 21
 P92430
 ID P92430 PRELIMINARY; PRT; 7 AA.

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AC P92430;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OC NCBI_TaxID=37682;
RN [1]_TaxID=37682;
RP SEQUENCE FROM N.A.
RC STRAIN=H6688; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 22
P92221
ID P92221 PRELIMINARY; PRT; 7 AA.
AC P92221;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromae; Bromus.
OC NCBI_TaxID=15371;
RN [1]_TaxID=15371;
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 23
P92425
ID P92425 PRELIMINARY; PRT; 7 AA.
AC P92425;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OC NCBI_TaxID=4604;
RN [1]_TaxID=4604;
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 24
P92381
ID P92381 PRELIMINARY; PRT; 7 AA.
AC P92381;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=52712;
RN [1]_TaxID=52712;
RP SEQUENCE FROM N.A.
RC STRAIN=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 25
P92425

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P92387
ID P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 26
P92210
ID P92210 PRELIMINARY; PRT; 7 AA.
AC P92210;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01391.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

P92387
ID P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

P92210
ID P92210 PRELIMINARY; PRT; 7 AA.
AC P92210;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01391.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

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RESULT 27
P92440
ID P92440 PRELIMINARY; PRT; 7 AA.
AC P92440;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77769; CAB01385.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 28
P92218
ID P92218 PRELIMINARY; PRT; 7 AA.
AC P92218;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77767; CAB01379.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

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RESULT 29
P92390 ID P92390 PRELIMINARY; PRT; 7 AA.
AC P92390;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Heteranthelium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Heteranthelium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01328.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 1 PP 2

RESULT 30
P92372 ID P92372 PRELIMINARY; PRT; 7 AA.
AC P92372;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Haynaldia villosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoidae; Andropogoneae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5561; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01301.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 1 PP 2

RESULT 23
P92390 ID P92390 PRELIMINARY; PRT; 7 AA.
AC P92390;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Heteranthelium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Heteranthelium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01328.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 1 PP 2

RESULT 31
P92442 ID P92442 PRELIMINARY; PRT; 7 AA.
AC P92442;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Taeniatherum caput-medusae (Medusahead).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01358.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 1 PP 2

RESULT 32
P92226 ID P92226 PRELIMINARY; PRT; 7 AA.
AC P92226;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Crithopsis delileana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Crithopsis.
OX NCBI_TaxID=37674;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5558; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77751; CAB01331.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 1 PP 2
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Db          1 PP 2

RESULT 33
P23385
ID P23385 PRELIMINARY; PRT; 7 AA.
AC P23385;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAY-1997 (TREMBlrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96435920; PubMed=8838806;
RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Anand R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT ESTs including 3 members of the Cystatin gene family and
RT identification of CpG islands.";
RL Genomics 32:425-430(1996).
DR EMBL; X88976; CAA61407.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 34
P2421
ID P2421 PRELIMINARY; PRT; 7 AA.
AC P2421;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAY-1997 (TREMBlrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96435920; PubMed=8838806;
RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Anand R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT ESTs including 3 members of the Cystatin gene family and
RT identification of CpG islands.";
RL Genomics 32:425-430(1996).
DR EMBL; X88976; CAA61407.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 35
P2685
ID P2685 PRELIMINARY; PRT; 8 AA.
AC P2685;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Kinin-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RX TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -|- (MYOTROPIC ACTIVITY).
CC -|- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 6 SW 7

RESULT 37

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P82686
 ID P82686 PRELIMINARY; PRT; 8 AA.
 AC P82686;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE Kinin-2 (PEA-K-2).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;
 Query Match 28.6%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 Db 6 SW 7

RESULT 38
 ID P82687 PRELIMINARY; PRT; 8 AA.
 AC P82687;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE Kinin-3 (PEA-K-3).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;
 Query Match 28.6%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 Db 6 SW 7

RESULT 39
 ID P82688 PRELIMINARY; PRT; 8 AA.
 AC P82688;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE Kinin-4 (PEA-K-4).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;
 Query Match 28.6%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 Db 6 SW 7

RESULT 40
 ID P82689 PRELIMINARY; PRT; 8 AA.
 AC P82689;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE Kinin-5 (PEA-K-5).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 865 MW; C76365B449DC775 CRC64;
 Query Match 28.6%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 Db 6 SW 7

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QY      1 SW 2
Db      ||
        6 SW 7

RESULT 41
Q9GMH3
ID Q9GMH3 PRELIMINARY; PRT; 8 AA.
AC Q9GMH3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus obscurus (Dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140833; AAF98686.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 962 MW; 5BD1F417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HQ 5
Db      ||
        7 HQ 8

RESULT 42
Q28866
ID Q28866 PRELIMINARY; PRT; 8 AA.
AC Q28866;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Actin protein (Fragment).
GN ACTIN.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94285813; PubMed=7912407;
RA Palumbi S.R., Baker C.S.;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435 (1994).
DR EMBL; S73467; AAD14118.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 906 MW; 69C866D1F4177408 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HQ 5
Db      ||
        5 HQ 6

RESULT 43

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Q9J205
ID Q9J205 PRELIMINARY; PRT; 8 AA.
AC Q9J205;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Truncated polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Pan X.; Disisceglie A.M.;
RT "Identification of liver-specific quasispecies of the hepatitis C
RT virus in chronically infected patients.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF211054; AAF30114.1; -.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; B1D41AFAF7776DCA CRC64;

Query Match 28.6%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PP 7
Db      ||
        3 PP 4

RESULT 44
Q64971
ID Q64971 PRELIMINARY; PRT; 8 AA.
AC Q64971;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative ORF (Fragment).
OS Alfalfa mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Alfamovirus.
OX NCBI_TaxID=12321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81124289; PubMed=6927843;
RA Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,
RA Bol J.F.;
RT "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus
RT RNAs and the intercalitronic junction in RNA 3.";
RL Nucleic Acids Res. 8:5635-5647 (1980).
DR EMBL; V00047; CAA23416.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;

Query Match 28.6%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SW 2
Db      ||
        2 SW 3

RESULT 45
Q53914
ID Q53914 PRELIMINARY; PRT; 9 AA.
AC Q53914;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Curd protein (Fragment).

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OS Streptomyces cyaneus (Streptomyces curacoi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1904;
RN [1]
RP SEQUENCE FROM N.A.
RA Bergh S.T., Uhlen M.;
RT "Cloning, analysis and heterologous expression of the polyketides
RT synthesis genes of Streptomyces curacoi.";
RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; M33704; AAA26724.1; -.
FT NON-TER 1
SQ SEQUENCE 9 AA; 1027 MW; 995BDDDC4140AB1 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 8 QP 9

RESULT 46
Q43960 Q43960 PRELIMINARY; PRT; 9 AA.
AC Q43960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hydrogenase-related protein (Fragment).
GN HUPA.
OS Azotobacter chroococcum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=353;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCD1.
RX MEDLINE=95055698; PubMed=7966281;
RA Du L., Tibelius K.H., Souza E.M., Garg R.P., Yates M.G.;
RT "Sequences, organization and analysis of the hupZMNORQTV genes from
RT the Azotobacter chroococcum hydrogenase gene cluster.";
RL J. Mol. Biol. 243:549-557(1994).
DR EMBL; L25315; AAA64455.1; -.
FT NON-TER 9
SQ SEQUENCE 9 AA; 1004 MW; EF421DD045B69B11 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MH 4
Db 1 MH 2

RESULT 47
Q99193 Q99193 PRELIMINARY; PRT; 9 AA.
AC Q99193;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RpoB beta-subunit of RNA polymerase (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;

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RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
RT RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 302:1261-1265(1988).
DR EMBL; X15849; CAA33847.1; -.
FT NON-TER 9
SQ SEQUENCE 9 AA; 852 MW; 5B416776DC76727 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 6 PP 7

RESULT 48
Q9UKJ6 Q9UKJ6 PRELIMINARY; PRT; 9 AA.
AC Q9UKJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Androgen receptor (Fragment).
GN AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Li X.Q., Wu Q.F.;
RT "A splice-site mutation in Androgen Receptor gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159087; AAF04001.1; -.
FT NON-TER 1
FT NON-TER 9
SQ SEQUENCE 9 AA; 1272 MW; 6F2B8415B331E684 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MH 4
Db 3 MH 4

RESULT 49
Q9UCS8 Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Ehnlholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metsa J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Biochim. Biophys. Acta 1086:255-260(1991).
FT NON-TER 1
FT NON-TER 9
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C776B CRC64;

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Query Match 28.6%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 3 PP 4

RESULT 50
Q15891 ID Q15891 PRELIMINARY; PRT; 9 AA.
AC Q15891;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP2E8B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinsault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32131; AAA73881.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1030 MW; E56635A1A33686D1 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
DB 2 HQ 3

RESULT 51
Q16386 ID Q16386 PRELIMINARY; PRT; 9 AA.
AC Q16386;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Mex40 protein (Fragment).
GN MEX40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95400293; PubMed=7670464;
RA Budarf M.L., Collins J., Gong W., Roe B., Wang Z., Bailey L.C.,
RA Sellinger B., Michaud D., Driscoll D.A., Emanuel B.S.;
RT "Cloning a balanced translocation associated with DiGeorge syndrome
RT and identification of a disrupted candidate gene.";
RL Nat. Genet. 10:269-278(1995).
DR EMBL; S79485; AAD14301.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1137 MW; 734911A69446837B CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 3 WM 4

RESULT 52
Q9TWV0 ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Antho-RPAMIDB-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=93126143; PubMed=1480510;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 2 PP 3

RESULT 53
Q9GJV2 ID Q9GJV2 PRELIMINARY; PRT; 9 AA.
AC Q9GJV2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus obliquidens (Pacific white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=90247;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140831; AAF98684.1; -.
DR EMBL; AF140826; AAF98679.1; -.
DR EMBL; AF140827; AAF98680.1; -.
DR EMBL; AF140828; AAF98681.1; -.
DR EMBL; AF140829; AAF98682.1; -.
DR EMBL; AF140830; AAF98683.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
DB 8 HQ 9

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RESULT 54
Q9TJ77
ID Q9TJ77 PRELIMINARY; PRT; 9 AA.
AC Q9TJ77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Wilm's tumor protein 1 (Fragment).
GN WTL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; PubMed=11130975;
RA Brouillette J.A., Andrew J.R., Venta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
method."
RL Mamm. Genome 11:1079-1086(2000).
DR EMBL; AF202074; AAF20919.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1231 MW; 58DDF41416D1F403 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 4 HQ 5

RESULT 55
Q9GJV3
ID Q9GJV3 PRELIMINARY; PRT; 9 AA.
AC Q9GJV3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus obscurus (Dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RX Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140834; AAF98687.1; -.
DR EMBL; AF140832; AAF98685.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 4 HQ 5

RESULT 56
Q9GJV1
ID Q9GJV1 PRELIMINARY; PRT; 9 AA.
AC Q9GJV1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus acutus (Atlantic white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=90246;
RN [1]
RP SEQUENCE FROM N.A.
RX Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140825; AAF98678.1; -.
DR EMBL; AF140822; AAF98675.1; -.
DR EMBL; AF140823; AAF98676.1; -.
DR EMBL; AF140824; AAF98677.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 8 HQ 9

RESULT 57
Q8WFT4
ID Q8WFT4 PRELIMINARY; PRT; 9 AA.
AC Q8WFT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Euechinozoa; Diadematozoa; Diadematozoa; Diadematozoa;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA3;
RC MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearce J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema."
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA3;
RC MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
Caribbean reefs."
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012858; AAL33832.2; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 28.6%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 QP 6
||
Db 8 QP 9

RESULT 58

P82440
ID P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 42 KDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture."
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON-TER
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5B1B07 CRC64;

Query Match 28.6%; Score 2; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
||
Db 1 QP 2

RESULT 59

O08979
ID O08979 PRELIMINARY; PRT; 9 AA.
AC O08979;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AML1 protein (fragment).
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=tumor;
RA MEDLINE=97332339; PubMed=9188573;
RX Amtoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; --
FT NON-TER 1
FT NON-TER 9
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match 28.6%; Score 2; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
||
Db 3 QP 4

RESULT 60

O90350
ID O90350 PRELIMINARY; PRT; 9 AA.
AC O90350;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyprotein (fragment).
OS Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=45255;
RN [1]_TaxID=45255;
RP SEQUENCE FROM N.A.
RC STRAIN=SG3419;
RX MEDLINE=99266893; PubMed=10335862;
RA Wong S.B.J., Chan S.H., Ren E.C.;
RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
RT predominance of group 2a and the Asian group 3 variant.";
RL J. Med. Virol. 58:145-153(1999).
DR EMBL; AF078065; AAC32371.1; --
FT NON-TER 9
SQ SEQUENCE 9 AA; 989 MW; D95CA5A5BB9CDDD CRC64;

Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 8 SW 9

RESULT 61

O71069
ID O71069 PRELIMINARY; PRT; 9 AA.
AC O71069;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]_TaxID=11232;
RP SEQUENCE FROM N.A.
RC STRAIN=Dog EPM;
RA Liermann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026238; AAC09168.1; --
FT NON-TER 9
SQ SEQUENCE 9 AA; 984 MW; F29CB32760587331 CRC64;

Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
||
Db 1 MH 2

RESULT 62

O92766
ID O92766 PRELIMINARY; PRT; 9 AA.
AC O92766;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026237; AAC09167.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;
Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 MH 4
Db 1 MH 2
RESULT 63
O71066 PRELIMINARY; PRT; 9 AA.
ID O71066;
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F290045760440441 CRC64;
Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 MH 4
Db 1 MH 2
RESULT 64
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
ID Q9PRJ4
AC Q9PRJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bradykinin.
OS Lepisosteus osseus (Long-nosed gar), and
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus
OX NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar."
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;
Query Match 28.6%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 PP 7
Db 2 PP 3
RESULT 65
Q8AYL5 PRELIMINARY; PRT; 9 AA.
ID Q8AYL5
AC Q8AYL5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two CYP19 genes differentially expressed
RT in the brain and ovary of teleost fish."
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR EMBL; AF324897; AAN32618.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;
Query Match 28.6%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QP 6
Db 7 QP 8
RESULT 66
Q8AUM7 PRELIMINARY; PRT; 9 AA.
ID Q8AUM7
AC Q8AUM7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.

```

OX NCBI_TaxID=7957;
RN [1]_TaxID=7957;
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two CYP19 genes differentially expressed
   in the brain and ovary of teleost fish.";
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR EMBL; AF324895; AN32616.1; -.
DR EMBL; AF324896; AN32617.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match      28.6%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
   ||
Db 7 QP 8

RESULT 67
Q9R5T2 PRELIMINARY; PRT; 10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]_
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
   dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
   ||
Db 4 PP 5

RESULT 68
P83062 PRELIMINARY; PRT; 10 AA.
ID P83062;
AC P83062;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE 92 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]_
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dows B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1044 MW; 36E840B73AEB0777 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
   ||
Db 3 SW 4

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
   ||
Db 3 PP 4

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
   ||
Db 3 PP 4

RESULT 69
Q14096 PRELIMINARY; PRT; 10 AA.
ID Q14096;
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P450IIB6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308828;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P450IIB6 gene: use of a
   cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1; -.
SQ SEQUENCE 10 AA; 885 MW; 4181B9D87DC77767 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
   ||
Db 4 PP 5

RESULT 70
Q15342 PRELIMINARY; PRT; 10 AA.
ID Q15342;
AC Q15342;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Aml1 protein (Fragment).
GN AML1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=96226397; PubMed=8634147;
RA Levanon D., Bernstein Y., Negraru V., Ghozi M.C., Bar-Am I.,
RA Aloya R., Goldenberg D., Lotem J., Groner Y.;
RT "A large variety of alternatively spliced and differentially expressed
   mRNAs are encoded by the human acute myeloid leukemia gene AML1.";
RL DNA Cell Biol. 15:175-185(1996).
DR EMBL; X90978; CAA62465.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1254 MW; 8D99287B441AF365 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
   ||
Db 3 SW 4

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RESULT 71
Q9UCR0          PRELIMINARY;      PRT;      10 AA.
ID Q9UCR0
AC Q9UCR0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffman E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 2 PP 3

RESULT 72
Q9UE86          PRELIMINARY;      PRT;      10 AA.
ID Q9UE86
AC Q9UE86
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92042176; PubMed=1939261;
RA Hawkins J.R., Superti-Furga A., Steinmann B., Dalglish R.;
RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis
RT imperfecta.";
RL J. Biol. Chem. 266:22370-22374(1991).
DR EMBL; S66556; AAB20361.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 777 MW; 2D20F6D8676DD867 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 2 PP 3

RESULT 73
Q8WFT6          PRELIMINARY;      PRT;      10 AA.
ID Q8WFT6
AC Q8WFT6
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA1;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA1;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012856; AAL33830.2; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1301 MW; EDBB101B173B46CA CRC64;

Query Match      28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 9 QP 10

RESULT 74
Q8WFT5          PRELIMINARY;      PRT;      10 AA.
ID Q8WFT5
AC Q8WFT5
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA2;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA2;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012857; AAL33831.2; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1301 MW; EDBB101B173B46CA CRC64;

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SQ SEQUENCE 10 AA; 1262 MW; COBB101B173B46DD CRC64;
Query Match      28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 9 QP 10

RESULT 75
Q8SHA8
ID Q8SHA8 PRELIMINARY; PRT; 10 AA.
AC Q8SHA8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Rhampholeon spectrum.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Rhampholeon.
OX NCBI_TaxID=179929;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448772; AAL90598.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1279 MW; 35BF8E27336409D7 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 2 QP 3

Search completed: November 25, 2003, 19:34:03
Job time : 14.1453 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 17.8663 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-24

03-03-041-8
 Perfect score: 7
 Sequence: 1 SWMHOPP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size :

Total number of hits satisfying chosen parameters: 399878

Minimum	DB	seq	length:	3
Maximum	DB	seq	length:	20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*

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- 24: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	%			Description		
	Score	Match	Length	DB	ID	
1	7	100.0	7	22	AAB72269	Colostrinin derive
2	7	100.0	7	22	AAB72522	Colostrinin peptid
3	7	100.0	7	22	AAB72554	Colostrinin peptid
4	7	100.0	7	22	AAB59332	Ewe colostrinin pe
5	7	100.0	7	23	AAE20251	Colostrinin consti
6	7	100.0	7	23	AAM51058	Colostrinin consti
7	7	100.0	7	23	AAO14600	Neural cell regula
8	6	85.7	19	19	AAW40310	Human IRAK protein
9	5	71.4	15	22	AAB72279	Colostrinin derive

83 3 42.9 7 22 AAM44329 H11 binding site c
84 3 42.9 7 22 AAM45562 H11 binding site c
85 3 42.9 7 22 AAM45567 H11 binding site c
86 3 42.9 7 22 AAM45582 H11 binding site c
87 3 42.9 7 22 AAM45587 H11 binding site c
88 3 42.9 7 22 AAM45619 H11 binding site c
89 3 42.9 7 22 AAM45624 H11 binding site c
90 3 42.9 7 22 AAM45639 H11 binding site c
91 3 42.9 7 22 AAM45644 H11 binding site c
92 3 42.9 7 22 AAM45649 H11 binding site c
93 3 42.9 7 22 AAM45654 H11 binding site c
94 3 42.9 7 22 AAM45659 H11 binding site c
95 3 42.9 7 22 AAM45664 H11 binding site c
96 3 42.9 7 22 AAM45669 H11 binding site c
97 3 42.9 7 22 AAM45674 H11 binding site c
98 3 42.9 7 22 AAM45679 H11 binding site c
99 3 42.9 7 22 AAM45684 H11 binding site c
100 3 42.9 7 22 AAM45689 H11 binding site c

ALIGNMENTS

RESULT 1
AAB72269
ID AAB72269 standard; peptide; 7 AA.
XX
AC AAB72269;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 24.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
FN WO20011937-A2.
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SWMHQPP 7
Db 1 SWMHQPP 7
RESULT 2
AAB72522
ID AAB72522 standard; Peptide; 7 AA.
XX
AC AAB72522;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #23.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
FN WO200112650-A2.
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 26; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SWMHQPP 7
Db 1 SWMHQPP 7
RESULT 3
AAB72554
ID AAB72554 standard; Peptide; 7 AA.
XX
AC AAB72554;
XX
DT 09-MAY-2001 (first entry)
XX

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SWMHQPP 7
 |||||
 Db 1 SWMHQPP 7

RESULT 6
 AAM51058
 ID AAM51058 standard; Peptide; 7 AA.
 AC AAM51058;
 XX 30-MAY-2002 (first entry)
 DT Colostrinin constituent peptide (casein amino acids 157-163).
 XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 7 /note= "optional C-terminal amidation"
 FT
 XX WO200213849-A1.
 XX 21-FEB-2002.
 XX 17-AUG-2000; 2000WO-US22775.
 XX 17-AUG-2000; 2000WO-US22775.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI WPI; 2002-269150/31.
 DR Modulation of blood cell proliferation in a patient involves use of
 XX blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX Claim 1; Page 34; 54pp; English.

CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 157-163. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SWMHQPP 7
 |||||
 Db 1 SWMHQPP 7

RESULT 7
 AAO14600
 ID AAO14600 standard; peptide; 7 AA.
 XX AAO14600;
 AC AAO14600;
 XX 27-MAY-2002 (first entry)
 DT Neural cell regulatory colostrinin peptide 23.
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX neural cell treatment.
 XX Unidentified.

XX Key Location/Qualifiers
 FT Modified-site 7 /note= "Optional C-terminal amide"
 FT
 XX WO200213851-A1.
 XX 21-FEB-2002.
 XX 17-AUG-2000; 2000WO-US22777.
 XX 17-AUG-2000; 2000WO-US22777.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA Boldogh I, Stanton JG, Hughes TK;
 PI WPI; 2002-269152/31.
 DR Promoting cell differentiation in a patient involves use of blood cell
 XX regulator selected from colostrinin, its constituent peptide and/or
 PT analog -
 XX Claim 7; Page 21; 37pp; English.

CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

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CC the method of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
Db 1 SWMHQPP 7

RESULT 8
AAW40310
ID AAW40310 standard; Protein; 19 AA.
XX
AC AAW40310;
XX
XX
XX 23-JUN-1998 (first entry)
XX
DE Human ITAK protein peptide substrate.
XX
XX Interleukin-1/tumour necrosis factor activated kinase; ITAK; inhibitor;
XX cytokine mediated inflammation; antagonist; disorder; therapy.
XX
XX Synthetic.
XX
XX WO9747750-A1.
XX
XX 18-DEC-1997.
XX
XX 09-JUN-1997; 97WO-US08516.
XX
XX 10-JUN-1996; 96US-0633414.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX
XX Anderson DM, Bird TA, Sims JE, Virca G;
XX
XX WPI; 1998-052314/05.
XX
XX Nucleic acid encoding interleukin-1/tumour necrosis factor activated
XX kinase - used to identify specific antagonists for treatment of
XX cytokine-mediated inflammation
XX
XX Claim 20; Page 33; 80pp; English.
XX
XX This sequence represents a peptide substrate used to assay a novel
XX interleukin-1/tumour necrosis factor alpha activated kinase (ITAK).
XX Antagonists of ITAK are used to treat IL-1 or TNF alpha-mediated
XX inflammatory disorders e.g. rheumatoid arthritis, inflammatory bowel
XX disease, type I diabetes, psoriasis, Alzheimer's disease, reperfusion
XX injury, malignancy, transplant rejection, neuropathy associated with
XX human immunodeficiency virus etc. Cells containing ITAK can be used to
XX raise antibodies for assay of ITAK or to inhibit IL-1 and TNF alpha
XX activity. Gene products that associate with ITAK are potential inhibitors
XX and can be used to detect ITAK genes. Antisense sequences inhibit
XX expression of ITAK. Inhibition of ITAK selectively blocks cell responses
XX to IL-1 and TNF alpha, but not responses to other cytokines.
XX
XX Sequence 19 AA;

Query Match 85.7%; Score 6; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQP 6
Db 12 SWMHQP 17

RESULT 9
AAW72279
ID AAW72279 standard; peptide; 15 AA.
XX
XX AAW72279;
AC
XX
XX 14-MAY-2001 (first entry)
XX
XX Colostrinin derived cytokine inducing peptide SEQ ID 34.
XX
XX Colostrinin; immune response; cytokine; blood cell proliferation;
XX central nervous system disorder; neurological disorder; mental disorder;
XX dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX neurosis; infection.
XX
XX Synthetic.
XX
XX WO200111937-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22818.
XX
XX 17-AUG-1999; 99US-0149311.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
XX WPI; 2001-202804/20.
XX
XX Inducing a cytokine and modulating an immune response, useful for
XX treating central nervous system diseases and bacterial and viral
XX infections, comprises administering colostrinin as an immunological
XX regulator -
XX
XX Claim 1; Page 34; 50pp; English.
XX
XX Sequences AAW72246 - AAW72275 represent peptides derived from colostrinin,
XX a proline rich polypeptide aggregate contained in colostrum. The
XX peptides have immune response modulatory activity, and are capable of
XX inducing cytokines. Colostrinin and its derived peptides are useful for
XX inducing cytokine production, for modulating an immunological response
XX and for inducing blood cell proliferation. The peptides are useful in the
XX treatment of disorders of the central nervous system, neurological
XX disorders, mental disorders, dementia, neurodegenerative diseases,
XX Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
XX disorders of the immune system, bacterial and viral infections and
XX acquired immunological deficiencies.
XX
XX Sequence 15 AA;

Query Match 71.4%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7
Db 1 MHQPP 5

RESULT 10
AAW72531
ID AAW72531 standard; Peptide; 15 AA.
XX
XX AAW72531;
AC
XX
XX 09-MAY-2001 (first entry)
XX
XX Colostrinin peptide #32.
XX
XX Dermatological; oxidative stress regulator; colostrinin.
XX

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OS Unidentified.
XX WO200112650-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22665.
XX
XX 17-AUG-1999; 99US-0149310.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2001-218342/22.
XX
XX Modulating oxidative stress level in a cell, involves contacting the
XX cell with an oxidative stress regulator selected from colostrinin, its
XX constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 26; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.
XX
XX Sequence 15 AA;
SQ
  Query Match          71.4%; Score 5; DB 22; Length 15;
  Best Local Similarity 100.0%; Pred. No. 5.9;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 3 MHQPP 7
  Db 1 MHQPP 5
  |||||
  |||||

RESULT 11
AAB72563
ID AAB72563 standard; Peptide; 15 AA.
XX
XX AAB72563;
AC
XX
XX 09-MAY-2001 (first entry)
DT
XX
XX Colostrinin peptide #32.
DE
XX
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrinum.
XX
XX Unidentified.
OS
XX
XX WO200112651-A2.
PN
XX
XX 22-FEB-2001.
PD
XX
XX 17-AUG-2000; 2000WO-US22774.
PF
XX
XX 17-AUG-1999; 99US-0149633.
PR
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
  Query Match          71.4%; Score 5; DB 22; Length 15;
  Best Local Similarity 100.0%; Pred. No. 5.9;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 3 MHQPP 7
  Db 1 MHQPP 5
  |||||
  |||||

RESULT 12
AAB59334
ID AAB59334 standard; Peptide; 15 AA.
XX
XX AAB59334;
AC
XX
XX 21-MAR-2001 (first entry)
DT
XX
XX Ewe colostrinin peptide fragment C-9.
DE
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO200075173-A2.
PN
XX
XX 14-DEC-2000.
PD
XX
XX 02-JUN-2000; 2000WO-GB02128.
PF
XX
XX 02-JUN-1999; 99GB-0012852.
PR
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
DR
XX
XX Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
PS
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 15 AA;
SQ
  Query Match          71.4%; Score 5; DB 22; Length 15;
  Best Local Similarity 100.0%; Pred. No. 5.9;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 3 MHQPP 7
  Db 1 MHQPP 5
  |||||
  |||||

  Query Match          71.4%; Score 5; DB 22; Length 15;
  Best Local Similarity 100.0%; Pred. No. 5.9;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 3 MHQPP 7
  Db 1 MHQPP 5
  |||||
  |||||

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RESULT 13

AAE20261
ID AAE20261 standard; peptide; 15 AA.

AAE20261;
AC

XX 18-JUN-2002 (first entry)

XX Colostrinin constituent peptide #32.

XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.

XX Unidentified.

XX Key Location/Qualifiers

PH Modified-site 15 /note= "Optionally C-terminal amide"

FT WO200213850-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22776.

XX 17-AUG-2000; 2000WO-US22776.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2002-269151/31.

XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog

XX Claim 6; Page 26; 51pp; English.

XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidizing species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.

XX Sequence 15 AA;

Query Match 71.4%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7

DB 1 MHQPP 5

RESULT 14

AA51066

XX ID AA51066 standard; Peptide; 15 AA.

XX AC AA51066;

XX 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 159-173).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

XX Blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Modified-site 15 /note= "optional C-terminal amidation"

FT WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified
CC as having a beta-casein homologue precursor, and corresponds to
CC casein amino acids 159-173. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture, a tissue, an organ
CC or an organism, and the cell is mammalian, including human;
CC modulating an immune response in a cell by contact with the
CC immunological regulator under conditions effective to induce a
CC cytokine; modulating an immune response in a patient by administering
CC an immunological regulator under conditions effective to induce a
CC cytokine, where the immunological regulator is administered topically
CC or as part of a dietary supplement, and where the immune response is
CC specific or non specific, an interferon response or an antibody
CC response; modulating blood cell proliferation by contacting blood
CC cells with a blood cell regulator, where the blood cells are present
CC in a cell culture or an organism, are mammalian or human, and where
CC the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patient. A
CC claimed cytokine-inducing composition comprises a pharmaceutical
CC carrier and an active agent such as the present peptide.

XX Sequence 15 AA;

Query Match 71.4%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7

DB 1 MHQPP 5

KW	antibiotic; SERCA2 inhibitor; heart insufficiency; circulatory system;
KW	diabetes; infection.
XX	
OS	Stachybotrys echinata.
XX	
FN	EP1130027-A1.
PD	
XX	05-SEP-2001.
XX	
PF	29-FEB-2000; 2000EP-0104114.
XX	
PR	29-FEB-2000; 2000EP-0104114.
XX	
PA	(AVET) AVENTIS PHARMA DEUT GMBH.
XX	
PI	Vertesy L, Kogler H, Markus A, Schiell M;
XX	
DR	WPI; 2001-627636/73.
XX	
PT	New isoindole derivatives prepared by microbial fermentation, useful
PT	for the treatment and prevention of heart insufficiency, diabetes
PT	mellitus and microbial infection
XX	
PS	Claim 6; Page 18; 21pp; German.
XX	
CC	The present invention relates to isoindole derivatives capable of acting
CC	as SERCA2 inhibitors. These can be used in the prevention and treatment
CC	of heart insufficiency, weakness in the heart and circulatory system,
CC	diabetes and microbial infection. The present sequence is a peptide which
CC	may form part of the compound of the invention.
XX	
SQ	Sequence 10 AA;
	Query Match 57.1%; Score 4; DB 22; Length 10;
	Best Local Similarity 100.0%; Pred. No. 79;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 MHQP 6
Db	1 MHQP 4
	RESULT 17
ABG95549	
ID	ABG95549 standard; Peptide; 11 AA.
XX	
AC	ABG95549;
XX	
DT	15-JAN-2003 (first entry)
XX	
DE	Human novel secreted protein gene 86 polypeptide #1.
XX	
KW	Human; secreted protein; autoimmune disease; chemotaxis;
KW	rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW	liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW	cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW	nervous system disorders; Alzheimer's disease; infection;
KW	ocular disorder; corneal infection; wound healing; tissue regeneration;
KW	epithelial cell proliferation; organ transplantation; food additive;
XX	preservative; nutritional.
XX	
OS	Homo sapiens.
XX	
PN	US6420526-B1.
XX	
PD	16-JUL-2002.
XX	
PF	08-SEP-1998; 98US-0149476.
XX	
PR	07-MAR-1997; 97US-038621P.
PR	07-MAR-1997; 97US-040161P.
PR	07-MAR-1997; 97US-040162P.
PR	07-MAR-1997; 97US-040163P.
XX	

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PR 07-MAR-1997; 97US-040333P.
PR 07-MAR-1997; 97US-040334P.
PR 07-MAR-1997; 97US-040336P.
PR 07-MAR-1997; 97US-040626P.
PR 11-APR-1997; 97US-043311P.
PR 11-APR-1997; 97US-043312P.
PR 11-APR-1997; 97US-043313P.
PR 11-APR-1997; 97US-043314P.
PR 11-APR-1997; 97US-043315P.
PR 11-APR-1997; 97US-043568P.
PR 11-APR-1997; 97US-043569P.
PR 11-APR-1997; 97US-043576P.
PR 11-APR-1997; 97US-043578P.
PR 11-APR-1997; 97US-043580P.
PR 11-APR-1997; 97US-043669P.
PR 11-APR-1997; 97US-043670P.
PR 11-APR-1997; 97US-043671P.
PR 11-APR-1997; 97US-043672P.
PR 11-APR-1997; 97US-043674P.
PR 23-MAY-1997; 97US-047492P.
PR 23-MAY-1997; 97US-047500P.
PR 23-MAY-1997; 97US-047501P.
PR 23-MAY-1997; 97US-047502P.
PR 23-MAY-1997; 97US-047503P.
PR 23-MAY-1997; 97US-047581P.
PR 23-MAY-1997; 97US-047582P.
PR 23-MAY-1997; 97US-047583P.
PR 23-MAY-1997; 97US-047584P.
PR 23-MAY-1997; 97US-047585P.
PR 23-MAY-1997; 97US-047586P.
PR 23-MAY-1997; 97US-047587P.
PR 23-MAY-1997; 97US-047588P.
PR 23-MAY-1997; 97US-047589P.
PR 23-MAY-1997; 97US-047590P.
PR 23-MAY-1997; 97US-047592P.
PR 23-MAY-1997; 97US-047593P.
PR 23-MAY-1997; 97US-047594P.
PR 23-MAY-1997; 97US-047595P.
PR 23-MAY-1997; 97US-047596P.
PR 23-MAY-1997; 97US-047597P.
PR 23-MAY-1997; 97US-047598P.
PR 23-MAY-1997; 97US-047599P.
PR 23-MAY-1997; 97US-047600P.
PR 23-MAY-1997; 97US-047601P.
PR 23-MAY-1997; 97US-047612P.
PR 23-MAY-1997; 97US-047613P.
PR 23-MAY-1997; 97US-047614P.
PR 23-MAY-1997; 97US-047615P.
PR 23-MAY-1997; 97US-047617P.
PR 23-MAY-1997; 97US-047618P.
PR 23-MAY-1997; 97US-047632P.
PR 23-MAY-1997; 97US-047633P.
PR 06-JUN-1997; 97US-048964P.
PR 06-JUN-1997; 97US-048974P.
PR 13-JUN-1997; 97US-049610P.
PR 08-JUL-1997; 97US-051926P.
PR 16-JUL-1997; 97US-052874P.
PR 18-AUG-1997; 97US-052724P.
PR 22-AUG-1997; 97US-056630P.
PR 22-AUG-1997; 97US-056631P.
PR 22-AUG-1997; 97US-056632P.
PR 22-AUG-1997; 97US-056633P.
PR 22-AUG-1997; 97US-056637P.
PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056845P.
PR 22-AUG-1997; 97US-056862P.
PR 22-AUG-1997; 97US-056864P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.

PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056888P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056894P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057761P.
PR 05-SEP-1997; 97US-057650P.
PR 05-SEP-1997; 97US-057669P.
PR 12-SEP-1997; 97US-058785P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98WO-US04493.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bedharik DR;
PI Endress GA, Yu G, Ni J, Feng P, Young PS, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 2002-634796/68.
XX
XX New isolated human secreted protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -
XX
PS Disclosure; Column 78; 129pp; English.
XX
CC The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of
CC 309 cDNA sequences also given in the specification. The protein is used
CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents one of the novel human
CC secreted proteins of the invention.
XX
XX Sequence 11 AA;
Query Match 57.1%; Score 4; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HQPP 7
Db 1 HQPP 4

```

RESULT 18

AAU93631
ID AAU93631 standard; Peptide; 11 AA.
AC AAU93631;
XX
DT 02-JUL-2002 (first entry)
XX
DE Granulocyte-colony stimulating factor receptor binding peptide #437.
XX
KW G-CSFR; granulocyte-colony stimulating factor receptor; cytokine;
KW haematopoietic growth factor; neutrophil proliferation; AIDS;
KW neutrophil differentiation; acquired immunodeficiency syndrome;
KW chemotherapy-induced neutropaenia; community acquired pneumonia;
KW depressed neutrophil count; immunostimulant.
XX
OS Synthetic.
XX
PN WO200207676-A2.
XX
PD 31-JAN-2002.
XX
PF 20-JUL-2001; 2001WO-US23046.
XX
PR 20-JUL-2000; 2000US-0620091.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Cwila SE, Balu P, Duffin DJ, Piplani S, McEwen-Merrill B;
PI Schatz PJ;
DR
XX WPI; 2002-329382/36.
XX
PT Novel compounds, useful for treating depressed neutrophil count,
PT comprise peptide chains of approximately 6 to 40 amino acids in length
PT that bind to granulocyte-colony stimulating factor receptor -
XX
PS Claim 41; Page 66; 90pp; English.
XX
CC The invention relates to compounds comprising a peptide chain
CC approximately 6 to 40 amino acids in length that binds to granulocyte-
CC colony stimulating factor receptor (G-CSFR). The compounds contain
CC specific sequences of the generic peptides appearing as AAU79402-AAU79406
CC and the generic sequences XV 1XV 2XV 3XV 4XV 5XV 6XV 7XV 8 (where
CC XV 1 = E, C, Q, V or Y; XV 2 = E, A, L, M, S, W or Q; XV 3 = K, R or T;
CC XV 4 = L, A or G; and XV 5 = R, A, M, H, E, V, L, G, D, Q or S; XV 6 = E or
CC V; XV 7 = A or G; and XV 8 = R, H, G or L) and XVI 1XVI 2XVI 3XVI 4XVI 5
CC XVI 6XVI 7XVI 8XVI 9 (where XVI 1 = A, E or G; XVI 2 = E, H or D;
CC XVI 3 = R or G; XVI 4 = K, Y, M, N, Q, R, D, I, S or E; XVI 5 = A, S or
CC P; XVI 6 = E, D, T, Q, K or A; XVI 7 = R, W, K, L, S, A or Q; XVI 8 = R
CC or E; and XVI 9 = W, G or R). The compounds are used for treating
CC conditions associated with depressed neutrophil count e.g. chemotherapy-
CC induced neutropaenia, AIDS-induced neutropaenia or community-acquired
CC pneumonia-induced pneumonia. The compounds are useful as in vitro as
CC tools for understanding the biological role of granulocyte-colony
CC stimulating factor (G-CSF) a haematopoietic growth factor and
CC cytokine that stimulates neutrophil proliferation and differentiation),
CC including evaluation of many factors thought to influence, and be
CC influenced by, production of white blood cells, in the development of
CC compounds that bind to G-CSFR, as reagents for detecting G-CSF receptor
CC or related receptor on living cells, fixed cells, in biological fluid, in
CC tissue homogenates or in purified natural biological materials, in situ
CC staining, fluorescence-activated cell sorting (FACS), Western blotting or
CC enzyme-linked immunoadsorbent assay (ELISA), in receptor purification or
CC in purifying cells expressing G-CSFR on the cell surface (or inside
CC permeabilised cells) as a commercial research reagent for various medical
CC and diagnostic uses or to treat a disease that would benefit from the
CC ability to of a compound to mimic the effects of G-CSF in vivo.
CC The compounds bind specifically to G-CSFR and allow for studies of
CC biological activities mediated by the receptor and for the treatment of
CC diseases, disorders and conditions that would benefit from activating or
CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
CC the invention.
XX

SQ Sequence 11 AA;
Query Match 57.1%; Score 4; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SWMH 4
DB 5 SWMH 8
RESULT 19
ABR00957
ID ABR00957 standard; peptide; 11 AA.
XX AC ABR00957;
XX 12-MAY-2003 (first entry)
XX Human gene 11-encoded secreted protein HAGEQ79, SEQ ID NO:438.
XX Human; secreted protein; cancer; tumour; hyperproliferative disorder;
KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;
KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
KW drug screening; chromosome identification; chromosome mapping;
KW cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
KW antianaemic; vulnery.
XX Homo sapiens.
XX WO200277013-A2.
XX 03-OCT-2002.
XX 26-MAR-2002; 2002WO-US09370.
XX 27-MAR-2001; 2001US-278650P.
PR 12-SEP-2001; 2001US-0950082.
PR 12-SEP-2001; 2001US-0950083.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-040578/03.
DR N-PSDB; ABZ73291.
XX New human secreted proteins and nucleic acids, useful for detecting or
XX treating cancer or other hyperproliferative disorders, autoimmune
XX disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
PS Claim 13; Page 1384; 2474pp; English.
XX ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted
XX protein genes, and ABR00947-ABP01363 represent the proteins they encode.
XX ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The
XX invention also encompasses antibodies specific for the secreted proteins,
XX the use of the secreted proteins in drug screening and recombinant
XX vectors and host cells comprising a nucleic acid of the invention. The
XX secreted proteins are thought to be involved in biological activities
XX associated with cellular signalling, cellular differentiation, cell
XX migration, prohormone activation and neurotransmitter activity. The
XX secreted proteins, nucleic acids encoding them, antibodies or antibody
XX fragments specific for the secreted proteins, and modulators of protein
XX activity are useful for diagnosing or treating cancers or other
XX hyperproliferative disorders. Additionally, the secreted proteins and
XX their nucleic acids may also be used in the treatment of autoimmune
XX disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
XX (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote
XX wound healing. Nucleic acids of the invention may be used for chromosome
XX identification, chromosome mapping, in gene therapy, for identifying
XX individuals from minute biological samples, as hybridisation probes, and
XX as molecular weight markers. The present sequence represents a human

CC secreted protein of the invention.
 XX Sequence 11 AA;
 SQ

Query Match 57.1%; Score 4; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 |||||
 Db 1 MHQP 4

RESULT 20
 ABP99483
 ID ABP99483 standard; Protein; 11 AA.
 XX
 AC ABP99483;
 XX
 DT 26-MAR-2003 (first entry)
 DE Human secreted protein SEQ ID NO 427.
 XX
 KW Human; secreted protein; neurotropic; neuroprotective; cytostatic;
 KW virucide; dermatological; immunosuppressive; anti-infectious; anti-HIV;
 KW vulnary; antibacterial; antiparkinsonian; antitickling; antianaemic;
 KW antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective;
 KW antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant;
 KW antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine;
 KW cardiovascular disorder; neurological disease; nephrotropic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO20027186-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US09188.
 XX
 PR 27-MAR-2001; 2001US-278650P.
 PR 12-SEP-2001; 2001US-0950082.
 PR 12-SEP-2001; 2001US-0950082.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 XX WPI; 2003-040583/03.
 DR N-PSDB; ABZ66904.
 XX
 PT New human secreted proteins encoded by genes contained in cDNA clones
 PT (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g.
 PT AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne
 PT encephalitis or West Nile fever -
 PS
 PS Claim 1; Page 1393; 2423pp; English.
 XX
 CC The invention relates to novel human genes (ABZ66891-ABZ68209) and the
 CC encoded secreted proteins (ABP99470-ABP99872) useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The genes are isolated from a range of human tissues disclosed
 CC in the specification. The nucleic acids, proteins, antibodies and
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:
 CC (a) cancer, e.g. breast and ovarian cancer and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
 CC bacterial, fungal and parasitic infections.

XX Sequence 11 AA;
 SQ

Query Match 57.1%; Score 4; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 |||||
 Db 1 MHQP 4

RESULT 21
 AAB28056
 ID AAB28056 standard; peptide; 12 AA.
 XX
 AC AAB28056;
 XX
 DT 02-FEB-2001 (first entry)
 DE Human secreted protein SEQ ID NO: 104.
 XX
 KW Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200055177-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US06058.
 XX
 PR 12-MAR-1999; 99US-0124145.
 PR 03-DEC-1999; 99US-0168654.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 XX WPI; 2000-638177/61.
 DR N-PSDB; AAC59152.
 XX
 PT Novel nucleic acids encoding 49 human secreted proteins useful for
 PT treating cancers, hyperproliferative disorders, inflammatory disorders,
 PT neurological disorders and cardiovascular disorders -
 PS
 PS Claim 11; Page 363; 389pp; English.
 XX
 CC Sequences AAB28012-B28060 represent the amino acid sequences of 49
 CC human secreted proteins encoded by the genes AAC59108-C59156. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

XX Sequence 12 AA;
 SQ

Query Match 57.1%; Score 4; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 91;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 Db 1 MHQP 4

RESULT 22
 AAY92771
 ID AAY92771 standard; peptide; 14 AA.
 XX
 AC AAY92771;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Oligopeptide mimotope C19 of surface LOS of serogroup B meningococcus.
 XX
 KW Heptapeptide; epitope; mimotope; surface lipo-oligosaccharide; LOS;
 KW meningitis; anti-bacterial; anti-inflammatory; vaccine.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 2..10
 XX
 PN WO200025814-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 27-OCT-1999; 99WO-GB03559.
 XX
 PR 30-OCT-1998; 98GB-0023835.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 XX
 PI Charalambous BM, Feavers IM;
 XX
 DR WPI; 2000-365403/31.
 XX
 PT Use of a mimotope of a surface lipooligosaccharide of a serogroup B
 PT meningococcus for a vaccine against serogroup B meningococci
 XX
 PS Example 2; Page 19; 39pp; English.
 XX
 CC Minotopes of a surface lipooligosaccharide (LOS) of a serogroup B
 CC meningococcus comprise an oligopeptide which is structurally more
 CC constrained than an unsubstituted linear form of the oligopeptide. The
 CC oligopeptide is cyclic and contains a heptapeptide, such as the generic
 CC sequence of AAY92767. The minotopes are useful in vaccines against
 CC serogroup B meningococci, especially Neisseria meningitidis, which
 CC causes meningitis. The LOS is a surface glycolipid that forms a major
 CC outer membrane component and possesses a terminal galactose acceptor
 CC sites for sialic acid. Sialylation of the LOS in immunotype B
 CC meningococci may enhance the ability of the organism to evade the human
 CC immune response. Therefore alternative target antigens on the surface of
 CC serogroup B meningococci are important.
 XX
 SQ Sequence 14 AA;

Query Match 57.1%; Score 4; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMH 4
 Db 3 SWMH 6

RESULT 23
 AAU88216
 ID AAU88216 standard; Peptide; 17 AA.
 XX

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 Db 12 MHQP 15

RESULT 24
 AAU90013
 ID AAU90013 standard; Peptide; 17 AA.
 XX
 AC AAU90013;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Insulin/insulin-like growth factor receptor-binding peptide #1969.
 XX

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 Db 12 MHQP 15

Query Match 57.1%; Score 4; DB 23; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAU88216;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Insulin/insulin-like growth factor receptor-binding peptide #180.
 XX
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke;
 KW diabetic neuropathy.
 XX
 OS Synthetic.
 XX
 PN WO200172771-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2000; 2000WO-US08528.
 XX
 PR 29-MAR-2000; 2000WO-US08528.
 XX
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Beasley J, Blume AJ, Schaeffer L, Pillurla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandrecki WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX
 DR WPI; 2002-025774/03.
 XX
 PT Modulating insulin activity in mammalian cells, for treating e.g.
 PT diabetes and tumours, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors
 XX
 PS Disclosure; Page 44; 390pp; English.
 XX
 CC The invention relates to a method of modulating insulin activity in
 CC mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR
 CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
 CC of the invention.
 XX
 SQ Sequence 17 AA;

KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke;
 KW diabetic neuropathy.
 XX
 OS Synthetic.
 XX WO200172771-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 29-MAR-2000; 2000WO-US08528.
 XX
 XX 29-MAR-2000; 2000WO-US08528.
 XX
 XX (DGB-) DGI BIOTECHNOLOGIES LLC.
 XX (NOVO) NOVO NORDISK AS.
 XX
 XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 XX Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
 XX Hansen PH, Ravera M, Hsiao K;
 XX WPI; 2002-025774/03.
 XX
 XX Modulating insulin activity in mammalian cells, for treating e.g.
 XX diabetes and tumours, comprises using peptides that bind to insulin or
 XX insulin-like growth factor receptors -
 XX
 XX Disclosure; Figure 3C; 390pp; English.
 XX
 XX The invention relates to a method of modulating insulin activity in
 XX mammalian cells by administering a peptide that binds the insulin
 XX receptor (IR). A composition containing a peptide, optionally expressed
 XX from gene therapy vectors, that binds to Site 1 of IR and an insulin
 XX agonist are useful for treating diabetes. Also, peptides that are
 XX antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 XX useful for treating insulin-like growth factor (IGF)-sensitive tumours
 XX (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 XX receptor agonists are useful for treating neurological diseases,
 XX including stroke and diabetic neuropathy. The peptides are also useful in
 XX screening for compounds that bind to IR or IGF-1 receptor, potential
 XX therapeutics and research reagents. AAU88034-AAU90957 represent IR
 XX and/or IGF-1 receptor-binding peptides and related amino acid sequences
 XX of the invention.
 XX
 XX Sequence 17 AA;
 XX
 XX Query Match 57.1%; Score 4; DB 23; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 3 MHQP 6
 XX |||||
 XX Db 12 MHQP 15
 XX
 XX RESULT 25
 XX ABB50820
 XX ID ABB50820 standard; Protein; 20 AA.
 XX
 XX AC ABB50820;
 XX
 XX 07-FEB-2002 (first entry)
 XX
 XX Human secreted protein encoded by gene 75 SEQ ID NO:773.
 XX
 XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 KW cytotatic; cardiant; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;

KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200162891-A2.
 XX
 XX 30-AUG-2001.
 XX
 XX 21-FEB-2001; 2001WO-US05614.
 XX
 XX 24-FEB-2000; 2000US-184836P.
 XX
 XX 29-MAR-2000; 2000US-193170P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 XX Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 XX Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
 XX Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
 XX Zeng Z, Greene JM;
 XX
 XX WPI; 2001-625724/72.
 XX
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 XX preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 XX disease and diabetic retinopathy -
 XX
 XX Disclosure; Page 178; 1533pp; English.
 XX
 XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 XX proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 XX activities based on the tissues and cells the genes are expressed in.
 XX Example of these activities include: immunomodulatory; antisclerotic;
 XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 XX anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 XX antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 XX in gene therapy and vaccine production. (I) and (II) can be used in the
 XX prevention, diagnosis and treatment of immune disorders (e.g. multiple
 XX sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 XX (HIV) infections), hyperproliferative disorders (e.g. cancers and
 XX Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 XX Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 XX disorders (e.g. corneal graft neovascularisation and diabetic
 XX retinopathy), neurological disorders (e.g. Huntington's chorea,
 XX Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 XX for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 XX ABA83193 and ABB50300 represent sequences used in the exemplification of
 XX the present invention.
 XX
 XX Sequence 20 AA;
 XX
 XX Query Match 57.1%; Score 4; DB 22; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 4 HQPP 7
 XX |||||
 XX Db 1 HQPP 4
 XX
 XX RESULT 26
 XX AAR12685
 XX ID AAR12685 standard; Protein; 5 AA.
 XX
 XX AC AAR12685;
 XX
 XX 31-JUL-1991 (first entry)
 XX

XX Pentapeptide paralogue for use as chromatographic affinity ligand.
 DE HPLC.
 KW Synthetic.
 XX WO9106356-A.
 PN
 XX 16-MAY-1991.
 PD
 XX 31-OCT-1990; 90WO-EP06333.
 PF
 XX 31-OCT-1989; 89US-0429721.
 PR
 XX (TERR-) TERRAPIN TECHN INC.
 PA
 XX Kauvar LM;
 PI
 XX WPI; 1991-163985/22.
 DR
 XX Identifying paralog with specific affinity for analyte - using
 PT candidate paralogs with systematically varied values of at least
 PT 2 parameters.
 XX
 PS Claim 41; Fig 8; 95pp; English.
 XX
 CC Peptide is one of a panel, each of which have systemically varied
 CC values of at least two parameters. A test protein is matched against
 CC the panel, and the paralogues with highest binding affinity are
 CC selected. Selected paralogues are bound to a matrix which is
 CC incorporated into the HPLC gel and used as affinity ligands.
 CC Technique is useful in chromatographic separation, purification
 CC and binding assay.
 XX
 SQ Sequence 5 AA;
 XX
 Query Match 42.9%; Score 3; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 WMH 4
 Db 1 WMH 3
 XX
 RESULT 27
 AAR27038
 ID AAR27038 standard; peptide; 5 AA.
 XX
 AC AAR27038;
 XX
 XX 25-MAR-2003 (updated)
 DT 01-MAR-1993 (first entry)
 XX
 XX Consensus heavy chain CDR1 used in humanised Mab.
 DE
 XX Monoclonal antibody; complementarity determining region; framework;
 KW antigens; tumour; melanoma; carcinoma; glioma.
 KW
 XX Non human.
 OS
 XX WO9215683-A1.
 PN
 XX 17-SEP-1992.
 PD
 XX 04-MAR-1992; 92WO-EP00480.
 PF
 XX 06-MAR-1991; 91EP-0103389.
 PR
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Bendig WM, Kettleborough CA, Saldanha J;
 PI

XX WPI; 1992-331729/40.
 DR
 XX Human monoclonal antibodies binding to human receptors - for
 PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma
 XX
 XX Claim 4; Page 62; 89pp; English.
 PS
 XX The CDR1 sequence was that of a consensus sequence of CDR1 deduced
 CC from antigen binding sites of non-human origin. The sequence is
 CC from the heavy chain hypervariable region. The sequence may be used
 CC to produce humanised monoclonal antibodies comprising CDRs of non
 CC human origin and frameworks of variable and constant regions of
 CC human heavy and light chains. The humanised antibodies or their
 CC chimeric variants may be used as therapeutic or diagnostic agents in
 CC order to combat e.g. glioma, melanoma or carcinoma.
 CC See also AAR27299-300 and AAR27037-51.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 5 AA;
 XX
 Query Match 42.9%; Score 3; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 WMH 4
 Db 3 WMH 5
 XX
 RESULT 28
 AAR51549
 ID AAR51549 standard; peptide; 5 AA.
 XX
 AC AAR51549;
 XX
 XX 25-MAR-2003 (updated)
 DT 19-OCT-1994 (first entry)
 XX
 XX Mimotope peptide #43 from panel of maximally diverse mimotopes.
 DE
 XX mimotope panel; rational drug design; candidate drug;
 KW screening assay; hydrophobicity; antibody repertoire.
 KW
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 PH Modified-site 1 /note= "acetylated"
 FT
 XX US5300425-A.
 PN
 XX 05-APR-1994.
 PD
 XX 06-DEC-1989; 89US-0447009.
 PF
 XX 13-OCT-1987; 87US-0108130.
 PR
 XX 11-OCT-1988; 88US-0255906.
 PR
 XX 06-DEC-1989; 89US-0447009.
 XX
 PA (TERR-) TERRAPIN TECHNOLOGIES INC.
 XX
 XX Kauvar LM;
 PI
 XX WPI; 1994-109390/13.
 DR
 XX Screening of candidate drugs for binding to receptor - by
 PT comparing inverse image antibody profile of drug with
 PT mimotype-binding profile of receptor
 XX
 XX Example 3; Fig 3; 29pp; English.
 PS
 XX A panel of 88 pentapeptides was designed on the basis of decreasing
 CC

CC hydrophobicity and periodic variation of hydrophobic moment. The
 CC peptides were labelled with iodine-125 and tested with individual
 CC members of a basal antibody repertoire. (Spleen cells were
 CC harvested from mice and used to provide a panel of
 CC antibody-secreting hybridoma cells as a subset of the complete
 CC B-cell repertoire). Nearly uniform binding to all antibody members
 CC of the repertoire was observed. The test was then repeated with the
 CC addition of a defined amount of analyte to the mixture. A small
 CC number of wells showed greatly decreased labelling and these
 CC antibodies represented the successful result of an initial screen
 CC for those which preferentially bind analyte.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 ||||
 Db 1 WMH 3

RESULT 29
 AAR69917
 ID AAR69917 standard; peptide; 5 AA.
 XX
 AC AAR69917;

DT 25-MAR-2003 (updated)
 DT 18-OCT-1995 (first entry)

XX Pentameric mimotope 43 used to obtain highly specific antibodies.

XX mimotope; antibody; production; high specificity; detection;
 KW immunoassay; high performance liquid chromatography.

XX Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Acetyl-Trp"

XX US5384263-A.

XX 24-JAN-1995.

XX 04-JUN-1993; 93US-0072190.

XX 11-OCT-1988; 88US-0255906.

PR 13-OCT-1987; 87US-0108110.

PR 04-JUN-1993; 93US-0072190.

XX (TERR-) TERRAPIN TECHNOLOGIES INC.

XX Kauvar LM;

XX WPI; 1995-105497/14.

XX Producing antibodies with high specificity and affinity for an
 PT analyte - by immunisation with selected mimotope, also analyte
 PT detection kits, useful for immunoassay of materials usually
 PT analysed by HPLC

XX Example 3; Fig 3; 25pp; English.

XX AAR69875-969 are pentameric mimotopes designed on the basis of
 CC decreasing hydrophobicity and periodic variation of hydrophobic
 CC moment. All the pentapeptides are acetylated at the N-terminus except
 CC E12 (for FITC) (sic). E12 is not identified in the specification.
 CC The mimotopes are used in the method of the invention to obtain
 CC antibodies specifically and strongly reactive with a desired

CC analyte. The mimotope is obtd. by reacting a panel of starting
 CC antibodies (Abs) representative of the resting B cell repertoire of a
 CC mammal with an analyte (so as to identify analyte-reacting Abs) and
 CC then reacting each of a panel of candidate mimotopes representative
 CC of a random set of 3D contours with the analyte-reacting Abs. A
 CC subject is immunised with one or more mimotopes identified and the
 CC product Abs are recovered from the serum of the subject.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 ||||
 Db 1 WMH 3

RESULT 30
 AAR74929
 ID AAR74929 standard; peptide; 5 AA.
 XX
 AC AAR74929;

DT 19-JAN-1996 (first entry)

XX H-CDR-1 of anti-idiotypic antibody against human anticancer antibody.

XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.

XX Mus sp.

XX JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX WPI; 1995-182987/24.

XX Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.

XX Claim 1; Page 2; 28pp; Japanese.

XX A new anti-idiotypic antibody against a human anticancer monoclonal
 CC antibody is claimed. This antibody contains in its heavy chain 3
 CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2
 CC (AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the
 CC light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
 CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
 CC encoding it are useful in pharmacological, medical and biochemical
 CC fields.
 XX
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 ||||
 Db 3 WMH 5

RESULT 31
 AAR98663
 ID AAR98663 standard; peptide; 5 AA.
 XX
 AC AAR98663;
 XX
 DT 25-MAR-2003 (updated)
 DT 11-MAR-1997 (first entry)
 XX
 DE Peptide 43 from 88 member diverse mimotope panel.
 XX
 KW Panel; mimotope; decreasing hydrophobicity; periodic variation;
 KW hydrophobic moment; antibody; repertoire; identification; drug;
 KW candidate; receptor; binding; ligand; rational; design; selection;
 KW treatment; tumour; production; immunological reagent; analyte;
 KW detection; trace contaminant; mimotope.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acylated"
 FT
 XX US5541070-A.
 XX
 PD 30-JUL-1996.
 XX
 XX 08-SEP-1993; 93US-0118133.
 XX
 PR 06-DEC-1989; 89US-0447009.
 PR 13-OCT-1987; 87US-0108130.
 PR 11-OCT-1988; 88US-0255906.
 PR 08-SEP-1993; 93US-0118133.
 XX
 PA (KAUV/) KAUVAR L M.
 XX
 PI Kauvar LM;
 XX
 DR WPI; 1996-361955/36.
 XX
 PT Identifying candidate drugs that bind a specific receptor by
 PT competitive reaction with panel of mimotope(s) - useful in rational
 PT drug design
 XX
 PS Example 3; Fig 3; 27pp; English.
 XX
 CC The present peptide is a member of a panel of 88 pentapeptide
 CC mimotopes designed on the basis of decreasing hydrophobicity, and
 CC periodic variation of hydrophobic moment. The panel was synthesised
 CC using the method of Geyzen, H. M., et al, Proc. Natl. Acad. Sci.
 CC USA (1984), which uses lots of 96 pins; the remaining 8
 CC polyethylene pins being controls. The mimotopes were then mixed,
 CC 125-I labelled and tested with individual members of a basal
 CC antibody (Ab) repertoire. Nearly uniform binding to all members was
 CC found. The test was then repeated with the addition of a defined
 CC amt. of analyte. A small number showed greatly increased labelling,
 CC these Ab representing the successful result of an initial screen
 CC for those that pref. bind analyte.
 CC The above is an example of a claimed method for identifying members
 CC of a panel of candidate drugs, that bind to a receptor having a
 CC known ligand. It is useful in rational drug design, e.g. selection
 CC of monoclonal Ab for treating individual tumours, and for the prodn.
 CC of immunological reagents for any analyte, including those not
 CC normally detectable by immunoassay, e.g trace contaminants in soil,
 CC air or water.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
 Db 1 WMH 3
 XX
 RESULT 32
 AAW39866
 ID AAW39866 standard; peptide; 5 AA.
 XX
 AC AAW39866;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Heavy chain CDR1 of catalytic antibody 8G4E.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 OS
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 PS Claim 19; Page 94; 147pp; English.
 XX
 CC AAW39866-68 represent the sequences of the heavy chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 8G4E, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 8G4E antibody was
 CC identified using TSAs, and has a per minute Kcat of 0.12. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved).
 XX
 SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 Db 3 WMH 5
 XX
 RESULT 33
 AAW44181
 ID AAW44181 standard; peptide; 5 AA.
 XX
 AC AAW44181;
 XX
 DT 16-JUN-1998 (first entry)

XX Monoclonal antibody 12H5 heavy chain CDR SEQ ID NO:25.
DE
XX
XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
KW amelioration; kidney disorder; nephrotoxicity; anticancer.
XX
XX Unidentified.
XX
XX WO9749427-A1.
XX
XX 31-DEC-1997.
XX
XX 27-JUN-1997; 97WO-JP02241.
XX
XX 19-SEP-1996; 96JP-0247635.
XX
XX 27-JUN-1996; 96JP-0167286.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX Hayashi K, Kawauchi Y, Masuho Y, Takasaki J;
XX WPI; 1998-076914/07.
XX
XX Amelioration of kidney disorders caused by cisplatin administration
PT - by treatment with an antibody inhibiting type II phospholipase A2
PT activity
XX
XX Disclosure; Page 50; 74pp; Japanese.
XX
XX The present sequence represents a complementary determining region
CC (CDR) from monoclonal antibody 12H5 heavy chain against type II
CC phospholipase A2, from the present invention. The present invention
CC describes a novel method for the amelioration of kidney disorders
CC (such as acute renal failure) associated with the administration of
CC cisplatin for the treatment of cancer. The method comprises treatment
CC with a monoclonal antibody which inhibits the activity of type II
CC phospholipase A2 (particularly of type II phospholipase A2 of human
CC origin), or with a protein or peptide possessing the same inhibitory
CC activity and containing a part of the antibody sequence. Preferably the
CC antibody also inhibits the activity of ape and/or mouse type II
CC phospholipase A2, and has the ability to release type II phospholipase
CC A2 bound to a cell membrane. Three specific monoclonal antibodies
CC having these properties which can be used are 12H5, 10.1 and 1.4.
CC derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM BP-5297
CC respectively. The method can be used for suppressing the nephrotoxicity
CC which is a characteristic feature of cisplatin administration, and
CC therefore allowing more efficient use of this drug as an anticancer
CC agent, e.g. by allowing an increased dosage to be used.
XX
XX Sequence 5 AA;
SQ
Query Match 42.9%; Score 3; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 WMH 4
Db 3 WMH 5
RESULT 34
AAV48891
ID AAY48891 standard; Peptide; 5 AA.
XX
XX AAY48891;
AC
XX 20-MAR-2003 (updated)
DT 10-DEC-1999 (first entry)
XX
XX Membrane dipeptidase-binding prostate homing peptide #7.
DE
XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
XX

KW membrane dipeptidase.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9946284-A2.
XX
XX 16-SEP-1999.
XX
XX 10-MAR-1999; 99WO-US05284.
XX
XX 13-MAR-1998; 98US-0042107.
XX
XX 26-FEB-1999; 99US-0258754.
XX
XX (BURN-) BURNHAM INST.
XX
XX Rajotte D, Pasqualini R, Ruoslahti EI;
XX WPI; 1999-571717/48.
XX
XX New peptides which selectively home to organs or tissues, used for,
PT e.g. identifying target ligands and for therapy of pathological
PT conditions -
XX
XX Example 6; Page 151; 193pp; English.
XX
XX The present invention describes peptides that selectively home to a
CC tissue or organ. The peptides can be used for identifying an organ
CC or tissue, for identifying a target molecule expressed by an organ or
CC tissue or for treating an organ or tissue pathology, where the organ or
CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,
CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the
CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences
CC which are used in the exemplification of the present invention.
XX (Updated on 20-MAR-2003 to correct PR field.)
XX
XX Sequence 5 AA;
SQ
Query Match 42.9%; Score 3; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HQP 6
Db 2 HQP 4
RESULT 35
AAB21923
ID AAB21923 standard; Peptide; 5 AA.
XX
XX AAB21923;
AC
XX 22-MAR-2001 (first entry)
DT
XX Human prostate-homing peptide #16.
DE
XX Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
XX
XX Homo sapiens.
OS
XX WO200042973-A2.
XX
XX 27-JUL-2000.
XX
XX 21-JAN-2000; 2000WO-US01602.
XX
XX 22-JAN-1999; 99US-0235902.
XX
XX (BURN-) BURNHAM INST.
XX
XX Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti EI;
XX

XX WPI; 2000-499174/44.
 DR Homing pro-apoptotic conjugate comprising a tumor homing molecule that
 PT selectively homes to a mammalian cell type or tissue linked to an
 PT antimicrobial peptide, useful for the treatment of prostate cancer -
 XX Example 9; Page 99; 118pp; English.
 XX The present invention relates to homing pro-apoptotic conjugates,
 CC comprising of a tumour homing molecule that selectively homes to a
 CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
 CC homing pro-apoptotic conjugates are selectively internalised by the
 CC mammalian cell type or tissue and exhibits high toxicity, especially to
 CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
 CC toxicity when not linked to the tumor homing molecule. The conjugates are
 CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
 CC prostate cancer or melanoma. The present sequence is a homing peptide
 CC isolated in the present invention, which can be conjugated to an
 CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
 CC present invention.
 XX SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQP 6
 Db 2 HQP 4
 RESULT 36
 AAB19754
 ID AAB19754 standard; Peptide; 5 AA.
 AC AAB19754;
 XX 19-FEB-2001 (first entry)
 DT Erythropoietin receptor agonist Mab 3G9 VH region CDR1.
 DE Erythropoietin receptor; agonist; monoclonal antibody; Mab; mouse;
 XX heavy chain variable region; antibody engineering; erythropoiesis;
 KW anaemia; cytopenia; acute renal failure; antianaemic; therapy;
 KW complementarity determining region; CDR.
 XX Mus sp.
 OS WO2000061637-A1.
 PN 19-OCT-2000.
 XX 14-APR-2000; 2000WO-US10284.
 PF 14-APR-1999; 99US-0129263.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA Erickson-Miller CL, Holmes SD, Taylor AH, Young PR;
 XX WPI; 2000-679469/66.
 DR Novel erythropoietin receptor agonist antibody useful for enhancing
 XX erythropoiesis in the treatment of anemia, cytopenia or acute renal
 PT failure -
 PT Claim 28; Page 50; 70pp; English.
 XX The present sequence is that of complementarity determining region
 CC 1 (CDR1) of the heavy chain variable region (VH) (see AAB19745) of
 CC 3G9, a murine erythropoietin receptor (EpoR) agonist monoclonal

CC antibody. Claimed EpoR agonist antibodies comprise a VH region
 CC that includes the 3G9 VH CDRs. These include humanised agonist
 CC antibodies in which the 3G9 VH CDRs are incorporated into a human
 CC framework. The EpoR agonist antibodies are used in a claimed
 CC method for enhancing erythropoiesis, for the treatment of anaemia,
 CC cytopenia, acute renal failure, and other conditions with depressed
 CC erythrocyte production. Agonist antibodies of EpoR have the same
 CC therapeutic utility as the natural ligand, but with the advantages
 CC of easier purification and longer half-life in vivo.
 XX SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 Db 3 WMH 5
 RESULT 37
 AAB12174
 ID AAB12174 standard; peptide; 5 AA.
 XX AC AAB12174;
 XX 10-NOV-2000 (first entry)
 DT Human CDR1 for IL-2R monoclonal antibody.
 DE Human; CDR; humanised antibody; complementarity determining region;
 XX IL-2Ralpha; interleukin-2 receptor; transplant rejection; CD25;
 KW immunosuppression.
 XX Homo sapiens.
 OS WO2000030679-A1.
 PN 02-JUN-2000.
 XX 22-NOV-1999; 99WO-EP08988.
 PF 23-NOV-1998; 98GB-0025632.
 PR (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Feutren G, Howell RK, Marbach P, Roberts A, Schreier MH, Schulz M;
 PI WPI; 2000-399934/34.
 DR Preventing or treating transplant rejection in a recipient comprises
 XX administering a monoclonal antibody specific for interleukin-2 receptor
 PT beyond the very early phase following transplantation -
 PT Disclosure; Page 2; 17pp; English.
 XX The present sequence is a human complementarity determining region (CDR).
 CC This sequence was used to generate a humanised antibody specific for the
 CC alpha subunit of interleukin-2 receptor (IL-2Ralpha). The humanised
 CC IL-2Ralpha antibody would be useful for preventing or treating transplant
 CC rejection in a recipient of organ, tissue or modified or unmodified cell
 CC transplant. The use of a monoclonal antibody specific for IL-2R decreases
 CC transplant rejection in an immunosuppression-intolerant or non-compliant
 CC recipient compared with available therapies. Also, undesirable side
 CC effects associated with current treatments e.g. renal dysfunction,
 CC hirsutism, gingival hyperplasia and hypertension are avoided.
 XX SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 38
AA92158
ID AA92158 standard; Peptide; 5 AA.
XX AC
XX AAY92158;
XX DT 01-AUG-2000 (first entry)
XX DE Murine 15B8 heavy chain variable region CDR 1.
XX Heavy chain; variable region; complementarity determining region; CDR 1;
KW anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic;
KW vascular-general; proliferative; antiischemic; cerebroprotective;
KW cardiant; agonist; antibody inhibition.
XX OS Mus musculus.
XX PN WO200018804-A1.
XX PD 06-APR-2000.
XX PF 28-SEP-1999; 99WO-US22428.
XX PR 28-SEP-1998; 98US-0102098.
XX PA (SMIK) SMITHKLINE BEECHAM PUC.
XX PI Holmes SD, Erickson-miller CL, Winkler JD;
XX WPI; 2000-293114/25.
XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in
PT patients suffering from strokes and myocardial infarctions
XX Claim 12; Page 40; 50pp; English.
XX AA92158-60 are heavy chain CDR (complementarity determining regions)
CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal
CC antibody 15B8. Tie2 is a single-transmembrane, tyrosine kinase receptor
CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and
CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2
CC antibodies may be administered to enhance angiogenesis in mammals
CC suffering from ischemic disease, myocardial infarction or cerebral stroke
CC or other vascular diseases such as diabetes. It may also be used to
CC enhance endothelial cell survival and to promote haematopoietic or
CC megakaryocyte cell proliferation (claimed).
XX SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 39
AA92158
ID AA92158 standard; Peptide; 5 AA.
XX AC
XX AAY92158;
XX DT 19-MAY-2000 (first entry)

XX Chimeric anti-CD25 antibody Ig heavy chain hypervariable region CDR1.
DE XX
XX Chimeric anti-CD25 antibody; CD25 binding molecule; immunoglobulin;
KW hypervariable region; complementary determining region; CDR1; CDR2; CDR3;
KW inflammation; rheumatoid arthritis; hyperproliferative skin disease.
XX OS Homo sapiens.
XX PN WO200006604-A2.
XX PD 10-FEB-2000.
XX PF 26-JUL-1999; 99WO-EP05316.
XX PR 27-JUL-1998; 98GB-0016281.
XX PR 27-MAY-1999; 99GB-0012460.
XX PA (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PA (UNLO) UNIV COLLEGE LONDON.
XX PI Amlot PL, Schreier MH;
XX WPI; 2000-183090/16.
XX Use of CD25 binding molecules in the treatment of rheumatoid arthritis
PT and inflammatory or hyperproliferative skin diseases -
XX Claim 1; Page 11; 14pp; English.
XX The present invention describes CD25 binding molecules, which are used
CC to treat rheumatoid arthritis and inflammatory or hyperproliferative
CC skin diseases. The CD25 binding molecule comprises at least one
CC antigen binding site comprising at least one domain which comprises in
CC sequence, the hypervariable regions CDR1 (having the sequence RYWH),
CC CDR2 (having the sequence AYPGNSTSYNQKPEG) and CDR3 (having the
CC sequence DGYVDFP), or their direct equivalents. The CD25 binding
CC molecules are used in the treatment of rheumatoid arthritis and
CC inflammatory or hyperproliferative skin diseases, such as psoriasis,
CC atypical dermatitis, contact dermatitis and further eczematous
CC dermatitises, seborrheic dermatitis. Lichen planus, Pemphigus,
CC bullous Pemphigoid, Epidermolysis bullosa, urticaria, angiodemas,
CC vasculitides, erythemas, cutaneous eosinophilias, Lupus erythematosus
CC and acne. A more preferred CD25 binding molecule for use in accordance
CC with the present invention is selected from a chimeric anti-CD25 antibody
CC which comprises at least: (i) one immunoglobulin heavy chain, or
CC fragment, which comprises (i) a variable domain comprising in sequence
CC the hypervariable regions CDR1, CDR2 and CDR3 (as above) and (ii) the
CC constant part, or fragment, of a human heavy chain; and (2) one
CC immunoglobulin light chain, or fragment, which comprises (i) a variable
CC domain comprising in sequence the hypervariable regions CDR1', CDR2',
CC and CDR3' (ISASSISMQ, DTSKLAS and HQRSYT, respectively) and (ii) the
CC constant part, or fragment, of a human light chain.
XX SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 40
AA014422
ID AA014422 standard; peptide; 5 AA.
XX AC
XX AA014422;
XX DT 03-MAY-2002 (first entry)


```

XX DE CD25 binding protein domain 1 hypervariable region CDR1.
XX XX
XX KW CD25 binding protein; hypervariable region; CDR1; gastrointestinal tract;
XX KW inflammatory disease; irritable bowel syndrome; IBS; Crohn's disease;
XX KW ulcerative colitis; inflammatory intestinal disease; medicament.
XX XX
XX OS Unidentified.
XX PN WO200172845-A1.
XX XX
XX PD 04-OCT-2001.
XX XX
XX PF 28-MAR-2001; 2001WO-EP03541.
XX XX
XX PR 30-MAR-2000; 2000GB-0007911.
XX XX
XX PA (NOVS ) NOVARTIS AG.
XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX FI Adam H, Faerber L;
XX XX
XX DR WPI; 2001-626258/72.
XX XX
XX PF CD25 binding molecule which comprises antigen binding site comprising
XX PT fully defined CDR1, CDR2, CDR3 hypervariable regions, for treating
XX PT Crohn's disease, ulcerative colitis, irritable bowel syndrome -
XX XX
XX PS Claim 1; Page 12; 19pp; English.
XX XX
XX CC The invention comprises a CD25 binding protein comprising at least one
XX CC CD25 binding domain containing the hypervariable regions CDR1, CDR2 and
XX CC CDR3. The CD25 binding domain 1 hypervariable regions are shown in
XX CC AA014422 - AA014424, CD25 binding domain 2 hypervariable regions are
XX CC shown in AA014425 - AA014427. The CD25 binding protein is useful for
XX CC treating an inflammatory disease of the gastrointestinal tract, such as:
XX CC irritable bowel syndrome, IBS; Crohn's disease; ulcerative colitis; or
XX CC other inflammatory intestinal disease. The CD25 binding protein is also
XX CC useful in the manufacture of a medicament for the treatment of
XX CC inflammatory disease of the intestinal tract. The present amino acid
XX CC sequence represents the CD25 binding domain 1 hypervariable region CDR1.
XX XX
XX SQ Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 WHH 4
XX DB |||
XX 3 WHH 5
XX
XX RESULT 41
XX AAG63123
XX ID AAG63123 standard; Protein; 5 AA.
XX AC
XX DE AAG63123;
XX XX
XX DT 01-OCT-2001 (first entry)
XX XX
XX DE Amino acid sequence of a human adenovirus 5 Elb 8.3 kDa protein.
XX KW Adenovirus protein; Ad; complementing cell line; Ad vector;
XX KW replication-incompetent Ad vector; El-deleted virus;
XX KW transgene expression; Ad5.
XX XX
XX OS Human adenovirus type 5.
XX XX
XX PN WO200144280-A2.
XX XX
XX PD 21-JUN-2001.
XX XX
XX PF 07-DEC-2000; 2000WO-US33123.
XX XX
XX PR 14-DEC-1999; 99US-0170550.
XX XX
XX PR 11-APR-2000; 2000US-0196266.
XX XX
XX PA (GENO-) GENOVO INC.
XX XX
XX PI Himes VB, Rasty S, Peluso RW;
XX XX
XX DR WPI; 2001-475764/51.
XX DR N-PSDB; AAH42482.
XX XX
XX PT New nucleic acids for creating complementing cell lines that enable
XX PT production of high titer adenovirus vectors, comprises a sequence of a
XX PT polynucleotide which is not a naturally-occurring adenoviral nucleotide
XX PT sequence -
XX XX
XX PS Example 1; Page 96; 104pp; English.
XX XX
XX CC The specification describes a nucleic acid molecule, comprising a
XX CC polynucleotide encoding 5 contiguous amino acids of a naturally-occurring
XX CC adenovirus (Ad) polypeptide, where the polynucleotide is not a
XX CC naturally-occurring adenoviral nucleotide sequence and is useful for
XX CC creating complementing cell lines that enable the efficient production
XX CC of high titer Ad vectors. The nucleic acid molecule is useful for
XX CC creating Ad-complementary cell lines which are useful for high yield
XX CC production of recombinant replication-incompetent Ad vectors, in the
XX CC absence of detectable replication competent Ad. The adenoviruses
XX CC free of contamination with RCA are suitable for preclinical and
XX CC clinical use. El-deleted viruses are suitable for applications in which
XX CC transient transgene expression is therapeutic (e.g. p53 gene transfer
XX CC in cancer, beta-interferon gene transfer in cancer, platelet derived
XX CC growth factor (PDGF) gene transfer in wound healing, and vascular
XX CC endothelial growth factor (VEGF) gene transfer in vascular diseases of
XX CC the heart and limbs). The present sequence encodes a human Ad5 Elb 8.3
XX CC kDa protein. It is used to construct an El complementation element, for
XX CC use in the course of the invention.
XX XX
XX SQ Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 QPP 7
XX DB |||
XX 1 QPP 3
XX
XX RESULT 42
XX AAE06499
XX ID AAE06499 standard; peptide; 5 AA.
XX XX
XX AC AAE06499;
XX XX
XX DT 25-SEP-2001 (first entry)
XX XX
XX DE Mouse prostate homing peptide #16.
XX XX
XX KW Mouse; chimeric prostate-homing pro-apoptotic peptide;
XX KW prostate-homing peptide; antimicrobial peptide; prostate cancer;
XX KW tumour homing molecule; cytostatic.
XX XX
XX OS Mus sp.
XX XX
XX PN WO200153342-A1.
XX XX
XX PD 26-JUL-2001.
XX XX
XX PF 16-JAN-2001; 2001WO-US01362.
XX XX
XX PR 21-JAN-2000; 2000US-0489582.
XX XX

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PA (BURN-) BURNHAM INST.
XX
XX
XX Ruoslahti EI, Pasqualini R, Arap W, Bredesen DE, Ellerby HM;
XX
XX WPI; 2001-451901/48.
XX
XX Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
XX prostate cancer, comprises a prostate-homing peptide linked to an
XX antimicrobial peptide -
XX
XX Example 9; Page 98; 176pp; English.
XX
XX The patent discloses novel chimeric prostate-homing pro-apoptotic
XX peptide which comprises a prostate-homing peptide linked to an
XX antimicrobial peptide, where the chimeric peptide is selectively
XX internalised by and exhibits high toxicity to prostate tissue and
XX where the antimicrobial peptide has low mammalian cell toxicity when
XX not linked to prostate-homing peptide. The chimeric peptide is used
XX to direct an antimicrobial peptide in vivo to a prostate cancer, to
XX induce selective toxicity in vivo in a prostate cancer, and to treat
XX a patient with prostate cancer. The present sequence is mouse prostate
XX homing peptide. This sequence is useful in the homing of pro-apoptotic
XX conjugates of the invention.
XX
XX SQ Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 HQP 6
XX ||||
XX 2 HQP 4
XX
XX DB
XX
XX RESULT 43
XX AAB71236
XX ID AAB71236 standard; peptide; 5 AA.
XX
XX AC AAB71236;
XX
XX XX 26-NOV-2002 (first entry)
XX DT
XX DE Murine IgG1 catabolic site fragment SEQ ID 26.
XX
XX XX IgG; 9E10; immunoglobulin G; Fc receptor; FcRn; drug; murine;
XX KW T-cell receptor binding ligand.
XX
XX OS Mus musculus.
XX
XX PN US2002098193-A1.
XX
XX PD 25-JUL-2002.
XX
XX XX 20-AUG-2001; 2001US-0933497.
XX
XX XX 03-MAR-1997; 97US-0811463.
XX
XX XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX XX Ward ES;
XX
XX XX WPI; 2002-681920/73.
XX
XX XX Composition for increasing serum half-life of agent, comprises mutant
XX immunoglobulin G molecule or IgG Fc-hinge fragment and having increased
XX serum half-life relative to IgG or relative to serum half-life of IgG -
XX
XX PS Disclosure; Page 10; 68pp; English.
XX
XX XX This invention describes a novel composition comprising a mutant
XX immunoglobulin G (IgG) molecule or IgG Fc-hinge fragment. The mutant IgG
XX molecule has an increased serum half-life relative to IgG and has one

CC amino acid substitution in the Fc-hinge region. The mutant IgG Fc-hinge
CC fragment has an increased serum half-life relative to serum half-life of
CC IgG, where the fragment has increased binding affinity for Fc receptor
CC (FcRn) or has same or slightly lower affinity than IgG for binding to
CC FcRn. The composition is useful for increasing the serum half-life of an
CC agent, by conjugating the agent to a mutant IgG or IgG Fc hinge fragment
CC having an increased serum half life, where the agent is a therapeutic
CC drug, antigen binding polypeptide, antigen or receptor binding ligand.
CC The receptor binding ligand is a T-cell receptor binding ligand. The
CC composition is broadly applicable to an unlimited number of the
CC therapeutic uses for the treatment of diseases or disorders as it can be
CC used to reduce costs and discomfort to the patient by reducing the number
CC of therapeutic doses needed. This sequence represents a fragment of
CC murine IgG1 corresponding to the catabolic site described in the
CC disclosure of the invention.
XX
XX SQ Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 23; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 MHQ 5
XX ||||
XX 2 MHQ 4
XX
XX DB
XX
XX RESULT 44
XX AAU86924
XX ID AAU86924 standard; Peptide; 5 AA.
XX
XX AC AAU86924;
XX
XX XX 21-MAY-2002 (first entry)
XX DT
XX DE Immunoglobulin catalytic domain associated peptide #1.
XX
XX KW Immunoglobulin; IgG; fragment of crystallisation; Fc; Fc receptor;
XX KW FcRn; Immunotherapeutic; vaccination.
XX
XX OS Synthetic.
XX
XX PN US6277375-B1.
XX
XX PD 21-AUG-2001.
XX
XX XX 03-MAR-1997; 97US-0811463.
XX
XX PR 03-MAR-1997; 97US-0811463.
XX
XX XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX XX Ward ES;
XX
XX XX WPI; 2002-214477/27.
XX
XX XX Composition comprising mutant immunoglobulin (Ig)G molecule having
XX increased half-life relative to IgG, decreasing endogenous serum IgG in
XX a subject, comprises amino acid substitutions in Fc-hinge fragment -
XX
XX PS Disclosure; Column 83; 62pp; English.
XX
XX XX The invention describes a composition comprising mutant immunoglobulin
XX (Ig)G and IgG domains such as crystallisation fragment (Fc)-hinge
XX fragments having an increased serum half-life allowing extended
XX interaction with the Fc receptor, FcRn. The mutant IgG has amino acid
XX substitutions (in CH2 domain of the Fc-hinge) of Thr to Leu at position
XX 252, Thr to Ser at position 254, and Thr to Phe at position 256, or has
XX amino acid substitutions (in CH3 domain of Fc-hinge) of His to Lys at
XX position 433, His to Tyr at position 435, and His to Tyr at position 436.
XX The composition has immunotherapeutic uses e.g. in vaccination, and is
XX useful for decreasing endogenous serum IgG in a subject. The composition
XX reduces the cost and discomfort to the patient by reducing the number of

CC therapeutic doses since the mutant immunoglobulin has increased serum
 CC half-life and persistence. This sequence represents a peptide associated
 CC with catalytic domains of the immunoglobulin and mutant immunoglobulin
 CC discussed in the invention.

SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
 |||
 Db 2 MHQ 4

RESULT 45

AAU11183
 ID AAU11183 standard; Peptide; 5 AA.

XX AC AAU11183;

XX DT 25-FEB-2002 (first entry)

XX DE Mouse antibody Act-1/LDP-02, heavy chain variable region CDRI.

XX KW Mouse; antibody; Act-1; alpha4beta7 integrin; anti-inflammatory;
 KW anti-asthmatic; immunosuppressive; heavy chain variable region;
 KW humanised antibody; LDP-02; leukocyte infiltration; mucosal tissue;
 KW quiescent inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; ileitis; Crohn's disease; nontropical sprue;
 KW enteropathy; seronegative arthropathy; collagenous colitis;
 KW eosinophilic gastroenteritis; pouchitis; ileoanal anastomosis;
 KW pancreatitis; insulin-dependent diabetes mellitus; mastitis;
 KW cholecystitis; cholangitis; pericholangitis; chronic bronchitis;
 KW chronic sinusitis; asthma; graft versus host disease; CDRI;
 KW complementarity determining region.

XX OS Mus musculus.

XX PN WO200178779-A2.

XX PD 25-OCT-2001.

XX PF 13-APR-2001; 2001WO-US12234.

XX PR 14-APR-2000; 2000US-0550082.

XX PR 27-DEC-2000; 2000US-0748960.

XX XX (MILL-) MILLENNIUM PHARM INC.

XX PA (GETH) GENENTECH INC.

XX PI Brettman LR, Fox JA, Allison DE;

XX DR WPI; 2002-0552333/07.

XX PT Treating a human with a disease associated with leukocyte infiltration
 PT of mucosal tissues, e.g. inflammatory bowel disease, asthma or graft
 PT versus host disease, by administering an anti-alpha4 beta 7 integrin
 PT antibody -

XX PS Claim 8; Fig 5; 81pp; English.

XX CC The invention relates to treating a human having a disease associated
 CC with leukocyte infiltration of mucosal tissues, comprising administering
 CC a humanised immunoglobulin (e.g. the humanised version of mouse
 CC antibody Act-1, LDP-02) or its antigen-binding fragment, which has
 CC binding specificity for alpha4beta7 integrin. The immunoglobulin or its
 CC fragment comprises an antigen binding region of non-human origin and at
 CC least a portion of an antibody of human origin. Also included is a method
 CC for inhibiting relapse and/or recurrence of quiescent inflammatory bowel
 CC disease in a human by administering the humanised immunoglobulin or its
 CC antigen-binding fragment, which has binding specificity for alpha4beta7

CC integrin. The treatment is used for treating a human having a disease
 CC associated with leukocyte infiltration of mucosal tissues, e.g.
 CC inflammatory bowel disease (e.g. ulcerative colitis, Crohn's disease,
 CC ileitis, Crohn's disease, nontropical sprue, enteropathy associated with
 CC seronegative arthropathies, microscopic or collagenous colitis,
 CC eosinophilic gastroenteritis, pouchitis and ileoanal anastomosis),
 CC pancreatitis, insulin-dependent diabetes mellitus, mastitis,
 CC cholecystitis, cholangitis, pericholangitis, chronic bronchitis,
 CC chronic sinusitis, asthma or graft versus host disease. The method is
 CC also useful for inhibiting relapse and/or recurrence of quiescent
 CC inflammatory bowel disease in a human, where quiescence has been induced
 CC by medical or surgical therapy. The present sequence is a mouse
 CC Act-1/LDP-02 antibody heavy chain variable region complementarity
 CC determining region as incorporated into the humanised antibody of the
 CC invention.

XX SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
 |||
 Db 3 WMH 5

RESULT 46

ABB82654

ID ABB82654 standard; peptide; 5 AA.

XX AC ABB82654;

XX DT 19-FEB-2003 (first entry)

XX DE CDRI fragment of a chimeric anti-CD25 antibody.

XX KW CD25; immunosuppressive; hepatotropic; antiasthmatic; dermatological;
 KW antiarthritic; cytostatic; nephrotropic; neuroprotective; antiulcer;
 KW antiinflammatory; vasotropic; complementarity determining region;
 KW steroid; CDR; anti-CD25 antibody.

XX OS Unidentified.

XX PN WO200281508-A2.

XX PD 17-OCT-2002.

XX PF 05-APR-2002; 2002WO-EP03808.

XX PR 06-APR-2001; 2001GB-0008816.

XX PR 06-APR-2001; 2001GB-0008817.

XX PR 06-APR-2001; 2001GB-0008821.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Hearing SD, Dayan CM, Norman MR;

XX DR WPI; 2003-067514/06.

XX PT CD25 binding molecules useful for prevention and treatment of
 PT autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,
 PT leukemia, multiple sclerosis and Crohn's disease in steroid-resistant
 PT patients -

XX PS Claim 1; Page 20; 22pp; English.

XX CC The invention relates to a CD25 binding molecule (I) comprising at least
 CC one antigen binding site having at least one domain which comprises in
 CC sequence, the hypervariable regions CDRI, CDR2 and CDR3 (complementarity
 CC determining region), for use in prevention or treatment of diseases such
 CC as autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,
 CC leukemia, glomerulonephritis, multiple sclerosis and Crohn's disease in a

DT 03-MAY-1995 (first entry)
 DE U1 snRNP 70K protein amino acids 156-161, homologous to rubella virus.
 XX Small ribonucleoprotein complex; U1 snRNP; 70K protein; epitope;
 XX autoantibody; immunoinfective cluster virus; nuclear protein antigen;
 KW systemic rheumatic disorder; Rubella virus; German measles;
 KW systemic lupus erythematosus; scleroderma.
 XX Homo sapiens.
 OS
 PN WO9420141-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 10-MAR-1994; 94WO-US02631.
 XX
 PR 11-MAR-1993; 93US-0029850.
 XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 XX Douvas A, Ehresmann G, Takehana Y;
 DR WPI; 1994-302689/37.
 XX
 PT Methods for treating immunoinfective cluster virus infections -
 PT utilise antibodies or fragments characteristic of auto antibodies
 PT produced by patients with rheumatic disorders
 XX
 PS Disclosure; Page 67; 106pp; English.
 XX
 CC A comparison of the U1 snRNP 70K protein sequence with proteins
 CC from immunoinfective cluster viruses revealed widespread
 CC homologies. The importance of these homologous motifs is that they
 CC are epitopes for autoantibodies occurring in high titres in systemic
 CC rheumatic disorders. Sera from such patients could be used for
 CC treatment of immunoinfective cluster virus infections.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 6 AA;
 Query Match 42.9%; Score 3; DB 15; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 Db |||
 2 QPP 4
 RESULT 50
 ID AAR73901 standard; peptide; 6 AA.
 AC AAR73901;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-DEC-1995 (first entry)
 XX
 DE Neisseria meningitidis opacity related protein POPM3 peptide 1-5.
 XX
 KW Neisseria meningitidis; opacity related protein POPM3; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KW viral; peptide 1-5.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO9509232-A2.
 XX
 PD 06-APR-1995.
 XX
 PD 28-SEP-1994; 94WO-CA00516.

XX 28-SEP-1993; 93US-0127499.
 PR (SHAR/) SHARMA I R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 PI Sharma LR, Van Alstyne D;
 XX WPI; 1995-147431/19.
 DR
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 35; Page 76; 98pp; English.
 XX
 CC AAR73911 is the Neisseria meningitidis opacity related protein POPM3.
 CC It contains the meningitis related antigenic sequences (MRHAS)
 CC claimed in AAR73889 and AAR73901, which are recognised by a monoclonal
 CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
 CC peptides may be used in immunoassays to diagnose the presence of
 CC bacterial and/or viral meningitis agents in a sample, or in
 CC prophylactic and therapeutic meningitis treatments. The peptides may
 CC also be used as vaccines against meningitis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 6 AA;
 Query Match 42.9%; Score 3; DB 16; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 Db |||
 2 QPP 4
 RESULT 51
 ID AAW08657 standard; peptide; 6 AA.
 XX
 AC AAW08657;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-FEB-1997 (first entry)
 XX
 DE Met-enkephalin analogue DAGO inhibitory peptide #51.
 XX
 KW Ligand; synthetic combinatorial peptide library; hexamer; antibody;
 KW antigen; receptor; inhibitor; enkephalin; opioid receptor.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= OTHER
 FT /note= "Ac-Arg"
 FT Modified-site 6
 FT /label= OTHER
 FT /note= "His-NH2"
 XX
 XX US5556762-A.
 PN
 XX 17-SEP-1996.
 PD
 XX 11-SEP-1992; 92US-0943709.
 XX
 PR 11-SEP-1992; 92US-0943709.
 PR 21-NOV-1990; 90US-0617023.
 PR 16-MAY-1991; 91US-0701658.
 PR 19-NOV-1991; 91US-0797551.
 XX

PA (HOUG-) HOUGHTEN PHARM INC.
 PI Appel JR, Houghten RA, Pinilla C;
 XX WPI; 1996-432985/43.
 XX
 XX Identifying oligopeptide ligands for an acceptor - by scanning
 PT synthetic peptide combinatorial libraries comprising
 PT self-solubilising, unsupported mixed oligopeptide(s)
 XX
 XX Example 5; Column 52; 75pp; English.
 PS
 CC The invention relates to a method of identifying oligopeptide ligands to
 CC a protein by scanning synthetic combinatorial peptide libraries (SCPL).
 CC The SCPL comprise sets of hexamers which contain either one of 6
 CC predetermined amino acids at one predetermined position in the hexamer
 CC and each set may have one predetermined amino acid at 1 of 6
 CC predetermined pos. in the hexamer. The method is useful for identifying
 CC biologically active sequences of e.g. pharmaceutical use. The peptides
 CC esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to
 CC its receptor, etc.
 CC met-enkephalin
 CC The peptides AAW08641-66 and AAW09226-35 are N-terminally acylated and
 CC C-terminally amidated peptides, isolated from a SCPL, which inhibit the
 CC Met-enkephalin analogue (D-Ala, MePhe, Gly-O)-enkephalin (DAGO) from
 CC binding to the mu opioid receptor. This peptide inhibits binding with
 CC an IC50 of about 21 nM.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 6 AA;
 SQ

Query Match 42.9%; Score 3; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 ||||
 Db 4 WMH 6

RESULT 52
 AAY29633
 ID AAY29633 standard; peptide; 6 AA.
 XX
 AC AAY29633;
 XX
 XX 19-OCT-1999 (first entry)
 DT
 DE Phosphoenolpyruvate carboxylase peptide #2.
 XX
 KW Phosphoenolpyruvate carboxylase; PEPc; organic acid; succinic acid;
 KW aerobic Coryneform microbe; Brevibacterium flavum MJ-233.
 XX
 OS Brevibacterium flavum.
 XX
 PN JP11196887-A.
 XX
 PD 27-JUL-1999.
 XX
 XX 16-JAN-1998; 98JP-0020360.
 PF
 XX 16-JAN-1998; 98JP-0020360.
 XX
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 XX WPI; 1999-496658/42.
 DR
 XX Preparation of organic acid e.g. succinic acid - comprises reacting
 PT phosphoenol-pyruvate carboxylase gene recombinant microbe
 PT anaerobically with substrate
 PT
 XX Example 1; Page 13; 18pp; Japanese.
 PS
 XX

CC The present invention describes the preparation of an organic acid
 CC comprising reacting an aerobic Coryneform microbe recombined by
 CC phosphoenolpyruvate carboxylase (PEPC) gene anaerobically with an
 CC organic raw material in a reaction liquid containing carbonate ion,
 CC bicarbonate ion or carbon dioxide gas. The method can prepare an
 CC organic acid such as succinic acid efficiently in a high yield. The
 CC present sequence represents a peptide from Brevibacterium flavum MJ-233
 CC PEPc, used in the exemplification of the present invention.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 42.9%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SWM 3
 ||||
 Db 1 SWM 3

RESULT 53
 AAY36355
 ID AAY36355 standard; Protein; 6 AA.
 XX
 AC AAY36355;
 XX
 DT 17-SEP-1999 (first entry)
 XX
 DE Fragment of human secreted protein encoded by gene 3.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO9931117-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 17-DEC-1998; 98WO-US27059.
 XX
 XX 19-DEC-1997; 97US-0068369.
 PR 18-DEC-1997; 97US-0068006.
 PR 18-DEC-1997; 97US-0068007.
 PR 18-DEC-1997; 97US-0068008.
 PR 18-DEC-1997; 97US-0068053.
 PR 18-DEC-1997; 97US-0068054.
 PR 18-DEC-1997; 97US-0068057.
 PR 18-DEC-1997; 97US-0068064.
 PR 18-DEC-1997; 97US-0070923.
 PR 13-DEC-1997; 97US-0068169.
 PR 19-DEC-1997; 97US-0068365.
 PR 19-DEC-1997; 97US-0068367.
 PR 19-DEC-1997; 97US-0068368.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Carter KC, Duan RD, Feng P, Ferrie AM, Florence C;
 PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;
 PI Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y;
 PI Yu G;
 XX
 DR WPI; 1999-418749/35.
 XX
 XX New isolated human genes encoding secreted polypeptides
 PT
 PT Disclosure; Page 419; 537pp; English.
 PS
 XX AAX97916 to AAX98029 represent 110 isolated human secreted protein
 CC

CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by
 CC the 110 human genes. The genes and their corresponding secreted
 CC polypeptides are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new genes.
 CC Specific uses are described for each of the 110 genes, based on which
 CC tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, tumours, developmental
 CC abnormalities and foetal deficiencies, blood disorders, diseases of the
 CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's
 CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,
 CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular
 CC disorders, kidney disorders, digestive/endocrine disorders, infections
 CC and AIDS. The polypeptides are also useful for identifying their binding
 CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are
 CC used in the exemplification of the present invention.

XX Sequence 6 AA;
 Query Match 42.9%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6
 DB 4 HQP 6

RESULT 54
 AAB28300
 ID AAB28300 standard; Peptide; 6 AA.

AC AAB28300;
 XX
 DT 14-FEB-2001 (first entry)

XX Human secreted peptide #17 encoded by cDNA#23.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.
 OS
 XX WO200058355-A1.
 PN
 XX 05-OCT-2000.

XX 22-MAR-2000; 2000WO-US07527.
 PF
 XX 26-MAR-1999; 99US-0126501.
 PR
 XX 22-DEC-1999; 99US-0171551.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-602358/57.
 DR
 XX N-PSDB; AAC67653.

XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -

XX Claim 11; Page 346; 367pp; English.

XX Sequences AAB28278-B28326 represent the amino acid sequences of 50
 CC human secreted proteins encoded by the genes AAC67631-C67680. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from

CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
 DB 1 WMH 3

RESULT 55
 AAB72258
 ID AAB72258 standard; peptide; 6 AA.

XX AAB72258;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 13.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and

```

CC acquired immunological deficiencies.
XX
SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 56
AAB72511
ID AAB72511 standard; Peptide; 6 AA.
XX
AC AAB72511;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrin peptide #12.
XX
KW Dermatological; oxidative stress regulator; colostrin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 57
AAB72543
ID AAB72543 standard; Peptide; 6 AA.
XX
AC AAB72543;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrin peptide #12.
XX
KW Dermatological; oxidative stress regulator; colostrin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 58
AAB59319
ID AAB59319 standard; Peptide; 6 AA.
XX
AC AAB59319;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrin peptide fragment B-4.
XX
KW Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO2000075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GH02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX

```


PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -

XX Claim 7; Page 27; 63pp; English.

PS
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrin. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7

Db 3 QPP 5

RESULT 59

AAB55512

ID AAB55512 standard; Peptide; 6 AA.

XX AAB55512;

07-MAR-2001 (first entry)

Human elastase variant segment peptide SEQ ID NO:82.

Human; elastase; variant; substrate; mutant; mutagenesis; histidine;
KW human neutrophil elastase; H43A; cytostatic; proteolysis; ADEPT;
KW antibody-directed enzyme activated prodrug therapy.

XX Homo sapiens.

XX WO200068363-A2.

16-NOV-2000.

04-MAY-2000; 2000WO-US06692.

05-MAY-1999; 99US-0132640.

(GETH) GENENTECH INC.

Carter PJ, Dall'Acqua W, Rodrigues M;

WPI; 2001-007389/01.

Elastase variant (H43A) having altered substrate specificity useful for
antibody-directed enzyme activated prodrug therapy -

Example 4; Fig 3; 79pp; English.

The present invention describes a purified elastase variant (I) with
an amino acid sequence different from that of a precursor elastase,
the difference comprising a substitution of an active site histidine
residue corresponding to residue 43 in human neutrophil elastase with
a different amino acid residue so that (I) has substrate specificity
substantially different from the precursor elastase. (I) has cytostatic
activity, and can be used in antibody-directed enzyme activated prodrug
therapy. The elastase variant can be used to cleave a particular
substrate, especially those containing histidine residues at the
substrate site. Site-specific proteolysis is useful in therapeutic
applications, e.g. for antibody-directed enzyme activated prodrug

CC therapy (ADEPT). AAC89022, AAC89023 and AAB55432 to AAB55526 represent
CC sequences used in the exemplification of the present invention.

SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEQ 5

Db 2 MEQ 4

RESULT 60

AAE20240

ID AAE20240 standard; peptide; 6 AA.

XX AAE20240;

18-JUN-2002 (first entry)

Colostrinin constituent peptide #12.

Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.

XX Unidentified.

XX Key

Location/Qualifiers

FT Modified-site 6

FT /note= "Optionally C-terminal amide"

XX WO200213850-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22776.

XX 17-AUG-2000; 2000WO-US22776.

XX (TEXA) UNIV TEXAS SYSTEM.

Stanton GJ, Hughes TK, Boldogh I;

WPI; 2002-269151/31.

Composition useful for the modulation of blood cell proliferation in a
patient comprises a blood cell regulator selected from colostrinin, its
constituent peptide and/or analog -

Claim 6; Page 25; 51pp; English.

The invention relates to a composition which comprises a blood cell
regulator selected from colostrinin, its constituent peptide and/or
analogue. The invention is used for modulating the oxidative stress
level in a cell e.g. mammalian or human cell present in a cell culture,
tissue, organ, or organism; or for treating oxidative damage to the skin
of a patient e.g. animal or human; to modulate oxidative stress during/
after a premature birth or normal birth, preventing/delaying aging in a
patient, enhancing wound healing, and the reduction of side effects of
cosmetic procedures. The method changes the level of an oxidising species
in the cell, such as decreases or prevents increase in the level of
damage to a biomolecule of the patient selected from DNA, protein and/or
lipid, compared to the same conditions when the oxidative stress
regulator is not present. The modulation of oxidative stress results in
enhanced repair, regeneration, and replacement of cells, tissues and
organs (e.g. kidney, liver, pancreas, skin, and the other internal and
external organs) as well as enhanced preservation of such organs for
transplantation, implantation, or scientific research. The present
sequence is a colostrinin constituent peptide.

```
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPP 7
Db 3 QPP 5

RESULT 61
AAMS1047
ID AAMS1047 standard; Peptide; 6 AA.
XX
AC AAMS1047;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide.
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "optional C-terminal amidation"
XX
PN WO200213849-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22775.
XX
PR 17-AUG-2000; 2000WO-US22775.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. The peptide is
CC classified as having a beta-casein homologue precursor. Methods
CC are claimed for: inducing a cytokine in a cell by contact with an
CC immunological regulator, where the cell is present in a cell
CC culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell
CC by contact with the immunological regulator under conditions in a
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator
CC is administered topically or as part of a dietary supplement, and
CC where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation
CC by contacting blood cells with a blood cell regulator, where the
CC blood cells are present in a cell culture or an organism, are
CC mammalian or human, and where the blood cells are increased in
CC number or differentiated; and a method for modulating blood cell
CC proliferation in a patent. A claimed cytokine-inducing composition
CC comprises a pharmaceutical carrier and an active agent such as the
```

```
CC present peptide.
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPP 7
Db 3 QPP 5

RESULT 62
AAO14589
ID AAO14589 standard; peptide; 6 AA.
XX
AC AAO14589;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 12.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22777.
XX
PR 17-AUG-2000; 2000WO-US22777.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog -
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPP 7
Db 3 QPP 5
```

KW	immunooassay; diagnosis; treatment; prophylactic; bacterial;
KX	viral; peptide 423-429.
XX	
OS	Streptococcus pneumoniae.
XX	
PN	WO9509232-A2.
XX	
PD	06-APR-1995.
XX	
PB	28-SEP-1994; 94WO-CA00516.
XX	
PR	28-SEP-1993; 93US-0127499.
XX	
PA	(SHAR/) SHARMA L R.
PA	(VALS/) VAN ALSTYNE D.
XX	
PI	Sharma LR, Van Alstyne D;
XX	
DR	WFI; 1995-147431/19.
XX	
PT	New peptide(s) and corresp. antibodies for the treatment of
PT	meningitis - the peptide(s) corresp. to homologous antigenic
PT	sites on bacterial and viral agents and on chemokine(s), used for
PT	detecting and preventing meningitis
XX	
PS	Claim 35; Page 76; 98pp; English.
XX	
CC	AAR73912 is the Streptococcus pneumoniae surface protein A. It
CC	contains the meningitis related antigenic sequences (MRHAS) claimed
CC	in AAR73890 and AAR73902, which are recognised by a monoclonal
CC	antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
CC	peptides may be used in immunoassays to diagnose the presence of
CC	bacterial and/or viral meningitis agents in a sample, or in
CC	prophylactic and therapeutic meningitis treatments. The peptides may
CC	also be used as vaccines against meningitis.
CC	(Updated on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 7 AA;
Query Match 42.9%; Score 3; DB 16; Length 7;	
Best Local Similarity 100.0%; Pred.No. 9.3e+05;	
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	5 QPP 7
Db	
	3 QPP 5
RESULT 65	
AAR73893	
ID	AAR73883 standard; peptide; 7 AA.
XX	
AC	AAR73883;
AC	
XX	
DT	25-MAR-2003 (updated)
DT	05-DEC-1995 (first entry)
XX	
DE	Rubella virus glycosylated membrane-associated protein E2 313-319.
XX	
KW	Rubella virus; Glycosylated membrane associated protein E2; vaccine;
KW	meningitis related homologous antigenic sequence; MRHAS;
KW	RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
KW	viral; peptide 313-319; Therien strain.
XX	
OS	Rubella virus.
XX	
PN	WO9509232-A2.
XX	
PD	06-APR-1995.
XX	
PF	28-SEP-1994; 94WO-CA00516.
XX	

PR 28-SEP-1993; 93US-0127499.
PA (SHAR/) SHARMA L R.
PA (VALS/) VAN ALSTYNE D.
XX
PI Sharma LR, Van Alstyne D;
XX WPI; 1995-147431/19.
DR
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73917 is the Rubella virus Therein strain glycosylated membrane
CC associated protein E2. It contains the meningitis related antigenic
CC sequences (MRHAS) claimed in AAR73893-R73885 and AAR73897, which are
CC recognised by a monoclonal antibody from the hybridoma Rubella
CC virus (RV)-1. The claimed MRHAS peptides may be used in
CC immunoassays to diagnose the presence of bacterial and/or viral
CC meningitis agents in a sample, or in prophylactic and therapeutic
CC treatments. The peptides may also be used as vaccines
CC against meningitis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
Query Match 42.9%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
DB |||||
3 QPP 5

RESULT 66
AAR73897
ID AAR73897 standard; peptide; 7 AA.
XX
AC AAR73897;
XX
XX 25-MAR-2003 (updated)
DT 05-DEC-1995 (first entry)
XX
DE Rubella virus glycosylated membrane-associated protein E2 313-319.
XX
KW Rubella virus; glycosylated membrane associated protein E2; vaccine;
KW meningitis related homologous antigenic sequence; MRHAS;
KW RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
KW viral; peptide 313-319; Therien strain.
XX
OS Rubella virus.
XX
XX WO9509232-A2.
PN
XX 06-APR-1995.
XX
XX 28-SEP-1994; 94WO-CA00516.
PF
XX 28-SEP-1993; 93US-0127499.
PR
XX (SHAR/) SHARMA L R.
PA (VALS/) VAN ALSTYNE D.
XX
XX Sharma LR, Van Alstyne D;
PI WPI; 1995-147431/19.
DR
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73916 is the Rubella virus strain M33 core structural glycoprotein.
CC It contains the meningitis related antigenic sequences (MRHAS)
CC claimed in AAR73879-R73882, which are recognised by a monoclonal
CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
CC peptides may be used in immunoassays to diagnose the presence of
CC bacterial and/or viral meningitis agents in a sample, or in

PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73915 is the Rubella virus Therien strain glycosylated membrane
CC associated protein E2. It contains the meningitis related antigenic
CC sequences (MRHAS) claimed in AAR73893-R73885 and AAR73897, which are
CC recognised by a monoclonal antibody from the hybridoma Rubella
CC virus (RV)-1. The claimed MRHAS peptides may be used in
CC immunoassays to diagnose the presence of bacterial and/or viral
CC meningitis agents in a sample, or in prophylactic and therapeutic
CC treatments. The peptides may also be used as vaccines
CC against meningitis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
Query Match 42.9%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
DB |||||
3 QPP 5

RESULT 67
AAR73879
ID AAR73879 standard; peptide; 7 AA.
XX
AC AAR73879;
XX
XX 25-MAR-2003 (updated)
DT 05-DEC-1995 (first entry)
XX
DE Rubella virus strain M33 core structural peptide MRHAS 102-108.
XX
KW Rubella virus; strain M33; core structural glycoprotein; vaccine;
KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
KW viral; peptide 102-108.
XX
OS Rubella virus.
XX
XX WO9509232-A2.
PN
XX 06-APR-1995.
XX
XX 28-SEP-1994; 94WO-CA00516.
PF
XX 28-SEP-1993; 93US-0127499.
PR
XX (SHAR/) SHARMA L R.
PA (VALS/) VAN ALSTYNE D.
XX
XX Sharma LR, Van Alstyne D;
PI WPI; 1995-147431/19.
DR
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73916 is the Rubella virus strain M33 core structural glycoprotein.
CC It contains the meningitis related antigenic sequences (MRHAS)
CC claimed in AAR73879-R73882, which are recognised by a monoclonal
CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
CC peptides may be used in immunoassays to diagnose the presence of
CC bacterial and/or viral meningitis agents in a sample, or in

CC prophylactic and therapeutic meningitis treatments. The peptides
 CC may also be used as vaccines against meningitis.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 7 AA;

Query Match 42.9%; Score 3; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||

Db 3 QPP 5

RESULT 68

AAAY20876
 ID AAY20876 standard; Protein; 7 AA.

AC AAY20876;

DT 22-JUL-1999 (first entry)

DE Human presenilin I mutant protein fragment 22.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.

XX Synthetic.

OS Homo sapiens.

XX WO9845322-A2.

XX 15-OCT-1998.

PF 02-APR-1998; 98WO-TB00705.

XX 10-APR-1997; 97US-0043163.

XX (UYUT-) RIJKSUNIV UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX Burbach JPH, Grosveld FG, Van Leeuwen FW;

XX WPI; 1998-609901/51.

DR N-PSDB; AAX75761.

XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA

XX Disclosure; Figure 10; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be

CC caused by mutations in RNA rather than DNA. The invention describes the
 CC used of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.

SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||

Db 2 QPP 4

RESULT 69

AAW61049

ID AAW61049 standard; peptide; 7 AA.

AC AAW61049;

XX 25-SEP-1998 (first entry)

DE Peptide from mouse IgG1 that is important for FcRn binding.

XX Immunoglobulin G; IgG; FcRn binding; half-life; increase; decrease;
 KW treatment; idiopathic thrombocytopenic purpura; ITP;
 KW Kawasaki disease; AIDS; Guillain-Barre syndrome; dermatomyositis.

XX Synthetic.

OS Mus sp.

XX WO9823289-A1.

XX 04-JUN-1998.

XX 26-NOV-1997; 97WO-US21437.

XX 27-NOV-1996; 96US-0031607.

XX (GEHO) GEN HOSPITAL CORP.

PA (UYBR-) UNIV BRANDEIS.

XX Israel EJ, Simister NE;

XX WPI; 1998-322461/28.

XX New antibody having altered Fc receptor binding site - allows
 PT increased or decreased half-lives and clearance rates, useful for,
 PT e.g. tumour imaging or treatment of AIDS

XX Example 2; Fig 2A; 32pp; English.

XX AAW61048-57 represent partial amino acid sequence of different
 CC immunoglobulin G (IgG) molecules. These peptides have been identified
 CC as being important for FcRn binding. The specification describes a
 CC non-naturally occurring IgG having an altered amino acid sequence
 CC compared to native IgG, which binds to FcRn with increased or
 CC decreased affinity. FcRn is a receptor found on the intestinal surface
 CC of the neonate and is responsible passage of maternal milk IgG from the
 CC intestinal lumen to the systemic circulation via the intestinal
 CC epithelial cells. FcRn is also used to prevent clearance of circulating
 CC IgG from the circulation. Altering the binding site on an IgG for FcRn
 CC allows greater or lower affinity for the FcRn receptor, which
 CC subsequently increases or decreases the half-life of circulating IgG,
 CC respectively. IgG's with an increased half-life can be used to treat
 CC immune conditions or diseases such as idiopathic thrombocytopenic

CC purpura (ITP), Kawasaki disease, AIDS, Guillain-Barre syndrome and
 CC dermatomyositis.
 XX
 SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
 ||||
 Db 2 MHQ 4

RESULT 70
 AAY16906
 ID AAY16906 standard; peptide; 7 AA.
 XX
 AC AAY16906;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Heat shock protein (hsp) binding peptide.
 XX
 KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN WO9922761-A1.
 XX
 PD 14-MAY-1999.
 XX
 PF 22-OCT-1998; 98WO-US22335.
 XX
 PR 31-OCT-1997; 97US-0961707.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
 PI Querfelli O, Rothman JE;
 XX
 DR WPI; 1999-313177/26.
 XX
 PT Identifying peptides which bind heat shock proteins
 XX
 PS Examples; Page 20; 155pp; English.
 XX
 CC The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzquinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases.
 XX
 SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6

Db ||||
 1 HQP 3

RESULT 71
 AAB16495
 ID AAB16495 standard; Peptide; 7 AA.
 XX
 AC AAB16495;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE Linear peptide that binds to angiostatin SEQ ID # 86.
 XX
 KW Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
 KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
 KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
 KW cerebral collateral; arteriovenous malformation; rubecosis; cancer;
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
 KW Helicobacter related disease; fracture; cat scratch fever.
 XX
 OS Synthetic.
 XX
 PN WO200032631-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28897.
 XX
 PR 04-DEC-1998; 98US-0206059.
 XX
 PA (ENTR-) ENTREMED INC.
 XX
 PI MacDonald NJ, Sim KL;
 XX
 DR WPI; 2000-412290/35.
 XX
 PT New angiogenesis-inhibiting protein receptors, useful in methods for
 PT treating diseases and processes that are mediated by angiogenesis, such
 PT as solid tumours, psoriasis, scleroderma and myocardial angiogenesis -
 XX
 PS Claim 1; Page 50; 100pp; English.
 XX
 CC This invention relates to angiogenesis-inhibiting protein receptors, and
 CC the DNA sequences encoding them. Angiogenesis is the generation of new
 CC blood vessels into a tissue, and normally occurs in wound healing,
 CC foetal and embryonal development and the formation of the corpus luteum,
 CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
 CC AAA68202) involved in angiogenesis, and has an amino acid sequence
 CC similar to that of a plasminogen fragment (see murine plasminogen
 CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.
 CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
 CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein
 CC sequences of human laminin. Laminin is an angiostatin binding protein, of
 CC and some of the peptides of the invention share homology with regions of
 CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
 CC angiogenesis-inhibiting protein receptor fragments of the invention. The
 CC peptides bind either angiostatin or endostatin and can be used in methods
 CC for treating diseases and processes that are mediated by angiogenesis,
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
 CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
 CC Helicobacter related diseases, fractures, placenta and cat scratch
 CC fever. They are useful for the detection and prognosis of cancer. DNA
 CC sequences A628204-A628241 encode the peptides of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db
|||
2 QPP 4

RESULT 72
AAB17249
ID AAB17249 standard; Peptide; 7 AA.
XX
AC AAB17249;
XX
DT 31-OCT-2000 (first entry)
XX
DE SH3 antagonist peptide sequence SEQ ID NO:305.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 39; Page 302; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAB69443
CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 73
AAY92768
ID AAY92768 standard; peptide; 7 AA.
XX
AC AAY92768;
XX
DT 29-AUG-2000 (first entry)
XX
DE Heptapeptide mimotope of surface LOS of serogroup B meningococcus.
XX
KW Heptapeptide; epitope; mimotope; surface lipo-oligosaccharide; LOS;
KW meningitis; anti-bacterial; anti-inflammatory; vaccine.
XX
OS Neisseria meningitidis.
XX
PN WO200025814-A2.
XX
PD 11-MAY-2000.
XX
PF 27-OCT-1999; 99WO-GB03559.
XX
PR 30-OCT-1998; 98GB-0023835.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX
PI Charalambous BM, Feavers IM;
XX
DR WPI; 2000-365403/31.
XX
PT Use of a mimotope of a surface lipoooligosaccharide of a serogroup B
PT meningococcus for a vaccine against serogroup B meningococci
XX
PS Claim 13; Page 26; 39pp; English.
XX
CC This is a preferred heptapeptide epitope mimotope of a surface
CC lipoooligosaccharide (LOS) of a serogroup B meningococcus. The mimotopes
CC are useful in vaccines against serogroup B meningococci, especially
CC Neisseria meningitidis, which causes meningitis. The LOS is a surface
CC glycolipid that forms a major outer membrane component and possesses a
CC terminal galactose acceptor sites for sialic acid. Sialylation of the LOS
CC in immunotype B meningococci may enhance the ability of the organism to
CC evade the human immune response. Therefore alternative target antigens on
CC the surface of serogroup B meningococci are important.
XX
SQ Sequence 7 AA;
Query Match 42.9%; Score 3; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 QPP 6
|||
Db 4 QPP 6

RESULT 74
AAU72048
ID AAU72048 standard; Peptide; 7 AA.
XX
AC AAU72048;
XX
DT 26-FEB-2002 (first entry)
XX
DE Melanoma antigen, javelin peptide #34.
XX
KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;
KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;
KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
KW javelin molecule; melanoma antigen recognised by T cells-1; human.
XX

OS Bacteriophage M13.
 XX WO200178655-A2.
 XX
 XX 25-OCT-2001.
 XX
 XX 17-APR-2001; 2001WO-US12449.
 XX
 XX 17-APR-2000; 2000US-197462P.
 XX
 XX (HOUGH/) HOUGHTON A.
 XX (LIVI/) LIVINGSTON P.
 XX (ALAW/) AL-AWQATI Q.
 XX (MAYH/) MAYHEW M.
 XX (HOEM/) HOE M.
 XX
 XX Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;
 XX WPI; 2001-663092/76.
 XX
 XX Anti cancer vaccine for the treatment of melanoma comprises a heat
 XX shock protein and a melanoma antigen i.e. tyrosinase -
 XX
 XX Disclosure; Page 16; 150pp; English.
 XX
 XX The invention relates to a method of induction of an immune response,
 XX comprising administration of an immunotherapeutic composition, comprising
 XX a heat shock protein, and a melanoma antigen, where the melanoma
 XX antigen is selected from tyrosinase, tyrosinase related protein 1,
 XX tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,
 XX NYEs01, MART antigens, GM2, antigenic portions and combinations of these.
 XX The melanoma antigen is covalently bound to a javelin molecule, where the
 XX melanoma antigen bound to the javelin molecule is non-covalently bound to
 XX the heat shock protein. The composition is useful for inducing an immune
 XX response for the treatment of melanoma. AAU71980-AAU72481 represent
 XX melanoma antigen peptides of the invention.
 XX
 XX Sequence 7 AA;
 XX
 XX Query Match 42.9%; Score 3; DB 22; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 4 HQP 6
 XX Db 1 HQP 3
 XX
 XX
 XX RESULT 75
 XX AAU43873
 XX ID AAU43873 standard; Peptide; 7 AA.
 XX AC AAU43873;
 XX
 XX 25-OCT-2001 (first entry)
 XX
 XX H11 binding site consensus conforming peptide (CCP) #144.
 XX
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
 XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
 XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX
 XX Homo sapiens.
 XX Synthetic.
 XX
 XX CA2290722-A1.
 XX
 XX 08-JUN-2001.
 XX
 XX 08-DEC-1999; 99CA-2290722.

PR 08-DEC-1999; 99CA-2290722.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 XX Entwistle JM, MacDonald GC;
 XX WPI; 2001-425937/46.
 XX
 XX Composition useful for treating and diagnosing cancer, comprises stress
 XX protein-peptide complexes associated with tumor, and isolated
 XX antigen-binding fragments of an antibody that binds specifically to the
 XX complex -
 XX
 XX Example 4; Page 101; 154pp; English.
 XX
 XX The present invention describes a composition (I) comprising stress
 XX protein-peptide complexes (SPPC) associated with tumours that is
 XX specifically immunogenically cross-reactive with cell surface-associated
 XX SPPCs specific to target cancer (TC). Also described is an isolated
 XX antigen-binding fragment of an antibody that binds specifically to SPPCs
 XX or a population of different SPPCs consisting of immunogenic cancer cell
 XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
 XX used in vaccine production and as a tumour-specific immunogenic response
 XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
 XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
 XX or imaging cancer cells, and to monitor the course of amelioration of
 XX malignancy in an individual. AAU43707 to AAU47109 represent peptides
 XX which are used in the exemplification of the present invention.
 XX
 XX Sequence 7 AA;
 XX
 XX Query Match 42.9%; Score 3; DB 22; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 5 QPP 7
 XX Db 5 QPP 7
 XX
 XX Search completed: November 25, 2003, 19:27:12
 XX Job time : 19.8663 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 11.2326 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWNHQP 7

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Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Published Applications AA:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	15	US-10-281-652-24
2	7	100.0	10	15	US-10-185-815-89
3	6	85.7	19	12	US-10-372-736-3
4	5	71.4	15	15	US-10-281-652-34
5	4	57.1	10	9	US-09-794-346-1
6	4	57.1	11	11	US-09-809-391-689
7	4	57.1	11	12	US-09-882-171-689
8	4	57.1	17	12	US-09-962-756-1752
9	4	57.1	20	12	US-10-195-730-261
10	4	57.1	20	12	US-09-933-767-773
11	4	57.1	20	15	US-10-023-282-773
12	3	42.9	5	9	US-09-748-960-12
13	3	42.9	5	9	US-09-765-086-223
14	3	42.9	5	9	US-09-933-497B-26
15	3	42.9	5	10	US-09-770-002-1
16	3	42.9	3	42.9	US-09-940-727B-70
17	3	42.9	3	42.9	US-10-097-065-334
18	3	42.9	3	42.9	US-10-227-353-7
19	3	42.9	3	42.9	US-10-281-652-13
20	3	42.9	3	9	US-09-873-676-86
21	3	42.9	7	11	US-09-821-687-7
22	3	42.9	7	10	US-09-954-385-347
23	3	42.9	7	12	US-10-052-578-176
24	3	42.9	7	12	US-09-990-832C-10
25	3	42.9	7	12	US-10-053-520-176
26	3	42.9	7	12	US-10-286-457-92
27	3	42.9	7	12	US-10-038-899-4
28	3	42.9	7	12	US-10-220-033-21
29	3	42.9	7	12	US-10-053-498B-176
30	3	42.9	7	15	US-10-015-979-84
31	3	42.9	7	15	US-10-281-652-1
32	3	42.9	8	7	US-08-344-824-263
33	3	42.9	8	10	US-09-765-614B-6
34	3	42.9	8	10	US-09-925-715-2
35	3	42.9	8	10	US-09-791-378-285
36	3	42.9	8	10	US-09-883-825-35
37	3	42.9	8	10	US-09-826-290-124
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ALIGNMENTS

RESULT 1
US-10-281-652-24
; Sequence 24, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-24

Query Match 100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
Db 1 SWMHQPP 7

RESULT 2
US-10-185-815-89
; Sequence 89, Application US/10185815
; Publication No. US20030096354A1
; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
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; OTHER INFORMATION: Segment of CAPHI beta casein precursor
US-10-185-815-89

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; Publication No. US20030166223A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/10/372,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide substrate
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Db 12 SWMHQP 17

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; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 15

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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
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Best Local Similarity 100.0%; Pred.No.11;
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Db      1 MHQPP 5

RESULT 5
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; Patent No. US20010031857A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Memo Peptides, Process for Their Preparation and Use Thereof
; FILE REFERENCE: 02481.1728
; CURRENT APPLICATION NUMBER: US/09/794,346
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: EP 00104114.4
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Description of Artificial Sequence: Memmonniella echinata, FH 227
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Best Local Similarity 100.0%; Pred.No.1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MHQP 6
Db      1 MHQP 4

RESULT 6
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; Sequence 689, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 689
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred.No.1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 HOPP 7
Db      1 HOPP 4

RESULT 7
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; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
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; PRIOR APPLICATION NUMBER: PCT/US98/04493
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; PRIOR APPLICATION NUMBER: 60/040,162
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; PRIOR APPLICATION NUMBER: 60/038,621
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; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
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; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
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; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
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; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/047,594
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; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Quest Match 57.1%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQPP 7

Db 1 HQPP 4

RESULT 8

US-09-962-756-1752
; Sequence 1752, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLIUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1752
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1752

Query Match 57.1%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQP 6
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Db 12 MHQP 15

RESULT 9
US-10-195-730-261
; Sequence 261, Application US/10195730
; Publication No. US20030144492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 261
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-730-261

Query Match 57.1%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQPP 7
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Db 11 HQPP 14

RESULT 10
US-09-933-767-773
; Sequence 773, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
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; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06

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; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
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; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-773

Query Match      57.1%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HOPP 7
Db      1 HOPP 4

RESULT 11
US-10-023-282-773
; Sequence 773, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-773

Query Match          57.1%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQPP 7
Db 1 HQPP 4

RESULT 12
US-09-748-960-12
; Sequence 12, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 3 WMH 5

RESULT 13
US-09-765-086-223
; Sequence 223, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredeesen, Dale E.

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-773

Query Match          57.1%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQPP 7
Db 1 HQPP 4

RESULT 12
US-09-748-960-12
; Sequence 12, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 3 WMH 5

RESULT 13
US-09-765-086-223
; Sequence 223, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredeesen, Dale E.

; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-223

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 2 HQP 4

RESULT 14
US-09-933-497B-26
; Sequence 26, Application US/09933497B
; Patent No. US20020098193A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.
; TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTSID:483
; CURRENT APPLICATION NUMBER: US/09/933,497B
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/013,563
; PRIOR FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-09-933-497B-26

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 2 MHQ 4

RESULT 15
US-09-770-002-1
; Sequence 1, Application US/09770002
; Patent No. US20020110558A1
; GENERAL INFORMATION:
; APPLICANT: Peter Lloyd Amlot
; APPLICANT: Max H. Schreier
; APPLICANT: Karin Schreier
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; TITLE OF INVENTION: treatment of rheumatoid arthritis or skin diseases.
; FILE REFERENCE: 4-30583A/30967C1
; CURRENT APPLICATION NUMBER: US/09/770,002
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/EP99/05316
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; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mus musculus
; FEATURE:
US-09-770-002-1

Query Match      42.9%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 WMH 4
        |||
Db      3 WMH 5

RESULT 16
US-09-940-727B-70
; Sequence 70, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-70

Query Match      42.9%; Score 3; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 WMH 4
        |||
Db      3 WMH 5

RESULT 17
US-10-097-065-334
; Sequence 334, Application US/10097065
; Publication No. US2003005236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369

; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 334
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-334

Query Match      42.9%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HQP 6
        |||
Db      4 HQP 6

RESULT 18
US-10-227-353-7
; Sequence 7, Application US/10227353
; Publication No. US20030087383A1
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
;              ROMANOS, MICHAEL A.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd., Suite 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/227,353
; FILING DATE: 26-Aug-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,269C
; FILING DATE: 02-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
```


;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-227-353-7

Query Match 42.9%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 4 QPP 6
|||
|||

RESULT 19
US-10-281-652-13
; Sequence 13, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-13

Query Match 42.9%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5
|||
|||

RESULT 20
US-09-873-676-86
; Sequence 86, Application US/09873676
; Patent No. US2002007289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

;
; OTHER INFORMATION: Synthetic Peptide
US-09-873-676-86

Query Match 42.9%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4
|||
|||

RESULT 21
US-09-821-687-7
; Sequence 7, Application US/09821687
; Patent No. US20020106724A1
; GENERAL INFORMATION:
; APPLICANT: MIKOSHIBA, KATSUHIKO
; APPLICANT: MIZUTANI, AKIHIRO
; TITLE OF INVENTION: RNA-BINDING PROTEIN
; FILE REFERENCE: 081356/0162
; CURRENT APPLICATION NUMBER: US/09/821,687
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-299812
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-821-687-7

Query Match 42.9%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QPP 6
Db 2 QPP 4
|||
|||

RESULT 22
US-09-954-385-347
; Sequence 347, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Ahle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Gisele G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzkv, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-347

Query Match 42.9%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 23
US-10-052-578-176
; Sequence 176, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 176
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-176

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6
|||
Db 1 QPP 3

RESULT 24
US-09-990-832C-10
; Sequence 10, Application US/09990832C
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/P1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-10

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 4 QPP 6

RESULT 25

US-10-053-520-176
; Sequence 176, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 176
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-176

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6
|||
Db 1 QPP 3

RESULT 26
US-10-286-457-92
; Sequence 92, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, b
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-92

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 1 QPP 3

RESULT 27
US-10-038-899-4
; Sequence 4, Application US/10038899
; Publication No. US20030186406A1

APPLICANT: Verhaert, Raymond M.D.
APPLICANT: Beekwilder, Martinus J.
APPLICANT: Aehle, Wolfgang
TITLE OF INVENTION: Enzyme Selection
FILE REFERENCE: 2183-5207US
CURRENT APPLICATION NUMBER: US/10/015,979
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: PCT/NL00/00399
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,443
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 84
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CB4 mutant isolated by selected
OTHER INFORMATION: tion
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(7)
OTHER INFORMATION:
US-10-015-979-84

Query Match 42.9%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 5 WMH 7

RESULT 31
US-10-281-652-1
Sequence 1, Application US/10281652
Publication No. US20030091606A1
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
APPLICANT: BOLDOGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/10/281,652
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/09/641,803
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-281-652-1

Query Match 42.9%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 32

US-08-344-824-263
Sequence 263, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
FLOOR
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-263

Query Match 42.9%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 33
US-09-765-614B-6
Sequence 6, Application US/09765614B
Patent No. US20020102215A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial

; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-09-765-614B-6

Query Match 42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 34

US-09-925-715-2
; Sequence 2, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-09-925-715-2

Query Match 42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 35

US-09-791-378-285
; Sequence 285, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 285
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-285

Query Match 42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 1 QPP 3

RESULT 36

US-09-883-825-35
; Sequence 35, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-883-825-35

Query Match 42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
|||
Db 4 WMH 6

RESULT 37

US-09-826-290-124
; Sequence 124, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.

```

; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-124

Query Match      42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QPP 7
Db      2 QPP 4

RESULT 38
US-09-999-724-58
; Sequence 58, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-999-724-58

Query Match      42.9%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QPP 7

```

```

Db      2 QPP 4

RESULT 39
US-10-365-908-98
; Sequence 98, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-98

Query Match      42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QPP 7
Db      2 QPP 4

RESULT 40
US-09-829-382-11
; Sequence 11, Application US/09829382
; Publication No. US20030175293A1
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,382
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,065
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

```

```
;
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 600-1-158 ..
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-487-5800
;   TELEFAX: 201-343-1684
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-829-382-11

Query Match      42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QPP 7
        |||
Db      2 QPP 4

RESULT 41
US-10-038-899-3
; Sequence 3, Application US/10038899
; Publication No. US20030186406A1
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
;   SATO, NORIYUKI
;   SAHARA, HIROMITSU
;   YASOJIMA, TAKAHIRO
;   WADA, YOSHIMASA
;   SUZUKI, MANABU
;   HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
;   RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;   OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038,899
; FILING DATE: 08-Jan-2002
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,116
; FILING DATE: 30-SEP-1996
; APPLICATION NUMBER: JP 253491/1995
; FILING DATE: 29-SEP-1995
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
```

```
;
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   ORIGINAL SOURCE:
;   ORGANISM: HUMAN
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-038-899-3

Query Match      42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SWM 3
        |||
Db      2 SWM 4

RESULT 42
US-10-357-929A-21
; Sequence 21, Application US/10357929A
; Publication No. US20030216322A1
; GENERAL INFORMATION:
; APPLICANT: Tatiana I. Samoylova
; APPLICANT: Valery A. Petrenko
; APPLICANT: Nancy R. Cox
; APPLICANT: Nancy E. Morrison
; APPLICANT: Henry J. Baker
; APPLICANT: Ludmila P. Globa
; TITLE OF INVENTION: Peptides for Recognition and Targeting
; FILE REFERENCE: 35721/259047
; CURRENT APPLICATION NUMBER: US/10/357,929A
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 10/357,929
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 60/354,188
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-357-929A-21

Query Match      42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 HQP 6
        |||
Db      6 HQP 8

RESULT 43
US-10-158-596A-105
; Sequence 105, Application US/10158596A
; Publication No. US20030068900A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela
; APPLICANT: Flynn, Christine
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYST
; FILE REFERENCE: 119927-1052
; CURRENT APPLICATION NUMBER: US/10/158,596A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
```

; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-105

Query Match 42.9%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 4 MHQ 6

RESULT 44
US-10-017-193-4
; Sequence 4, Application US/10017193
; Publication No. US20030113478A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Mai Huong
; APPLICANT: Chiu, Phillip
; TITLE OF INVENTION: Surface Coating Method and Coated Device
; FILE REFERENCE: 52200-8010
; CURRENT APPLICATION NUMBER: US/10/017,193
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attachment peptide from fibronectin
US-10-017-193-4

Query Match 42.9%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 45
US-10-254-446A-232
; Sequence 232, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan
US-10-254-446A-232

Query Match 42.9%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 4 MHQ 6

RESULT 46
US-09-748-960-11
; Sequence 11, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Judith A.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(9)
; OTHER INFORMATION: CDR3 of the light chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-11

Query Match 42.9%; Score 3; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOP 6
|||
Db 5 HOP 7

RESULT 47
US-09-780-053-165
; Sequence 165, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129 5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-165

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 5 QPP 7

RESULT 48
US-09-780-053-456
; Sequence 456, Application US/097800053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 4 QPP 6

RESULT 49
US-09-780-053-517
; Sequence 517, Application US/097800053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-517

Query Match 42.9%; Score 3; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 4 QPP 6

RESULT 50
US-09-780-053-620
; Sequence 620, Application US/097800053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 620
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-620

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 4 QPP 6

RESULT 51
US-09-862-179A-11
; Sequence 11, Application US/09862179A
; Patent No. US20020147306A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Danny
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
; FILE REFERENCE: MTSI-P01-009
; CURRENT APPLICATION NUMBER: US/09/862,179A
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PDZ inhibitory peptide
US-09-862-179A-11

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
|||
Db 2 HQP 4

```

RESULT 52
US-09-862-179A-18
; Sequence 18, Application US/09862179A
; Patent No. US20020147306A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Danny
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
; TITLE OF INVENTION: AND PDZ DOMAINS
; FILE REFERENCE: MTSI-P01-009
; CURRENT APPLICATION NUMBER: US/09/862,179A
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Negative control peptide
US-09-862-179A-18

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 2 HQP 4

RESULT 53
US-09-017-743C-69
; Sequence 69, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:

```

; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-143

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 1 MHQ 3

RESULT 56

US-09-938-864-148
; Sequence 148, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT FILING DATE: 2001-08-24
; CURRENT APPLICATION NUMBER: US/09/938,864
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-148

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 2 MHQ 4

RESULT 57

US-09-938-864-180
; Sequence 180, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5

; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-180

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 5 MHQ 7

RESULT 58

US-09-938-864-243
; Sequence 243, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT FILING DATE: 2001-08-24
; CURRENT APPLICATION NUMBER: US/09/938,864
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-243

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 6 MHQ 8

RESULT 59

US-09-938-864-281
; Sequence 281, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5

```
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-281

Query Match
Best Local Similarity 42.9%; Score 3; DB 11; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
Db 1 MHQ 3

RESULT 60
US-09-791-477-108
; Sequence 108, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-108

Query Match
Best Local Similarity 42.9%; Score 3; DB 11; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
Db 4 MHQ 6

RESULT 61
US-09-791-477-143
; Sequence 143, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-143

Query Match
Best Local Similarity 42.9%; Score 3; DB 11; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
Db 5 MHQ 7

RESULT 62
US-09-791-477-148
; Sequence 148, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-148

Query Match
Best Local Similarity 42.9%; Score 3; DB 11; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
Db 2 MHQ 4

RESULT 63
US-09-791-477-180
; Sequence 180, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-180

Query Match
Best Local Similarity 42.9%; Score 3; DB 11; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
Db 5 MHQ 7

RESULT 64
US-09-791-477-243
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; Sequence 243, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-243

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 6 MHQ 8

RESULT 65
US-09-791-477-281
; Sequence 281, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-281

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 1 MHQ 3

RESULT 66
US-09-785-019-108
; Sequence 108, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 1 MHQ 3

RESULT 67
US-09-785-019-143
; Sequence 143, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-143

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 4 MHQ 6

RESULT 68
US-09-785-019-148
; Sequence 148, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376

```

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-148

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
DB      2 MHQ 4

RESULT 69
US-09-785-019-180
; Sequence 180, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-180

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
DB      5 MHQ 7

RESULT 70
US-09-785-019-243
; Sequence 243, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-785-019-243

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
DB      1 MHQ 3

RESULT 71
US-09-785-019-281
; Sequence 281, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-281

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
DB      1 MHQ 3

RESULT 72
US-09-932-165-66
; Sequence 66, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; FILE REFERENCE: 83P2H3 AND Cat#P2E11 USEFUL IN TREATMENT AND
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-66

Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QPP 7
      |||
Db      3 QPP 5

RESULT 73
US-09-932-165-669
; Sequence 669, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-669

Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QPP 7
      |||
Db      3 QPP 5

RESULT 74
US-09-932-165-1013
; Sequence 1013, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
```

```
;
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1013
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1013
```

```
Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      5 QPP 7
      |||
Db      5 QPP 7
```

```
RESULT 75
US-09-932-165-1212
; Sequence 1212, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1212
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```
Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      5 QPP 7
      |||
Db      1 QPP 3
```

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Search completed: November 25, 2003, 20:37:01
Job time : 12.2326 secs
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 5.65698 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-24
Perfect score: 7
Sequence: 1 SWHQPP 7

Scoring table: OIIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

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Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles.ppep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-641-803-24
2	6	85.7	19	3	US-08-870-529-3
3	6	85.7	19	4	US-09-544-794-3
4	5	71.4	15	4	US-09-641-803-34
5	4	57.1	11	4	US-09-149-476-689
6	4	57.1	20	4	US-09-205-258-773
7	3	42.9	4	3	US-08-810-720-12
8	3	42.9	5	1	US-08-014-979-52
9	3	42.9	5	1	US-07-946-421-4
10	3	42.9	5	1	US-08-318-970B-1
11	3	42.9	5	2	US-08-672-345C-70
12	3	42.9	5	2	US-08-774-354B-2
13	3	42.9	5	3	US-09-258-754-278
14	3	42.9	5	3	US-09-042-107-278
15	3	42.9	5	3	US-08-811-463-26
16	3	42.9	5	3	US-08-214-095D-70
17	3	42.9	5	4	US-09-406-532-5
18	3	42.9	5	4	US-08-479-089A-7
19	3	42.9	5	4	US-09-082-358B-31
20	3	42.9	5	4	US-07-669-545B-7
21	3	42.9	5	6	5217869-43
22	3	42.9	5	6	5464756-28
23	3	42.9	6	1	US-08-253-854-40
24	3	42.9	6	1	US-08-127-499A-22
25	3	42.9	6	1	US-08-482-847-22
26	3	42.9	6	1	US-08-237-716-7
27	3	42.9	6	1	US-08-704-170-89

ALIGNMENTS

```
RESULT 1
US-09-641-803-24
; Sequence 24, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-24

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMHQPP 7
Db 1 SSMHQPP 7

RESULT 2
US-08-870-529-3
; Sequence 3, Application US/08870529
; Patent No. 6080557
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: IL-1/TNF-(-ACTIVATED KINASE (ITAK),
; TITLE OF INVENTION: AND METHODS OF MAKING AND USING THE SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,529
; FILING DATE: 06-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.418
; TELECOMMUNICATION INFORMATION:

US-09-641-803-24

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-870-529-3

Query Match 85.7%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMHQPP 6
Db 12 SSMHQPP 17

RESULT 3
US-09-544-794-3
; Sequence 3, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/09/544,794
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide substrate
US-09-544-794-3

Query Match 85.7%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMHQPP 6
Db 12 SSMHQPP 17

RESULT 4
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match      71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred.No. 0.81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MHQPP 7
Db      1 MHQPP 5

RESULT 5
US-09-149-476-689
; Sequence 689, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060

EARLIER FILING DATE: 1997-10-02
Query Match 57.1%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HOPP 7
DB 1 HOPP 4
RESULT 6
US-09-205-258-773
Sequence 773, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
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EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
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EARLIER APPLICATION NUMBER: 60/048,894
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 773
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-773

Query Match 57.1%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOPP 7
Db 1 HOPP 4

RESULT 7
US-08-810-720-12
Sequence 12, Application US/08810720
Patent No. 6037527
GENERAL INFORMATION:
APPLICANT: Barton, Kenneth A.
APPLICANT: Umbeck, Paul F.
TITLE OF INVENTION: INSECTICIDAL COTTON PLANTS (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nicholas J. Seay
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,720
FILING DATE: 03-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 670513.90163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608/251-9166
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-720-12

Query Match 42.9%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 8
US-08-014-979-52
Sequence 52, Application US/08014979
Patent No. 5510240
GENERAL INFORMATION:
APPLICANT: Lam, Kit S. et al.
TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,979
FILING DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7156-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-014-979-52

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 1 WMH 3

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RESULT 9
US-07-946-421-4
; Sequence 4, Application US/07946421
; Patent No. 555864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettlborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-4
;
; Query Match 42.9%; Score 3; DB 1; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 WMH 4
Db 3 WMH 5

RESULT 10
US-08-318-970B-1
; Sequence 1, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA

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; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR1-1
; OTHER INFORMATION: hypervariable region
US-08-318-970B-1
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; Query Match 42.9%; Score 3; DB 1; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 WMH 4
Db 3 WMH 5

RESULT 11
US-08-672-345C-70
; Sequence 70, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-70

Query Match 42.9%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
|||
Db 3 WMH 5

RESULT 12

US-08-774-354B-2
; Sequence 2, Application US/08774354B
; Patent No. 6063427
; GENERAL INFORMATION:
; APPLICANT: Michiko WATANABE
; TITLE OF INVENTION: METHOD FOR PRODUCING A
; TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; STATE:
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,354B
; FILING DATE: December 27, 1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 653-96F029US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
US-08-774-354B-2

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 3 QPP 5

US-09-258-754-278
; Sequence 278, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1998-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-278

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
|||
Db 2 HQP 4

RESULT 14

US-09-042-107-278
; Sequence 278, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-278

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
|||
Db 2 HQP 4

RESULT 15

US-08-811-463-26
; Sequence 26, Application US/08811463C
; Patent No. 6277375
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.

```
; TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTS0:483
; CURRENT APPLICATION NUMBER: US/08/811,463C
; CURRENT FILING DATE: 1997-03-03
; EARLIER APPLICATION NUMBER: 60/013,563
; EARLIER FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-08-811-463-26

Query Match      42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
Db      2 MHQ 4

RESULT 16
US-09-214-095D-70
; Sequence 70, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-70

Query Match      42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 WMH 4
Db      3 WMH 5

RESULT 17
US-09-406-532-5
; Sequence 5, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Maller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: 15B8 heavy chain CDR 1
US-09-406-532-5

Query Match      42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 WMH 4
Db      3 WMH 5

RESULT 18
US-08-479-089A-7
; Sequence 7, Application US/08479089A
; Patent No. 6383487
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6383487artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,089A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/669,545
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6924
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-479-089A-7

Query Match      42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 WMH 4
Db      3 WMH 5
```

RESULT 19
US-09-082-358B-31
; Sequence 31, Application US/09082358B
; Patent No. 6469153
; GENERAL INFORMATION:
; APPLICANT: Goff, Stephen P.
; APPLICANT: Li, Xingqiang
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
; TITLE OF INVENTION: EIP-1, and EIP-3
; FILE REFERENCE: 0575/54804
; CURRENT APPLICATION NUMBER: US/09/082,358B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 5
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-31

Query Match 42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 OPP 7
|||
Db 2 QPP 4

RESULT 20
US-07-669-545B-7
; Sequence 7, Application US/07669545B
; Patent No. 6521230
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6521230artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,545B
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9005962
; FILING DATE: 16-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6924
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-07-669-545B-7

Query Match 42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
|||
Db 3 WMH 5

RESULT 21
5217869-43
; Patent No. 5217869
; APPLICANT: KAUFAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:43
; LENGTH: 5
5217869-43

Query Match 42.9%; Score 3; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
|||
Db 1 WMH 3

RESULT 22
5464756-28
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:28
; LENGTH: 5
5464756-28

Query Match 42.9%; Score 3; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
|||
Db 2 SWM 4

RESULT 23
US-08-253-854-40
; Sequence 40, Application US/08253854
; Patent No. 5504190
; GENERAL INFORMATION:


```
; APPLICANT: Houghten, Richard A.
; APPLICANT: Cuervo, Julio H.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Appel Jr., Jon R.
; APPLICANT: Blondelle, Silvie
; TITLE OF INVENTION: Synthesis of Equimolar Multiple
; TITLE OF INVENTION: Oligomer Mixtures, Especially Of Oligopeptide Mixtures
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milanow, Ltd.
; STREET: 180 No. 5504190th Stetson Avenue, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: PRL.0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-253-854-40

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
   |||
Db 4 WMH 6

RESULT 24
US-08-127-499A-22
; Sequence 22, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-482-847-22

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-127-499A-22

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPP 7
   |||
Db 2 OPP 4

RESULT 25
US-08-482-847-22
; Sequence 22, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-482-847-22

Query Match 42.9%; Score 3; DB 1; Length 6;
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 2 Qpp 4

RESULT 26
US-08-237-716-7
; Sequence 7, Application US/08237716
; Patent No. 5589384
; GENERAL INFORMATION:
; APPLICANT: LIPSCOMBE, Martin J
; APPLICANT: CHARLES, Ian G
; APPLICANT: FAIRWEATHER, Neil F
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5589384th Glebe Road, 8th Floor
; City: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,716
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,003
; FILING DATE: 11-JUN-1992
; APPLICATION NUMBER: GB 9112553.4
; FILING DATE: 11-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-237-716-7

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 4 Qpp 6

RESULT 27
US-08-704-170-89
; Sequence 89, Application US/08704170
; Patent No. 5707626
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR

; TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 No. 5707626th Figueroa Street, Suite 500
; City: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-704-170-89

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 2 Qpp 4

RESULT 28
US-08-460-269C-7
; Sequence 7, Application US/08460269C
; Patent No. 6197548
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
; ROMANOS, MICHAEL A.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd., Suite 1400
; City: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,269C
; FILING DATE: 02-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067

```
; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-460-269C-7

Query Match 42.9%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 29
US-09-641-803-13
; Sequence 13, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-13

Query Match 42.9%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 3 QPP 5

RESULT 30
PCT-US94-02631-89
; Sequence 89, Application PC/TUS9402631
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-460-269C-7

Query Match 42.9%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 29
US-09-641-803-13
; Sequence 13, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-13

Query Match 42.9%; Score 3; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 31
US-08-169-524-3
; Sequence 3, Application US/08169524
; Patent No. 5496706
; GENERAL INFORMATION:
; APPLICANT: Kuusela, Pentti
; APPLICANT: Hilden, Pekka
; TITLE OF INVENTION: Methods and Materials for the
; TITLE OF INVENTION: Detection of
; TITLE OF INVENTION: Staphylococcus Aureus
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; Zip: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 28113/31832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
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; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-169-524-3

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 Db 1 QPP 3

RESULT 32
 US-08-081-539-113
 ; Sequence 113, Application US/08081539
 ; Patent No. 5501962

; GENERAL INFORMATION:
 ; APPLICANT: Braford-Goldberg, Sarah R.
 ; APPLICANT: Easton, Alan M.
 ; APPLICANT: Klein, Barbara K.
 ; APPLICANT: McKearn, John P.
 ; APPLICANT: Olins, Peter O.
 ; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
 ; TITLE OF INVENTION: Chimeric Hybrid Polypeptides
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
 ; ADDRESSEE: Patent Dept.
 ; STREET: P. O. Box 5110
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60680

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/081,539
 ; FILING DATE: 19930621
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kanady, Mary J.
 ; REGISTRATION NUMBER: 28623
 ; REFERENCE/DOCKET NUMBER: 2724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (708)470-6501
 ; TELEFAX: (708)470-6881

; INFORMATION FOR SEQ ID NO: 113:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-081-539-113

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 Db 1 QPP 3

RESULT 33
 US-08-127-499A-3

; Sequence 3, Application US/08127499A
 ; Patent No. 5510264
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/127,499A
 ; FILING DATE: 28-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 US-08-127-499A-3

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 Db 3 QPP 5

RESULT 34
 US-08-127-499A-7
 ; Sequence 7, Application US/08127499A
 ; Patent No. 5510264
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra

; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/127,499A
 ; FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 51916/102/INBI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-127-499A-7

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 35
 US-08-127-499A-10
 Sequence 10, Application US/08127499A
 Patent No. 5510264
 GENERAL INFORMATION:
 APPLICANT: VAN ALSTYNE, Diane
 APPLICANT: SHARMA, Lawrence Rajendra
 TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
 TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/127,499A
 FILING DATE: 28-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 51916/102/INBI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-127-499A-10

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 36
 US-08-127-499A-25
 Sequence 25, Application US/08127499A
 Patent No. 5510264
 GENERAL INFORMATION:
 APPLICANT: VAN ALSTYNE, Diane
 APPLICANT: SHARMA, Lawrence Rajendra
 TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
 TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/127,499A
 FILING DATE: 28-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 51916/102/INBI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-127-499A-25

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 37
 US-08-466-647-113
 Sequence 113, Application US/08466647
 Patent No. 5543141
 GENERAL INFORMATION:
 APPLICANT: Braford-Goldberg, Sarah R.
 APPLICANT: Easton, Alan M.
 APPLICANT: Klein, Barbara K.
 APPLICANT: McKearn, John P.
 APPLICANT: Olins, Peter O.
 TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
 TITLE OF INVENTION: Chimeric Hybrid Polypeptides
 NUMBER OF SEQUENCES: 121
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
 ADDRESSEE: Patent Dept.
 STREET: P. O. Box 5110
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60680

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,647
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,539
FILING DATE: 21-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-647-113

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 1 QPP 3

RESULT 38
US-08-482-847-3
Sequence 3, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PETIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-3

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 3 QPP 5

RESULT 39
US-08-482-847-7
Sequence 7, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PETIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-7

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 3 QPP 5

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 3 QPP 5

RESULT 40

US-08-482-847-10
 ; Sequence 10, Application US/08482847
 ; Patent No. 5556757
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 ; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,847
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/127,499
 ; FILING DATE: 28-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 51916/104/INBI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; US-08-482-847-10

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7

Db 3 QPP 5

RESULT 41

US-08-482-847-25
 ; Sequence 25, Application US/08482847
 ; Patent No. 5556757
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 ; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,847
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/127,499
 ; FILING DATE: 28-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 51916/104/INBI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-482-847-25

Query Match 42.9%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7

Db 3 QPP 5

RESULT 42

US-08-723-116-4
 ; Sequence 4, Application US/08723116
 ; Patent No. 5837248
 ; GENERAL INFORMATION:
 ; APPLICANT: KIKUCHI, KIKICHI
 ; APPLICANT: SATO, NORIYUKI
 ; APPLICANT: SAHARA, HIROMITSU
 ; APPLICANT: YASOJIMA, TAKAHIRO
 ; APPLICANT: WADA, YOSHIMASA
 ; APPLICANT: SUZUKI, MANABU
 ; APPLICANT: HAMURO, JUNJI
 ; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
 ; TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
 ; TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/723,116
 ; FILING DATE: 30-SEP-1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 253491/1995
 ; FILING DATE: 29-SEP-1995

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 217140/1996
;; FILING DATE: 19-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 10-821-0X
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: HUMAN
US-08-723-116-4

Query Match 42.9%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

RESULT 43
US-08-774-354B-4
; Sequence 4, Application US/08774354B
; Patent No. 6063427
; GENERAL INFORMATION:
; APPLICANT: Michiko WATANABE
; TITLE OF INVENTION: METHOD FOR PRODUCING A
; TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; STATE:
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,354B
; FILING DATE: December 27, 1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 653-96F029US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; IMMEDIATE SOURCE:
;; POSITION IN GENOME:
;; FEATURE:
;; PUBLICATION INFORMATION:
US-08-774-354B-4

Query Match 42.9%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 4 QPP 6

RESULT 44
US-09-103-808-4
; Sequence 4, Application US/09103808
; Patent No. 6368852
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; SAITO, NORIYUKI
; SAHARA, HIROMITSU
; YASOJIMA, TAKAHIRO
; WADA, YOSHIMASA
; SUZUKI, MANABU
; HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTIN
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,808
; FILING DATE: 24-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,116
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE: HUMAN


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; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-103-808-4
Query Match      42.9%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

RESULT 45
US-09-641-803-1
; Sequence 1, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-1

Query Match      42.9%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 46
US-07-872-644-35
; Sequence 35, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SEQUENCE CHARACTERISTICS:

; SEQUENCE CHARACTERISTICS:
; Query Match      42.9%; Score 3; DB 1; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 47
US-08-291-349A-5
; Sequence 5, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Mahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1, 8
OTHER INFORMATION: /note= "FN5 (1892-1899)
OTHER INFORMATION: fibronectin fragment : FN-C/H-V"
US-08-291-349A-5

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 48
US-08-297-494-35
; Sequence 35, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,494
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5580771and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-297-494-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHH 4
Db 4 WHH 6

RESULT 49
US-07-990-296-3
; Sequence 3, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Rucht, Leo T.
; APPLICANT: Allen, Janice B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; TITLE OF INVENTION: with Fibronectin Activity
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,296
FILING DATE: 19921210
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.252-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
FEATURE:
NAME/KEY: Fragment of the 33 kD carboxy
NAME/KEY: terminal heparin-binding fragment of the A
NAME/KEY: chain of fibronectin
LOCATION: Represents isolated fibronectin
LOCATION: Residues 1892-1899 from all plasma isoforms
LOCATION: of fibronectin
US-07-990-296-3

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 50
US-08-297-510-35
; Sequence 35, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-297-510-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 2 WMH 4
|||
Db 4 WMH 6

RESULT 51
US-08-479-532-35
Sequence 35, Application US/08479532
Patent No. 5776752
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,532
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5776752and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-479-532-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 2 WMH 4
|||
Db 4 WMH 6

RESULT 52
US-08-455-526-35
Sequence 35, Application US/08455526
Patent No. 5789553
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,526
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/297,494
FILING DATE: 29-AUG-1994

```
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 578953and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-455-526-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
DB 4 WMH 6

RESULT 54
US-08-723-116-3
; Sequence 3, Application US/08723116
; Patent No. 5837248
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; APPLICANT: SATO, NORIYUKI
; APPLICANT: SAHARA, HIROMITSU
; APPLICANT: YASOJIMA, TAKAHIRO
; APPLICANT: WADA, YOSHIMASA
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,116
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 253491/1995
; FILING DATE: 29-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; US-08-723-116-3

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
DB 4 WMH 6

RESULT 53
US-08-455-525-35
; Sequence 35, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 580098and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
|||
Db 2 SWM 4

RESULT 55
US-08-480-133A-3
; Sequence 3, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey E.
; TITLE OF INVENTION: Method for Treating Inflammatory
; DISEASES Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-133A-3

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 56
US-08-699-965-2
; Sequence 2, Application US/08699965
; Patent No. 5853744
; GENERAL INFORMATION:
; APPLICANT: MOORADIAN, DANIEL L.
; APPLICANT: FIELDS, GREGG B.
; TITLE OF INVENTION: METHOD FOR MODIFYING A SUBSTRATE SURFACE
; TO INCLUDE A BIOMOLECULE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 No. 5853744th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/699,965
; FILING DATE: 20-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00300101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-699-965-2

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 57
US-08-435-149-6
; Sequence 6, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABLA A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0989.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-149-6

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 58
US-09-025-706-10
Sequence 10, Application US/09025706
Patent No. 5958874
GENERAL INFORMATION:
APPLICANT: Clark, Richard A
APPLICANT: Greiling, Doris
APPLICANT: Gailit, James
TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jackie Fleischmann & Mugel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87653.97R263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-025-706-10

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 59
US-08-394-748A-13
Sequence 13, Application US/08394748A
Patent No. 6013628
GENERAL INFORMATION:
APPLICANT: Skubitz, Amy P.N.
APPLICANT: Furcht Leo T.
APPLICANT: Balles, Mark
APPLICANT: Gregerson, Dale S.
APPLICANT: Agarwal, Anita
APPLICANT: Wright, Martha M.
APPLICANT: Murali, Shobana
TITLE OF INVENTION: Method for Treating Conditions of the Eye
TITLE OF INVENTION: Using Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6013628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,748A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600.307US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: FN-C/H-V
US-08-394-748A-13

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 60
US-09-139-491-35
Sequence 35, Application US/09139491
Patent No. 6015677
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry

APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
SEQUENCE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 601567 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-139-491-35

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
DB 4 WMH 6

RESULT 61
US-08-774-354B-5
Sequence 5, Application US/08774354B
Patent No. 6063427
GENERAL INFORMATION:
APPLICANT: Michiko WATANABE
TITLE OF INVENTION: METHOD FOR PRODUCING A
TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington, D.C.
STATE:
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,354B
FILING DATE: December 27, 1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER: 653-96F029US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-08-774-354B-5

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 5 QPP 7

RESULT 62
US-08-916-913A-3
Sequence 3, Application US/08916913A
Patent No. 6121027
GENERAL INFORMATION:
APPLICANT: Clapper, David L.
APPLICANT: Swanson, Melvin J.
APPLICANT: Hu, Sheau-Ping
APPLICANT: Amos, Richard A.
APPLICANT: Everson, Terrence P.
TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOIETIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fredrikson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-97
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,913A
FILING DATE: 15 August 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: No. 6121027e
; FILING DATE: No. 6121027e
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-913A-3

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 63
US-09-025-622-10
; Sequence 10, Application US/09025622
; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaackle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-622-10

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
```

```
Db 2 QPP 4

RESULT 64
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-847-065-11

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 65
US-08-960-054A-6
; Sequence 6, Application US/08960054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-960-054A-6

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 66
US-08-958-993A-6
; Sequence 6, Application US/08958993A
; Patent No. 6264917
; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/993
; CURRENT APPLICATION NUMBER: US/08/958,993A
; CURRENT FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-958-993A-6

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 67
US-08-959-206A-2
; Sequence 2, Application US/08959206A
; Patent No. 6331289
; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/08/959,206A
; CURRENT FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-959-206A-2

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 68

US-09-103-808-3
; Sequence 3, Application US/09103808
; Patent No. 6388852
; GENERAL INFORMATION:

; APPLICANT: KIKUCHI, KOKICHI
; SAITO, NORIYUKI
; SAHARA, HIROMITSU
; YASOJIMA, TAKAHIRO
; WADA, YOSHIMASA
; SUZUKI, MANABU
; HAMURO, JUNJI

; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTID.

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/103,808

; FILING DATE: 24-Jun-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/723,116

; FILING DATE: <Unknown>

; APPLICATION NUMBER: JP 217140/1996

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-821-0X

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:

; ORGANISM: HUMAN

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-103-808-3

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
|||
Db 2 SWM 4

RESULT 69

US-09-101-751A-58

; Sequence 58, Application US/09101751A

; Patent No. 6465253

; GENERAL INFORMATION:

; APPLICANT: WICKHAM, THOMAS J.

; APPLICANT: KOVESDI, IMRE

; APPLICANT: BROUGH, DOUGLAS E.

; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS

; FILE REFERENCE: 85710

; CURRENT APPLICATION NUMBER: US/09/101,751A

; CURRENT FILING DATE: 1999-01-29

; PRIOR APPLICATION NUMBER: WO 96US19150

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 08/700,846

; PRIOR FILING DATE: 1996-08-21

; PRIOR APPLICATION NUMBER: US 08/701,124

; PRIOR FILING DATE: 1996-08-21

; PRIOR APPLICATION NUMBER: US 08/563,368

; PRIOR FILING DATE: 1995-11-28

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 58

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: ()..()

; OTHER INFORMATION: Description of Unknown Organism: Artificial

; OTHER INFORMATION: Sequence

US-09-101-751A-58

Query Match

Best Local Similarity 42.9%; Score 3; DB 4; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7

Db 2 Qpp 4

RESULT 70

US-09-591-564-3

; Sequence 3, Application US/09591564

; Patent No. 6514734

; GENERAL INFORMATION:

; APPLICANT: Clapper, David L.

; Swanson, Melvin J.

; Hu, Sheau-Fing

; Amos, Richard A.

; Everson, Terrence P.

; TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY

; ACTIVE MOIETIES

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fredrikson & Byron, P.A.

; STREET: 900 Second Avenue South

; CITY: Minneapolis

; STATE: Minnesota

; COUNTRY: USA

; ZIP: 55402-3397

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows-97

; SOFTWARE: ASCII files

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/591,564

; FILING DATE: 09-Jun-2000

; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/916,913

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Philip M.

REGISTRATION NUMBER: 31,162

REFERENCE/DOCKET NUMBER: 9896.116.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 347-7088

TELEFAX: (612) 347-7077

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acid residues

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-591-564-3

Query Match

Best Local Similarity 42.9%; Score 3; DB 4; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7

Db 2 Qpp 4

RESULT 71

PCT-US92-03222-35

; Sequence 35, Application PC/TUS9203222

; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.

; APPLICANT: Bentley, Kelley

; APPLICANT: Charbonneau, Harry

; APPLICANT: Sonnenburg, William K.

; TITLE OF INVENTION: DNA Encoding Mammalian

; TITLE OF INVENTION: Phosphodiesterases

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/03222

; FILING DATE: 19920420

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/688,356

; FILING DATE: 04-APR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/30822

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US92-03222-35

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 4 WMH 6

RESULT 72

PCT-US93-11781-3
; Sequence 3, Application PC/TUS9311781
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; APPLICANT: Morrill Hall
; APPLICANT: 100 Church Street, S.E.
; APPLICANT: Minneapolis, Minnesota 55455
; APPLICANT: U.S.A.
; APPLICANT: Represented By The Secretary of Health
and Human Services
; APPLICANT: 200 Independence Avenue S.W.
; APPLICANT: Washington, D.C. 20201
; APPLICANT: United States of America
TITLE OF INVENTION: Polypeptides Useful for Treating
Inflammatory Disorders
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Norwest Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11781
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.283-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11781-3

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 73

PCT-US95-02478-13
; Sequence 13, Application PC/TUS9502478
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for Treating Conditions
Of the Eye Using Polypeptides
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: FN-C/H-V
PCT-US95-02478-13

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 74

US-08-139-054-7
; Sequence 7, Application US/08139054
; Patent No. 5578710
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothea
; APPLICANT: Dony, Carola
; APPLICANT: Rudolph, Rainer
TITLE OF INVENTION: IMPROVED ACTIVATION OF RECOMBINANT
PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
STREET: 1725 K. St. N.W. Suite 1000
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,054
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/837,779
FILING DATE:
APPLICATION NUMBER: DE P 41 05 480.6
FILING DATE: 21-FEB-1991
ATTORNEY/AGENT INFORMATION:

NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: 920053
TELEPHONE: (202)859-2930
TELEFAX: (202)887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-139-054-7

Query Match 42.9%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 7 Qpp 9

RESULT 75

US-08-723-116-2
Sequence 2, Application US/08723116
Patent No. 5837248

GENERAL INFORMATION:

APPLICANT: KIKUCHI, KOKICHI
APPLICANT: SATO, NORIYUKI
APPLICANT: SAHARA, HIROMITSU
APPLICANT: YASOJIMA, TAKAHIRO
APPLICANT: WADA, YOSHIMASA
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI

TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE

TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING

TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,116

FILING DATE: 30-SEP-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 253491/1995

FILING DATE: 29-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 217140/1996

FILING DATE: 19-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-821-0X

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN
US-08-723-116-2

Query Match 42.9%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

Search completed: November 25, 2003, 20:30:00
Job time : 5.65698 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 6.86047 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QLPPTVMFP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database:

PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	40.0	8	2	S10783
2	4	40.0	12	2	PN0663
3	4	40.0	13	2	I84603
4	4	40.0	19	2	PH1352
5	4	40.0	20	2	PC2030
6	3	30.0	8	2	S16324
7	3	30.0	9	2	B38740
8	3	30.0	10	2	PC2171
9	3	30.0	10	2	S18396
10	3	30.0	10	2	C39745
11	3	30.0	11	1	XASNBA
12	3	30.0	11	2	C61497
13	3	30.0	11	2	I33098
14	3	30.0	13	2	A60856
15	3	30.0	13	2	S15755
16	3	30.0	13	2	A40207
17	3	30.0	14	2	PC0152
18	3	30.0	14	2	C33098
19	3	30.0	14	2	PH1566
20	3	30.0	14	2	PH1348
21	3	30.0	14	2	H83778
22	3	30.0	15	2	PQ0545
23	3	30.0	15	2	PQ109
24	3	30.0	15	2	S29366
25	3	30.0	15	2	FA0060
26	3	30.0	15	2	B61457
27	3	30.0	16	2	F44908
28	3	30.0	16	2	A54877
29	3	30.0	16	2	B54877

30	3	30.0	16	2	E58503
31	3	30.0	16	2	S01104
32	3	30.0	17	2	S15754
33	3	30.0	17	2	S32587
34	3	30.0	17	2	S59481
35	3	30.0	17	2	S56612
36	3	30.0	18	2	S04229
37	3	30.0	18	2	PC2280
38	3	30.0	18	2	S39845
39	3	30.0	18	2	B45138
40	3	30.0	18	2	S10452
41	3	30.0	18	2	A54135
42	3	30.0	19	2	S60633
43	3	30.0	19	2	C32735
44	3	30.0	19	2	B32735
45	3	30.0	19	2	B61409
46	3	30.0	19	2	A34467
47	3	30.0	20	2	S21737
48	3	30.0	20	2	S29817
49	3	30.0	20	2	A39328
50	3	30.0	20	2	A37111
51	3	30.0	20	2	A54519
52	3	30.0	20	2	T44453
53	3	30.0	20	2	PH1380
54	3	30.0	20	2	S65605
55	3	30.0	20	2	A61093
56	3	30.0	20	2	F24417
57	3	30.0	20	2	S03954
58	3	30.0	20	4	I53672
59	2	20.0	3	3	I78890
60	2	20.0	4	2	A32039
61	2	20.0	4	2	S53508
62	2	20.0	5	1	HORCHA
63	2	20.0	5	2	JN0860
64	2	20.0	5	2	E42364
65	2	20.0	5	2	F80324
66	2	20.0	5	2	B37988
67	2	20.0	5	2	A60411
68	2	20.0	5	2	G44817
69	2	20.0	5	2	I44817
70	2	20.0	5	2	E44817
71	2	20.0	5	2	C44817
72	2	20.0	5	2	A44817
73	2	20.0	6	2	A61049
74	2	20.0	6	2	A27696
75	2	20.0	6	2	B27696
76	2	20.0	6	2	A19780
77	2	20.0	6	2	I67345
78	2	20.0	6	4	A35039
79	2	20.0	7	2	PH1408
80	2	20.0	7	2	S08606
81	2	20.0	7	2	A61081
82	2	20.0	7	2	B61491
83	2	20.0	7	2	S71299
84	2	20.0	7	2	PC1316
85	2	20.0	7	2	PT0283
86	2	20.0	7	2	B39040
87	2	20.0	7	2	I48105
88	2	20.0	7	2	I48086
89	2	20.0	7	2	S66442
90	2	20.0	7	2	A39690
91	2	20.0	7	2	A58718
92	2	20.0	7	2	S45648
93	2	20.0	8	2	PH1407
94	2	20.0	8	2	A31570
95	2	20.0	8	2	B24749
96	2	20.0	8	2	S43971
97	2	20.0	8	2	PL0184
98	2	20.0	8	2	S21273
99	2	20.0	8	2	B39745
100	2	20.0	8	2	S21288

superoxide dismuta
hypothetical prote
actin 6 - soybean
L-ascorbate peroxi
hydroxyproline-ric
thyroid hormone re
N4-(beta-N-acetylgl
poly(lendopeptidas
2-aminobenzoate-Co
arsenite oxidase I
hypothetical prote
Na+/K+-exchanging
H+-transporting tw
thyroglobulin - pi
genome polypeptide
36K microfibrillar
coumarin 7-monooxy
cytochrome P450 2C
notechis II-5b non
ribulose-bisphosph
tubulin alpha chai
acetyl-CoA synthet
alpha-amylase (EC
dimeric protein (B
glue protein - Cal
interphotoreceptor
acidic fibroblast
somatotropin - syn
tyrosine protein k
tyrosine-melanocyt
starvation-induced
proctolin - Americ
peptidyl-dipeptida
flagellar protein
ribulose-bisphosph
acid proteinase li
proctolin - Atlant
27.5 kda structura
27.5K structural p
27.5K structural p
28K structural p
28K structural pro
halo-toxin - Pseud
contraction-inhibi
contraction-inhibi
transferrin - bovi
MHC H2-K-k cell su
hypothetical colla
Ig heavy chain V r
Ig heavy chain V r
tryptophyllin, bas
seed protein ws-5
ICL2 protein - Par
large granule L3 c
Ig heavy chain CRD
calcaequetrin, fas
dihydrofolate redu
DNA topoisomerase
glutathione S-tran
neural cell adhesi
carnocin U149 - Ca
Na+-transporting A
Ig heavy chain V r
angiotensin-conver
neuropeptide B - b
tumor-associated a
capsid protein VP-
cellulase (EC 3.2.
endoglycosylcerami
lectin - potato (f

ALIGNMENTS

RESULT 1
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
A:Title: Biochem. 191, 47-56, 1990
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||
DB 2 PLPP 5

RESULT 2
PN0663
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0663
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
A:Title: J. Biochem. 114, 634-639, 1993
A:Reference number: PN0662; MUID:94156881; PMID:8113213
A:Accession: PN0663
A:Molecule type: protein
A:Residues: 1-12 <YOS>
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match 40.0%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||
DB 3 PLPP 6

RESULT 3
I84603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I84603
R:Koizumi, O.; Kaneda, T.; Morishita, R.
A:Title: Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A:Reference number: I45884; MUID:87213162; PMID:3579900
A:Accession: I84603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:M26144; NID:9951194; PIDN:AAA74588.1; PID:9951195
C:Genetics:
A:Gene: GDB:DNTT
A:Cross-references: GDB:I19100; OMIM:187410
A:Map position: 10q23-10q24

Query Match 40.0%; Score 4; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
|||
DB 8 QPLP 11

RESULT 4
PHI352
Ig heavy chain DJ region (clone C100-115) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PHI352
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A:Title: Predominance of fetal type DJH joining in young children with B precursor 1;
J. Exp. Med. 176, 1577-1581, 1992
A:Reference number: PHI302; MUID:93094761; PMID:1460419
A:Accession: PHI352
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A:Note: the authors translated the stop codon for residue 2 as X
C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||
DB 8 PPTV 11

RESULT 5
PC2030
tumor-derived adhesion factor - human (fragment)
N:Alternate names: 30K protein
C:Species: Homo sapiens (man)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jan-2000
R:Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.;
Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994
A:Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder:
A:Reference number: PC2030; MUID:94161713; PMID:8117260
A:Accession: PC2030
A:Molecule type: protein
A:Residues: 1-20 <AKA>
A:Experimental source: cell line EJ-1
C:Comment: this protein relates with the aberrant cell adhesion of cancer cells.

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||
DB 16 PLPP 19

RESULT 6
S16324
Hypothetical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C:Accession: S16324
R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A:Title: A novel class of plant proteins containing a homeodomain with a closely lin
A:Reference number: S16323; MUID:91266907; PMID:1675603
A:Accession: S16324
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>

A;Cross-references: EMBL:X58821; NID:gi16327; PIDN:CAA41624.1; PID:g579259

Query Match 30.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 6 LPP 8

RESULT 7

B38740
Ig kappa chain C region (PY20) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: B38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: B38740
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-9 <RUF>

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
|||
Db 5 PTV 7

RESULT 8

PC2171
triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragm

C;Species: Rhizopus niveus
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2171
R;Kohno, M.; Kuginiwa, Y.; Hashimoto, Y.; Morita, Y.
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
A;Title: Purification, characterization, and crystallization of two types of lipase from
A;Reference number: PC2171; MUID:94319059; PMID:7765029
A;Accession: PC2171
A;Molecule type: protein
A;Residues: 1-10 <KOH>
C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
C;Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 5 LPP 7

RESULT 9

S18396
Probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fragm

C;Species: Acetobacter hansenii
C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C;Accession: S18396
R;Levy, H.R.; Cook, C.
Arch. Biochem. Biophys. 291, 161-167, 1991
A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase fr
A;Reference number: S18396; MUID:92027789; PMID:1929428
A;Accession: S18396
A;Molecule type: protein
A;Residues: 1-10 <LEV>

A;Experimental source: ATCC 23769

C;Function:

A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phospha
A;Pathway: pentose phosphate pathway
C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 3 LPP 5

RESULT 10

C39745
sphingomyelinase - Rhodococcus sp. (fragment)

C;Species: Rhodococcus sp.
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: C39745
R;Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidas.
ble using these activator proteins.
A;Reference number: A39745; MUID:91210321; PMID:1850427
A;Accession: C39745
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ITO>

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
|||
Db 3 PLP 5

RESULT 11

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C;Accession: A01254
R;Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A;Reference number: A01254
A;Accession: A01254
A;Molecule type: protein
A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analys
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; v
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 3 LPP 5

RESULT 12

C61497

seed protein ws-18 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: C61497
R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis
A:Reference number: A61491; PMID:89351606; PMID:2765119
A:Accession: C61497
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HR>
C:Keywords: glycoprotein; seed

Query Match 30.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
|||
Db 3 PTV 5

RESULT 13

I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: I33098

R.Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: I33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NC>

Query Match 30.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 2 LPP 4

RESULT 14

A60856
inhibin alpha chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60856
R.Leversha, L.J.; Robertson, D.W.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenhall
J. Endocrinol. 113, 213-221, 1987
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; PMID:87224684; PMID:3585232
A:Accession: A60856
A:Molecule type: protein
A:Residues: 1-13 <LEV>

C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
|||
Db 4 PLP 6

RESULT 15

S15755
actin 7 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C:Accession: S15755

R.Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated region
A:Reference number: S15754; PMID:91346640; PMID:2102831
A:Accession: S15755
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <PEA>

C:Cross-references: EMBL:X17120; NID:G18527; PIDN:CAA34980.1; PID:G18528
C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
|||
Db 8 QPL 10

RESULT 16

A40207
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Dec-1993
C:Accession: A40207
R.Gao, E.N.; Shier, P.; Siu, C.H.

J. Biol. Chem. 267, 9409-9415, 1992
A:Title: Purification and partial characterization of a cell adhesion molecule (gp150) from Dictyostelium discoideum
A:Reference number: A40207; PMID:92250549; PMID:1577768
A:Accession: A40207

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <GAO>
C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6
|||
Db 3 PPT 5

RESULT 17

PQ0152
18K iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)
N:Alternate names: frxB homolog
C:Species: chloroplast Chlamydomonas reinhardtii
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-Sep-1993
C:Accession: PQ0152
R.Wu, M.; Nie, Z.Q.; Yang, J.

Plant Cell, 1, 551-557, 1989
A:Title: The 18-KD protein that binds to the chloroplast DNA replicative origin is a component of the 18-KD protein complex
A:Reference number: PQ0152; PMID:92404720; PMID:2562513
A:Accession: PQ0152

A:Molecule type: protein
A:Residues: 1-14 <WUM>
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
|||
Db 1 MFP 3


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RESULT 18.
C33098
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: C33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: C33098
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-14 <NIC>

Query Match      30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 2 LPP 4

RESULT 19
PH1566
cerebrin 30 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: PH1566
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993
A:Title: Micropurification of two human cerebrospinal fluid proteins by high performance
A:Reference number: PH1566; MUID:93329419; PMID:8336140
A:Accession: PH1566
A:Molecule type: protein
A:Residues: 1-14 <LEO>

Query Match      30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 9 QPL 11

RESULT 20
PH1348
Ig heavy chain DJ region (clone C100-106) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1348
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1348; MUID:93094761; PMID:1460419
A:Accession: PH1348
A:Molecule type: DNA
A:Residues: 1-14 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match      30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 4 PPT 6

RESULT 21
H83778
hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)

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```

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H83778
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H83778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <STO>
A:Cross-references: GB:AP001510; GB:BA000004; NID:gl0173440; PIDN:BA04751.1; GSPDB:C
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1032

```

```

Query Match      30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8
Db 8 TVM 10

```

```

RESULT 22
PQ0545
capsid protein VP19C - human herpesvirus 1 (fragment)
C:Species: human herpesvirus 1
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PQ0545
R:Davidson, M.D.; Rixon, F.J.; Davidson, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herp
A:Reference number: PQ0544; MUID:93019027; PMID:1328483
A:Accession: PQ0545
A:Molecule type: protein
A:Residues: 1-15 <DAV>
A:Experimental source: strain 17
C:Genetics:
A:Gene: UL38
C:Keywords: capsid protein

```

```

Query Match      30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 5 PLP 7

```

```

RESULT 23
B39109
hypothetical 1.5K protein - hepatitis C virus
N:Alternate names: hypothetical protein 2
C:Species: hepatitis C virus
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C:Accession: B39109; JQ1585
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tek
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identific
A:Reference number: A39109; MUID:91156678; PMID:1705704
A:Accession: B39109
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <HAN>
A:Cross-references: GB:M58406
R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A:Title: Cloning and sequencing of the structural region and expression of putative c
A:Reference number: JQ1584; MUID:92300349; PMID:1318944
A:Accession: JQ1585

```

A:Molecule type: genomic RNA
 A:Residues: 1-15 <KUM>
 A:Experimental source: strain U.K.

Query Match 30.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 ||||
 Db 10 PLP 12

RESULT 24

S29386
 C:Species: Desulfovibrio vulgaris
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S29386
 R:Piezik, A.J.; Wolbert, R.B.G.; Portier, G.L.; Verhagen, M.F.J.M.; Hagen, W.R.
 Eur. J. Biochem. 212, 237-245, 1993
 A:Title: Nigerythrin and rubrerythrin from Desulfovibrio vulgaris each contain two monon
 A:Reference number: S29385; PMID:93185629; PMID:8383040
 A:Accession: S29386
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <PIE>

Query Match 30.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
 ||||
 Db 8 PTV 10

RESULT 25

PA0060
 C:Species: Fusarium sporotrichioides (fragment)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C:Accession: PA0060
 R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A:Reference number: PA0051
 A:Accession: PA0060
 A:Molecule type: protein
 A:Residues: 1-15 <CHO>

Query Match 30.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 ||||
 Db 4 PLP 6

RESULT 26

B61457
 C:Species: Tetrahymena pyriformis
 C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
 C:Accession: B61457
 R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
 J. Protozool. 36, 562-567, 1989
 A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purificatio
 A:Reference number: A61457; PMID:90095988; PMID:2689637
 A:Accession: B61457
 A:Molecule type: protein
 A:Residues: 1-15 <BAN>

C:Genetics:

A:Genetic code: SGCS

C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; m

Query Match 30.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 ||||
 Db 2 LPP 4

RESULT 27

F44908
 C:Species: Streptomyces olivaceoviridis (fragment)
 C:Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
 C:Accession: F44908
 R:Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.
 J. Bacteriol. 174, 3450-3454, 1992
 A:Title: Chitinases of Streptomyces olivaceoviridis and significance of processing f
 A:Reference number: A44908; PMID:92276319; PMID:1592803
 A:Accession: F44908
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <ROM>

A:Experimental source: ATCC 11238
 A>Note: sequence extracted from NCBI backbone (NCBI:104594)
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
 ||||
 Db 6 MFP 8

RESULT 28

AS4877
 C:Species: Conus pennaceus
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
 C:Accession: AS4877
 R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Z
 Biochemistry 33, 9523-9529, 1994
 A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine
 A:Reference number: AS4877; PMID:94347719; PMID:8068627
 A:Accession: AS4877
 A:Molecule type: protein
 A:Residues: 1-16 <PAI>

R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.
 submitted to the Brookhaven Protein Data Bank, January 1996
 A:Reference number: A66355; PDB:1PEN
 A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsy:
 C:Superfamily: alpha-conotoxin
 C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic ne
 F16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 ||||
 Db 5 LPP 7

RESULT 29

B54877
 A:Species: Conus pennaceus
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
 C:Accession: B54877
 R:Faizilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk
 Biochemistry 33, 9523-9529, 1994
 A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece
 A:Reference number: A54877; MUID:94347719; PMID:8068627
 A:Accession: B54877
 A:Molecule type: protein
 A:Residues: 1-16 <PAI>
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap
 C:Superfamily: alpha-conotoxin
 C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 F:2-6,3-16/Disulfide bonds: #status experimental
 F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
 |||
 Db 5 LPP 7

RESULT 30

E58503
 A:Species: unidentified bacterium (fragment)
 N:Alternate names: 21.3K bladder and kidney stone protein
 C:Keywords: unidentified bacterium
 C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 05-Mar-1999
 C:Accession: E58503
 R:Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A:Description: The proteins of kidney and gallbladder stones.
 A:Reference number: A58501
 A:Accession: E58503
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <BIN>
 A:Experimental source: human bladder and kidney stones
 C:Function:
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C:Keywords: metalloprotein; oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
 |||
 Db 5 LPP 7

RESULT 31

S01104
 A:Species: Drosophila melanogaster
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jul-2000
 C:Accession: S01104
 R:Evaleth, D.D.; Marsh, J.L.
 Mol. Gen. Genet. 209, 290-298, 1987
 A:Title: Overlapping transcription units in Drosophila: sequence and structure of the C
 A:Reference number: S01102; MUID:86038375; PMID:3478553
 A:Accession: S01104
 A:Molecule type: DNA
 A:Residues: 1-16 <EVE>
 A:Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762
 C:Genetics:

A:Gene: Cs
 A:Cross-references: FlyBase:FBgn0002036

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
 |||
 Db 13 PTV 15

RESULT 32

S15754
 A:Species: Glycine max (soybean)
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
 C:Accession: S15754; S08049
 R:Pearson, L.; Mesgher, R.B.
 Plant Mol. Biol. 14, 513-526, 1990
 A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untransla
 A:Reference number: S15754; MUID:91346640; PMID:2102831
 A:Accession: S15754
 A:Molecule type: DNA
 A:Residues: 1-17 <PEA>
 A:Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526
 C:Superfamily: actin
 C:Keywords: cytoskeleton

Query Match 30.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
 |||
 Db 8 QPL 10

RESULT 33

S32587
 A:Species: Spinacia oleracea (spinach)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
 C:Accession: S32587; S15878
 R:Kubo, A.; Saji, H.; Tanaka, K.; Kondo, N.
 Plant Mol. Biol. 18, 691-701, 1992
 A:Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidop
 A:Reference number: S20866; MUID:92216045; PMID:11558944
 A:Accession: S32587

A:Molecule type: protein
 A:Residues: 1-17 <KUB>
 A:Note: this is a revision to the sequence from reference S15878
 R:Tanaka, K.; Takeuchi, E.; Kubo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.
 Arch. Biochem. Biophys. 286, 371-375, 1991
 A:Title: Two immunologically different isozymes of ascorbate peroxidase from spinach
 A:Reference number: S15878; MUID:91378325; PMID:1897962
 A:Accession: S15878
 A:Molecule type: protein
 A:Residues: 1,3-17 <TAN>
 A:Note: this sequence has been revised in reference S20866
 C:Keywords: chloroplast; oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
 |||
 Db 5 PTV 7

RESULT 34

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
 C:Species: Phaseolus vulgaris (kidney bean)
 C>Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
 C:Accession: S59481
 R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to different
 A:Reference number: S59481; MUID:96011753; PMID:7548825
 A:Accession: S59481
 A:Molecule type: protein
 A:Residues: 1-17 <WOU>
 C:Keywords: glycoprotein; hydroxyproline
 F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 4 LPP 6

RESULT 35
 I55612
 thyroid hormone receptor beta - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I55612
 R:Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.
 J. Clin. Invest. 94, 506-515, 1994
 A:Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th
 A:Reference number: I55612; MUID:94314950; PMID:8040303
 A:Accession: I55612
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-17 <RES>
 A:Cross-references: GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:G633780
 C:Genetics:
 A:Gene: TRbeta

Query Match 30.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 5 LPP 7

RESULT 36
 S04229
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)
 A:Alternate names: glycosylasparaginase
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
 C:Accession: S04229
 R:Tollersrud, O.K.; Aronson Jr., N.N.
 Biochem. J. 260, 101-108, 1989
 A:Title: Purification and characterization of rat liver glycosylasparaginase.
 A:Reference number: S04228; MUID:89374025; PMID:2775174
 A:Accession: S04229
 A:Molecule type: protein
 A:Residues: 1-18 <TOL>
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
 C:Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 |||

Db

3 PLP 5

RESULT 37

PC2280

prolylendopeptidase-inhibiting peptide - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997

C:Accession: PC2280

R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.

Biochem. Biophys. Res. Commun. 202, 809-815, 1994

A:Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.

A:Reference number: PC2280; MUID:94324971; PMID:8048952

A:Accession: PC2280

A:Molecule type: protein

A:Residues: 1-18 <OHM>

A:Experimental source: brain

C:Superfamily: cytoskeletal keratin

Query Match 30.0%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4

|||

Db 4 PLP 6

RESULT 38

S39845

2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)

C:Species: Pseudomonas sp.

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

C:Accession: S39845

R:Altenschmidt, U.; Fuchs, G.

Eur. J. Biochem. 205, 721-727, 1992

A:Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization

from a denitrifying Pseudomonas sp.

A:Reference number: S22402; MUID:92241310; PMID:1315272

A:Accession: S39845

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10, 'X', 12-14, 'X', 16-18 <ALT>

Query Match

30.0%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5

|||

Db 12 LPP 14

Qy . 3 LPP 5
|||
Db 9 LPP 11

RESULT 40

S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C;Species: Aspergillus niger
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C;Accession: S10452
R;van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A;Reference number: S10452
A;Accession: S10452
A;Molecule type: DNA
A;Residues: 1-18 <VAN>
A;Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|||
Db 4 QPL 6

RESULT 41

A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002
C;Accession: A54195
R;Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase
A;Reference number: A54195; MUID:94297020; PMID:8025109
A;Accession: A54195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <ESM>
A;Experimental source: rectal gland
A;Note: sequence extracted from NCBI backbone (NCBIP:149363)
C;Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
|||
Db 9 PPT 11

RESULT 42

S60633
H+-transporting two-sector ATPase [EC 3.6.3.14] protein 8 - brine shrimp mitochondrion
C;Species: mitochondrion Artemia sp. (brine shrimp)
A;Variety: strain La Mata
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
C;Accession: S60633
R;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
J. Mol. Evol. 38, 156-168, 1994
A;Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic populations
A;Reference number: S60624; MUID:94223692; PMID:8165960
A;Accession: S60633
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-19 <PER>
A;Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
A;Experimental source: strain La Mata
A;Note: the source is designated as Artemia parthenogenetica

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Genetics:
A;Gene: ATP8
A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
|||
Db 6 PLP 8

RESULT 43

C32735
thyroglobulin - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
C;Accession: C32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bo
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: C32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat ho
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|||
Db 10 QPL 12

RESULT 44

B32735
thyroglobulin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
C;Accession: B32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bo
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: B32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat ho
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|||
Db 10 QPL 12

RESULT 45

B61409

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genome polypeptide (clone L3/S2) - Skalica virus (fragment)
C:Species: Skalica virus
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Nov-2000
C:Accession: B61409
R:Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Griesikova, M.
J. Gen. Virol. 72, 333-338, 1991
A:Title: The relationship between the flaviviruses Skalica and Langat as revealed by mon
A:Reference number: A61409; MUID:91132129; PMID:1847173
A:Accession: B61409
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: genomic RNA
A:Residues: 1-19 <GUI>
C:Superfamily: yellow fever virus genome polypeptide

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 1 LPP 3

RESULT 46
A34467
36K microfibril-associated protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34467
R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Hayakawa
J. Biol. Chem. 264, 17437-17444, 1989
A:Title: Isolation and characterization of a new 36-kDa microfibril-associated glycoprotein
A:Reference number: A34467; MUID:90008913; PMID:2793866
A:Accession: A34467
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KOB>

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db 16 QPL 18

RESULT 47
S21737
coulmarin 7-monoxygenase (EC 1.14.14.-) cytochrome P450 2A7 - western baboon (fragment)
N:Alternate names: coumarin 7-hydroxylase
C:Species: Papio papio (western baboon)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Mar-1999
C:Accession: S21737
R:Dalet-Beluche, I.; Boulenc, X.; Fabre, G.; Maurel, P.; Bonfils, C.
Eur. J. Biochem. 204, 641-646, 1992
A:Title: Purification of two cytochrome P450 isozymes related to CYP2A and CYP3A gene fa
A:Reference number: S21176; MUID:92174920; PMID:1541278
A:Accession: S21737
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <DAL>
C:Genetics:
A:Gene: CYP2A7
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
Db 1

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Db 16 TVM 18

RESULT 48
S29817
cytochrome P450 2C23 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
C:Accession: S29817
R:Marie, S.; Roussel, F.; Cresteil, T.
Biochim. Biophys. Acta 1172, 124-130, 1993
A:Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
A:Reference number: S29817; MUID:93176794; PMID:7679925
A:Accession: S29817
A:Molecule type: mRNA
A:Residues: 1-20 <MAR>
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; transmembrane protein

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 4 PLP 6

RESULT 49
A39328
notechis II-5b nontoxic venom protein - common tiger snake (fragment)
C:Species: Notechis scutatus (common tiger snake, mainland tiger snake)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
C:Accession: A39328
R:Yang, C.C.; Chang, L.S.; Wu, F.S.
Toxicol. 29, 1337-1344, 1991
A:Title: Venom constituents of Notechis scutatus (Australian tiger snake) f;
A:Reference number: A39328; MUID:92263371; PMID:1814009
A:Accession: A39328
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <VAN>
C:Superfamily: phospholipase A2

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db 17 QPL 19

RESULT 50
A37111
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C>Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 12-Apr-1995
C:Accession: A37111
R:Sato, M.H.; Hisabori, T.; Yoshida, M.
J. Biol. Chem. 265, 13419-13422, 1990
A:Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M L
A:Reference number: A37111; MUID:90337936; PMID:2143183
A:Accession: A37111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <SAT>
C:Superfamily: ribulose-bisphosphate carboxylase small chain
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 LPP 5
Db 18 LPP 20

RESULT 51
A54519
tubulin alpha chain - Leishmania enriettii (fragment)
C:Species: Leishmania enriettii
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 13-Aug-1999
C:Accession: A54519
R:Wirth, D.F.; Slater, C.
Mol. Biochem. Parasitol. 9, 83-92, 1983
A:Title: Isolation and characterization of an alpha-tubulin gene from Leishmania enriettii
A:Reference number: A54519; MUID:84142075; PMID:6321982
A:Accession: A54519
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <WIR>
A:Cross-references: GB:M28001; NID:g159409; PIDN:AAA29273.1; PID:g159410
C:Superfamily: tubulin

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
Db 2 PTV 4

RESULT 52
T44453
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44453
R:Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
J. Bacteriol. 180, 5559-5566, 1998
A:Title: Molecular characterization and regulation of an operon encoding a system for the
A:Reference number: 222777; MUID:99008987; PMID:9791103
A:Accession: T44453
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <NIS>
A:Cross-references: EMBL:AF012537; NID:g2668593; PIDN:AAC71069.1; PID:g2668594
A:Experimental source: strain PAO1

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 11 PLP 13

RESULT 53
PH1380
alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)
C:Species: Bacillus sp.
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999
C:Accession: PH1380
R:Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
Biosci. Biotechnol. Biochem. 56, 1792-1795, 1992
A:Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly
A:Reference number: PH1380; MUID:93113087; PMID:1369074
A:Accession: PH1380
A:Molecule type: protein
A:Residues: 1-20 <KAW>
A:Experimental source: strain NO.195
C:Comment: This enzyme has an optimum pH of 7.0.

C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VMF 9
Db 11 VMF 13

RESULT 54
S65605
dimeric protein (BDP) - barley (fragment)
C:Species: Hordeum vulgare (barley)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: S65605
R:Garcia-Casado, G.; Armentia, A.; Sanchez-Monge, R.; Sanchez, L.M.; Lopez-Otin, C.;
FEBS Lett. 364, 36-40, 1995
A:Title: A major baker's asthma allergen from rye flour is considerably more active t
A:Reference number: S65604; MUID:95269763; PMID:7750539
A:Accession: S65605
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GAR>

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 18 PLP 20

RESULT 55
A61093
glue protein - California mussel (fragments)
A:Alternate names: adhesive polyphenolic protein
C:Species: Mytilus californianus (California mussel)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A61093
R:Waite, J.H.
J. Comp. Physiol. B 156, 491-496, 1986
A:Title: Mussel glue from Mytilus californianus Conrad: a comparative study.
A:Reference number: A61093; MUID:86279063; PMID:3734192
A:Accession: A61093
A:Molecule type: protein
A:Residues: 1-20 <WAI>
A:Note: the amino terminal residue was tentatively identified as Ser
A:Note: 12-Ser was also found
C:Comment: This glue protein is a component of the adhesive plaque of the byssus, the

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 4 PPT 6

RESULT 56
F24417
F:4,14/Modified site: 3-hydroxyproline (Pro) #status experimental
F:5,9,15,19/Modified site: 4-hydroxyproline (Pro) #status experimental
F:7,17/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
F:13/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental

interphotoreceptor retinoid-binding protein - bush baby (fragment)
 N:Alternate names: interstitial retinol-binding protein
 C:Species: Galago sp. (bush baby)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 18-Jun-1993
 C:Accession: F24417
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A:Reference number: A91365; MUID:86301171; PMID:3743780
 A:Accession: F24417
 A:Molecule type: protein
 A:Residues: 1-20 <FON>

Query Match 30.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
 |||
 Db 5 QPL 7

RESULT 57

S03954
 acidic fibroblast growth factor - pig (fragment)
 N:Alternate names: alpha-endothelial cell growth factor
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
 C:Accession: S03954
 R:Quinkler, W.; Masberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape
 Eur. J. Biochem. 181, 67-73, 1989

A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
 A:Reference number: S03953; MUID:89231704; PMID:2714282
 A:Accession: S03954

A:Molecule type: protein
 A:Residues: 1-20 <QUI>
 C:Keywords: growth factor

Query Match 30.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 3 LPP 5

RESULT 58

I53672
 somatotropin - synthetic
 C:Species: synthetic
 C:Date: 07-Jun-1996 #sequence_revision 31-Jul-1997 #text_change 19-May-2000
 C:Accession: I53672
 R:Bogosian, G.; Bilyeu, K.; O'Neil, J.P.
 Gene 133, 17-22, 1993

A:Title: Genome rearrangements by residual IS10 elements in strains of Escherichia coli
 A:Reference number: I53672; MUID:94040791; PMID:8224890

A:Accession: I53672
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-20 <BOG>

A:Cross-references: GB:S67119; NID:g455674; PIDN:AB28847.1; PID:g455675
 A>Note: partial sequence of bovine somatotropin synthesized and expressed in Escherichia

Query Match 30.0%; Score 3; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
 |||
 Db 1 MFP 3

RESULT 59

I78890
 tyrosine protein kinase - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: I78890
 R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak,
 Oncogene 9, 3437-3448, 1994
 A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine pr
 A:Reference number: I58407; MUID:95060800; PMID:7970703

A:Accession: I78890
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3 <RES>

A:Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
 C:Genetics:
 A:Gene: p52ntk

Query Match 20.0%; Score 2; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 |||
 Db 2 PT 3

RESULT 60

A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989

A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fac
 A:Reference number: A32039; MUID:89123285; PMID:2563371
 A:Accession: A32039

A:Molecule type: protein
 A:Residues: 1-4 <HOR>
 A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
 |||
 Db 2 PL 3

RESULT 61

S53508
 starvation-induced ribonuclease - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53508
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995

A:Title: cDNA structure and regulatory properties of a family of starvation-induced
 A:Reference number: S53506; MUID:95201242; PMID:7894013

A:Accession: S53508
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <ROE>

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PT 6
||
Db 2 PT 3

RESULT 62

HOROHA

proctolin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C;Accession: A01644
R;Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects
A;Reference number: A93048; MUID:76074708; PMID:576
A;Accession: A01644
A;Molecule type: protein
A;Residues: 1-5 <STA>
A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological properties as the natural peptide.
Science 213, 567-569, 1981
A;Title: Pentapeptide (proctolin) associated with an identified neuron.
A;Reference number: A94260; MUID:81225865; PMID:6113690
A;Contents: annotation; biological source
A;Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles.
A;Superfamily: proctolin
C;Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
||
Db 3 LP 4

RESULT 63

JN0860

peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0860
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from the striped bonito.
A;Reference number: JN0859; MUID:94080036; PMID:7764272
A;Accession: JN0860
A;Molecule type: protein
A;Residues: 1-5 <MAT>
A;Experimental source: intestine
A;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide.
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
||
Db 2 LP 3

RESULT 64

E42364

flagellar protein flir - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991

A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and flagellar assembly
A;Reference number: A42364; MUID:91258342; PMID:1646201
A;Accession: E42364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <VOG>
A;Cross-references: GB:M62408

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
||
Db 4 LP 5

RESULT 65

PS0324

ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
R;Tsugita, A.
submitted to JIPID, April 1993

A;Reference number: PS0206
A;Accession: PS0324
A;Molecule type: protein
A;Residues: 1-5 <TSU>
A;Experimental source: leaf, chlorophyll

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PT 6
||
Db 4 PT 5

RESULT 66

B37988

acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C;Species: Physarum polycephalum
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C;Accession: B37988
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J.
J. Biol. Chem. 265, 19898-19903, 1990
A;Title: Purification and characterization of a novel intracellular acid proteinase from the slime mold Physarum polycephalum.
A;Reference number: A37988; MUID:91060608; PMID:2246266
A;Accession: B37988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MUR>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
||
Db 3 PP 4

RESULT 67

A60411

proctolin - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60411
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, J.
Peptides 11, 205-211, 1990
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab.

A:Reference number: A60411; MUID:90287800; PMID:2356151
A:Accession: A60411
A:Molecule type: protein
A:Residues: 1-5 <ARE>
C:Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse
C:Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
||
Db 3 LP 4

RESULT 68
G44817
27.5 kda structural protein - Leuconostoc oenos phase P32 (fragment)
C:Species: Leuconostoc oenos phase P32
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: G44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: G44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 69
I44817
27.5K structural protein - Leuconostoc oenos phase P37 (fragment)
C:Species: Leuconostoc oenos phase P37
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: I44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: I44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 70
E44817
27.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C:Species: Leuconostoc oenos phase P54
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: E44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.

A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: E44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 71
C44817
28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)
C:Species: Leuconostoc oenos phase PAT5-12
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: C44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: C44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 72
A44817
28K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)
C:Species: Leuconostoc oenos phase PZt11-15
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: A44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: A44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 73
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A:Note: host mulberry tree
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C:Accession: A61049
R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, Chem. Lett. 00, 679-680, 1989
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas :

A;Reference number: A61049
A;Accession: A61049
A;Molecule type: protein
A;Residues: 1-6 <KAJ>
A;Note: sequence confirmed by synthesis
C;Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C;Keywords: toxin

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 FP 10
||
Db 2 FP 3

RESULT 74

A27696
contraction-inhibiting peptide I - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995
C;Accession: A27696
E;Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A;Title: Structures and actions of Mytilus inhibitory peptides.
A;Reference number: A90142; MUID:88240357; PMID:337776
A;Accession: A27696
A;Molecule type: protein
A;Residues: 1-6 <HIR>
C;Keywords: amidated carboxyl end
F;6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MF 9
||
Db 4 MF 5

RESULT 75

B27696
contraction-inhibiting peptide II - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995
C;Accession: B27696
E;Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A;Title: Structures and actions of Mytilus inhibitory peptides.
A;Reference number: A90142; MUID:88240357; PMID:337776
A;Accession: B27696
A;Molecule type: protein
A;Residues: 1-6 <HIR>
C;Keywords: amidated carboxyl end
F;6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MF 9
||
Db 4 MF 5

Search completed: November 25, 2003, 19:36:10
Job time : 7.86047 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 3.54651 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPUPPTVMFP 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	8	1	CPD1_ENTPA
2	3	30.0	9	1	RT33_BOVIN
3	3	30.0	11	1	BPP3_AKGHA
4	3	30.0	11	1	TIN4_HOPTI
5	3	30.0	12	1	TIN2_HOPTI
6	3	30.0	12	1	TIN3_HOPTI
7	3	30.0	13	1	ACT7_SOYBN
8	3	30.0	14	1	ECDC_LYMDI
9	3	30.0	16	1	CXAA_CONPE
10	3	30.0	16	1	CXAB_CONPE
11	3	30.0	17	1	ACT6_SOYBN
12	3	30.0	18	1	UC21_MAIZE
13	3	30.0	20	1	BULB_NAPES
14	3	30.0	20	1	CPA7_PAPSP
15	2	20.0	5	1	E104_LITRU
16	2	20.0	5	1	PAP2_PARMA
17	2	20.0	5	1	PRCT_PERAM
18	2	20.0	6	1	CP1_MYTED
19	2	20.0	6	1	CP2_MYTED
20	2	20.0	6	1	TMOF_SARBU
21	2	20.0	6	1	TRPI_PSEPU
22	2	20.0	6	1	VF19_HSVIK
23	2	20.0	7	1	LANC_CARUI
24	2	20.0	7	1	TPFY_PACDA
25	2	20.0	7	1	MNFI_LEPDE
26	2	20.0	7	1	UF04_MOUSE
27	2	20.0	7	1	UN06_PINPS
28	2	20.0	8	1	ACI_THUAL
29	2	20.0	8	1	ALL5_CALVO
30	2	20.0	8	1	ALL6_CYPDPO
31	2	20.0	8	1	COW2_CONPU
32	2	20.0	8	1	NPB_BOVIN
33	2	20.0	8	1	PPK2_PERAM

34	2	20.0	9	1	AL10_CARMA
35	2	20.0	9	1	COXE_THUOB
36	2	20.0	9	1	FAR3_PENMO
37	2	20.0	9	1	FAR4_PENMO
38	2	20.0	9	1	FAR5_ASCSU
39	2	20.0	9	1	FAR9_ASCSU
40	2	20.0	9	1	FLA2_TREHY
41	2	20.0	9	1	FRF1_SARBU
42	2	20.0	9	1	KNL3_BONVA
43	2	20.0	9	1	LMT3_LOCMI
44	2	20.0	9	1	OXYA_SQUAC
45	2	20.0	9	1	OXYT_EISFO
46	2	20.0	9	1	OXYT_RABIT
47	2	20.0	9	1	SAMP_MUSCA
48	2	20.0	9	1	TKC1_CALVO
49	2	20.0	9	1	UPA3_HUMAN
50	2	20.0	9	1	YBFR_AZOVI
51	2	20.0	10	1	AH3_PRUSE
52	2	20.0	10	1	AL15_CARMA
53	2	20.0	10	1	BPP2_BOTIN
54	2	20.0	10	1	BPP2_BOTJA
55	2	20.0	10	1	BPP2_BOTIN
56	2	20.0	10	1	BPP_VIPAS
57	2	20.0	10	1	BRK_ONCMY
58	2	20.0	10	1	CATB_SHEEP
59	2	20.0	10	1	COXM_RAT
60	2	20.0	10	1	COXQ_RABIT
61	2	20.0	10	1	COXQ_SHEEP
62	2	20.0	10	1	FAR6_PANRE
63	2	20.0	10	1	GON1_ALIMI
64	2	20.0	10	1	GON3_ONCKE
65	2	20.0	10	1	GONL_SQUAC
66	2	20.0	10	1	LABA_JATMU
67	2	20.0	10	1	LPK2_LOCMI
68	2	20.0	10	1	NS1_MYCTU
69	2	20.0	10	1	ODP2_BOVIN
70	2	20.0	10	1	PVK_LOCMI
71	2	20.0	10	1	Q20B_COMTE
72	2	20.0	10	1	SLAP_BACTG
73	2	20.0	10	1	TEMK_RANTE
74	2	20.0	10	1	TKL2_LOCMI
75	2	20.0	10	1	TMOF_AEDAE
76	2	20.0	10	1	UHA3_HUMAN
77	2	20.0	10	1	UPA2_HUMAN
78	2	20.0	10	1	UPA5_HUMAN
79	2	20.0	10	1	UPA9_HUMAN
80	2	20.0	10	1	URE3_MORMO
81	2	20.0	11	1	BPP3_BOTIN
82	2	20.0	11	1	BPP4_BOTIN
83	2	20.0	11	1	BPP_AKHP
84	2	20.0	11	1	BRK_MEGFL
85	2	20.0	11	1	ERF_CLOPA
86	2	20.0	11	1	LADD_ONCMY
87	2	20.0	11	1	LPW_THETH
88	2	20.0	11	1	MLG_THETH
89	2	20.0	11	1	MORN_HUMAN
90	2	20.0	11	1	NXSN_PSETE
91	2	20.0	11	1	POQC_PSEFL
92	2	20.0	11	1	PVK1_PERAM
93	2	20.0	11	1	TKN1_PSEGU
94	2	20.0	11	1	TKN1_UPERU
95	2	20.0	11	1	TKN2_PSEGU
96	2	20.0	11	1	TKN3_PSEGU
97	2	20.0	11	1	TKN4_PSEGU
98	2	20.0	11	1	TKN5_PSEGU
99	2	20.0	11	1	TKN_ELEMO
100	2	20.0	12	1	FAR7_PENMO

ALIGNMENTS

RESULT 1

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CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPD1
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VNF 9
DB 3 VNF 5

RESULT 2
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRP33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc B.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT Identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
DB 5 QPL 7

RESULT 3
BPPB_AKGHA
ID BPPB_AKGHA STANDARD; PRT; 11 AA.

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AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 3 LPP 5

RESULT 4
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 2 PLP 4

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Db          7 PLP 9
RESULT 5
TIN2 HOPTI
ID TIN2 HOPTI STANDARD; PRT; 12 AA.
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
[1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
FT C2627D8EFD37605D CRC64;
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 7 PLP 9

RESULT 6
TIN3 HOPTI
ID TIN3 HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
[1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
FT C2627D8EFD37605D CRC64;
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 7 PLP 9

RESULT 7
TIN7 HOPTI
ID TIN7 HOPTI STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SAC7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Wayne.
RC MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
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EMBL; X17120; CAA34980.1; -.
DR PIR; S15755; S15755.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON TER 13 13
FT C2627D8EFD37605D CRC64;
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C6D4FD05A CRC64;

Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 8 QPL 10

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FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 7 PLP 9

RESULT 7
ACT7 SOYBN
ID ACT7 SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SAC7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Wayne.
RC MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
-----
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or send an email to license@isb-sib.ch).
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EMBL; X17120; CAA34980.1; -.
DR PIR; S15755; S15755.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON TER 13 13
FT C2627D8EFD37605D CRC64;
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C6D4FD05A CRC64;

Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 8 QPL 10

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RESULT 8
ECDC LYMDI          STANDARD;          PRT;          14 AA.
AC P80940;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide C (TR).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantridae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.W., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC -!- OF LARVAE AND PUPAE.
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match          30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 9 PLP 11

RESULT 9
CXAA_CONPE          STANDARD;          PRT;          16 AA.
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1A.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;

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RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
RT antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR, A54877; A54877.
DR PDB; IPEN; 2I-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT MOD_RES 3 16 SULFATION.
FT MOD_RES 15 15 AMIDATION.
FT MOD_RES 16 16
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match          30.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 5 LPP 7

RESULT 10
CXAB_CONPE          STANDARD;          PRT;          16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1B.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin Pn1B:
RT comparison with alpha-conotoxins Pn1A and GI.";

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RL Biochemistry 36:11323-11330(1997).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR: B54877; B54877.
DR PDB: 1AKG; 20-MAY-98.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT 3 16 SULFATION.
FT MOD_RES 15 15
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;
Query Match 30.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No.1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 LPP 5
Db 5 LPP 7
RESULT 11
ACT6_SOYBN STANDARD; PRT; 17 AA.
AC P15986;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 6 (Fragment).
GN SAG6.
OS Glycine max (Soybean).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
CC NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=21028311;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes."; Plant Mol. Biol. 14:513-526(1990).
RL
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC
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DR EMBL: X17119; CAA34979.1; -.
DR PIR: S15754; S15754.
DR InterPro: IPR004001; Actin.
DR InterPro: IPR004000; Actin_like.
DR Pfam: PF00022; actin; 1.
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;
Query Match 30.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPL 3
Db 8 QPL 10
RESULT 12
UC21_MAIZE STANDARD; PRT; 18 AA.
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
DE (Fragment).
OS Zea mays (Maize).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CC NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."; Theor. Appl. Genet. 93:997-1005(1996).
RL
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
CC Maize-2DPAGE; P80627; COLEOPTILE.
DR MaizeDB; 123953; -.
RN [1]
RP NON_TER 18
RP NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;
Query Match 30.0%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No.1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PTV 7
Db 5 PTV 7
RESULT 13
BULB_NARPS STANDARD; PRT; 20 AA.
AC P80554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Bulb protein (Fragment).
OS Narcissus pseudonarcissus (Daffodil).
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
CC Narcissus.


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OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSURE 2 2 OR N.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 13 LPP 15

RESULT 14
CPA7 PAPSP STANDARD; PRT; 20 AA.
AC P80055;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 2A7 (BC 1.14.14.1) (CYP11A7) (P450 FI) (Coumarin 7-
DE hydroxylase) (Fragment).
GN CYP2A7.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92174920; PubMed=1541278;
RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
RT "Purification of two cytochrome P450 isozymes related to CYP2A and
RT CYP3A gene families from monkey (baboon, Papio papio) liver
RT microsomes. Cross reactivity with human forms."
RL Eur. J. Biochem. 204:641-648(1992).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro; IPR001128; Cytochrome P450.
DR PROSITE; PS00086; CYTOCHROME P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT UNSURE 14 14
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2045 MW; 693102A1F0B50C96 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
Db 16 TVM 18

RESULT 15
EI04 LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5 AMIDATION.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
Db 3 TV 4

RESULT 16
PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FP 10
Db 4 FP 5

RESULT 17
PRCT_PERAM

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ID PRCT_PERAM STANDARD; PRT; 5 AA.
 AC P01373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Proctolin.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 6850, 6759;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 in insects.";
 RL Life Sci. 17:1253-1256(1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron.";
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus.";
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=8623789; PubMed=2872861;
 RA Stangler J., Dirksen H., Keller R.;
 RT Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, Carcinus maenas.";
 RL Peptides 7:67-72(1986).
 CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR; A01644; HOROHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LP 4
 DB 3 LP 4
 RESULT 18
 CIP1_MYTED STANDARD; PRT; 6 AA.
 ID CIP1_MYTED
 AC P13736;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide I (MIP I).
 OS Mytilus edulis (Blue mussel).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloida; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP II.
 DR PIR; A27696; A27696.
 KW Hormone; Amidation.
 FT MOD RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 MF 9
 DB 4 MF 5
 RESULT 19
 CIP2_MYTED STANDARD; PRT; 6 AA.
 ID CIP2_MYTED
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloida; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 DR PIR; B27696; B27696.
 KW Hormone; Amidation.
 FT MOD RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 MF 9
 DB 4 MF 5
 RESULT 20
 TMOP_SARBU STANDARD; PRT; 6 AA.
 ID TMOP_SARBU
 AC P41495;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOP).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 de Loof A.;
 RT "Sequencing and characterization of trypsin modulating oostatic
 factor (IMOF) from the ovaries of the grey fleshfly, Neobellieria
 (Sarcophaga) bullata.";
 RL Regul. Pept. 50:61-72(1994).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
 DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PT 6
 DB 2 PT 3
 RESULT 21
 TRPI_PSEPU
 ID TRPI_PSEPU STANDARD; PRT; 6 AA.
 AC F36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TrpBA operon transcriptional activator (Fragment).
 GN TRPI
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRG1 C1S;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
 putida.";
 RL Biochimie 71:521-531(1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
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 CC EMBL; X13299; CAA31660.1; -;
 DR InterPro: IPR000847; HTH LYSR.
 DR PROSITE: PS00044; HTH LYSR_FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 FW DNA-binding.
 FT NON_TER 6

SQ SEQUENCE 6 AA; 693 MW; 77672AA1EDD6F000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LP 4
 DB 5 LP 6
 RESULT 22
 VP19_HSVIK
 ID VP19_HSVIK STANDARD; PRT; 6 AA.
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN UL38.
 OS Herpes simplex virus (type 1 / strain KOS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
 Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
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 or send an email to license@isb-sib.ch).
 CC EMBL; M57646; AAA45830.1; -;
 DR Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PL 3
 DB 5 PL 6
 RESULT 23
 LANC_CARUI
 ID LANC_CARUI STANDARD; PRT; 7 AA.
 AC P36960;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lantibiotic carnocin UI49 (Fragment).
 OS Carnobacterium sp. (strain UI49).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 OC Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE.

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RX MEDLINE=92321768; PubMed=1622206;
RA Nes I.P.;
RT "Purification and characterization of a new bacteriocin isolated from
a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 5 QP 6

RESULT 24
MNPI_LBPDE
ID MNPI_LBPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (Led-MNP-I).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phycophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeulenberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leeuwen F., de Loof A.;
RT "Identification, characterization, and immunological localization of
a novel myotropic neuropeptide in the Colorado potato beetle,
Leptinotarsa decemlineata."
RL Peptides 16:365-374(1995).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
DB 5 PL 6

RESULT 25
TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-1 (PdT-1).
OS Pachymedusa dactyloides (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;

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[1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactyloides tryptophyllin-1 (PdT-1): structural
characterization, pharmacological activity and cloning of precursor
cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3
FT MOD RES 7
FT MOD RES 7
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 26
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC NON TER 7
CC NON TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 27
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC
CC PROTEIN IS: 6.6, ITS MW IS: 25 KDa.
FT NON TER 1 1
FT NON TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
DB 5 LP 6

RESULT 28
ACI_THUAL
ID ACI_THUAL STANDARD; PRT; 8 AA.
AC P18591;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
DE Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
DB 1 PT 2

RESULT 29
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calliostatin 5 (Met-calliostatin 1) ([HYP3]Met-calliostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.

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OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Calliostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-calliostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUOTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION (20%).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 30
ALL6_CVDPO
ID ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P821E7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
DB 1 LP 2

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RESULT 31
COW2_CONPU STANDARD; PRT; 8 AA.
ID COW2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
EA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
Db 5 LP 6

RESULT 32
NPB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QP 2
Db 4 QP 5

RESULT 33
PPK2_PERAM STANDARD; PRT; 8 AA.
ID PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca; PubMed=9210163;
RX MEDLINE=9735392; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=2018984; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 2 PP 3

RESULT 34
AL10_CARMA STANDARD; PRT; 9 AA.
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the

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RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTROSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
FW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 3 QP 4

RESULT 35
COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (SC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984;
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 3 QP 4

RESULT 36
FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLFP3 (AQP5MRLRF-amide).
OS Penaeus monodon (Pencoid shrimp).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaiyuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 2 QP 3

RESULT 37
FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLFP4 (SQP5MRLRF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaiyuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 2 QP 3

RESULT 38
FAR5 ASCSU STANDARD; PRT; 9 AA.
ID NCBI_TaxID=6687;
AC P43170;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF5.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RN SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
AScaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PT 6
Db 4 PT 5

RESULT 39
FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RN SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
AScaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PL 3
Db 6 PL 7

RESULT 40
FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein fliaA2 (35 kDa sheath protein)
(Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RN SEQUENCE.
RX STRAIN=CS;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE
THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND
FLA3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2
FT UNSURE 8 9
FT NON TER 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TV 7
Db 2 TV 3

RESULT 41
FRF1 SARBU STANDARD; PRT; 9 AA.
ID FRF1 SARBU
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RN SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6CSA7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
Db 1 QP 2


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RESULT 42
KML3 BOMVA
ID KML3 BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McLean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 PP 5
DB 2 PP 3

RESULT 43
LMT3 LOCMI
ID LMT3 LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytotropin 3 (LOW-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452 (1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE172C9D776C6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 PP 5
DB 2 PP 3

RESULT 44
OXYA SQUAC
ID OXYA SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspargtocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19 (1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316 (1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PL 3
DB 7 PL 8

RESULT 45
OXYT EISFO
ID OXYT EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Umi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399 (1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO

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CC      . PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC      NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC      NEPHRIDIAL FUNCTION.
CC      -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR      PIR; PC2021; PC2021.
DR      InterPro; IPR000981; Neurhyp_horm.
DR      Pfam; PF00220; hormone4; 1.
DR      PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW      Hormone; Amidation.
FT      DISULFID 1 6
FT      MOD RES 9 9
FT      SEQUENCE 9 AA; 996 MW; D4BEB76EB4542C9 CRC64;

Query Match      20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PT 6
Db      7 PT 8

RESULT 46
OXYT RABIT
ID _OXYT RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus).
OS Balaenoptera physalus (Finback whale), (Common rorqual),
OS Tachygyossus aculeatus aculeatus (Austrian echidna), and
OS Hydrolagus collieri (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9776, 49271, 7873;
RN [1]
RP SPECIES=Rabbit;
RC MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SPECIES=H. amphibius;
RC MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SPECIES=H. amphibius;
RC MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [4]
RP SPECIES=B. physalus;
RC MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [5]
RP SPECIES=H. collieri;
RC MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holocephalian

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RT      elasmobranch fish, Hydrolagus collei.";
RL      J. Endocrinol. 45:597-606(1969).
CC      -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC      UTERUS AND OF THE MAMMARY GLAND.
CC      -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR      PIR; A91466; A91466.
DR      PIR; A92774; A92774.
DR      PIR; A93147; A93147.
DR      PIR; A93408; A93408.
DR      PIR; B90667; B90667.
DR      PDB; 1XY1; 15-OCT-90.
DR      PDB; 1XY2; 15-OCT-90.
DR      InterPro; IPR000981; Neurhyp_horm.
DR      Pfam; PF00220; hormone4; 1.
DR      PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW      Hormone; Hypothalamus; Amidation; 3D-structure.
FT      DISULFID 1 6
FT      MOD RES 9 9
FT      SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match      20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PL 3
Db      7 PL 8

RESULT 47
SAMP MUSCA
ID _SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19095;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SPECIES=
RC MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC      -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC      ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC      IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC      -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR      PIR; B20569; B20569.
DR      InterPro; IPR001759; Pentaxin.
DR      PROSITE; PS00289; PENTAXIN; PARTIAL.
KW      Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT      DOMAIN 1 >9
FT      NON_TER 9 9
FT      SEQUENCE 9 AA; 965 MW; D05B573B3386769 CRC64;

Query Match      20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 FP 10
Db      2 FP 3

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RESULT 48
ID TKCI CALVO STANDARD; PRT; 9 AA.
AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins."
RL Peptides 15:761-768 (1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59DC1B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
DB 2 PT 3

RESULT 49
ID UP3 HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714 (1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
DB 2 PL 3
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RESULT 50
ID YBFR AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=3354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423 (1992).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M83692; AAA22122.1; -
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 51
ID AH3 PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RX TISSUE=Seed;
RX Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase."
RL Plant Physiol. 100:282-290 (1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
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KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PP 5
 ||
 Db 3 PP 4

RESULT 52
 AL19_CARMA STANDARD; PRT; 10 AA.
 AC P81822;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 19.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 EA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation; Multigene family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1101 MW; 96687CDSAB369AB1 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 PT 6
 ||
 Db 2 PT 3

RESULT 53
 BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; B37196; B37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PP 5
 ||
 Db 9 PP 10

RESULT 54
 BPP2_BOTJA STANDARD; PRT; 10 AA.
 AC P01022;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
 DE inhibitor V-6-II).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscac J., Weaver E.R.,
 RA Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 RT jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01255; XAVI68.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PP 5
 ||
 Db 9 PP 10

RESULT 55
 BPP8_BOTIN STANDARD; PRT; 10 AA.
 AC P30426;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]

```

RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 9 PP 10

RESULT 56
BPP VIPAS
ID - BPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
CC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 9 PP 10

RESULT 57
BRK ONCMY
ID - BRK ONCMY STANDARD; PRT; 10 AA.
AC Q9PRL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
Db 8 PL 9

RESULT 58
CATB_SHEEP
ID CATB SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CTSB.
OS Ovis aries (Sheep).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
CC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Moko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin B). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro; IPR000169; SHprot acsite.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; PARTIAL.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

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Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
 ||
 1 LP 2

Db

RESULT 59
 COXM RAT
 ID COXM RAT STANDARD; PRT; 10 AA.
 AC P80431;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 GN COX7B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform."
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 DR PIR; S65387; S65387.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 ||
 7 PT 8

Db

RESULT 60
 COXQ RABIT
 ID COXQ RABIT STANDARD; PRT; 10 AA.
 AC P80336;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 DE (Fragment).
 GN COX8H.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RA Freund R., Kadenbach B.;
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.

CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 ||
 9 PT 10

Db

RESULT 61
 COXQ SHEEP
 ID COXQ SHEEP STANDARD; PRT; 10 AA.
 AC P80337;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 DE (Fragment).
 DE Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RA Freund R., Kadenbach B.;
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 ||
 9 PT 10

Db

RESULT 62
 FAR6 PANRE
 ID FAR6 PANRE STANDARD; PRT; 10 AA.
 AC P82660;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OC NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Hulton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of RMRamide-related
 RT peptides (FarPs) from free-living nematode, Panagrellus redivivus."
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.

CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (PMFAMIDE RELATED PEPTIDE)
 CC FAMILY.

KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1132 MW; CH13EAC9D776C76D CRC64;

AMIDATION.

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
 DB 5 QP 6

RESULT 63

GONL_ALLMI
 ID GONL_ALLMI STANDARD; PRT; 10 AA.
 AC P37041; P20407;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
 DE (luliberin I).
 OS Alligator mississippiensis (American alligator).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=91352338; PubMed=1882082;
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
 Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure of two forms of gonadotropin-releasing hormone
 from brains of the American alligator (Alligator mississippiensis).";
 RL Regul. Pept. 33:105-116(1991).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GnRH family.

CC PIR; A60066; RHAQ1.

DR InterPro; IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
 DB 8 QP 9

RESULT 64

GON3_ONCKE
 ID GON3_ONCKE STANDARD; PRT; 10 AA.
 AC P20367; P81751;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-RH III)
 DE (luliberin III).
 GN GnRH3.

OS Oncorhynchus keta (Chum salmon), and

OS Clupea pallasii (Pacific herring).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018, 30724;

RN [1]

RP SEQUENCE.

RC SPECIES=O. keta;

RX MEDLINE=83195140; PubMed=6341999;

RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;

RT "Characterization of a teleost gonadotropin-releasing hormone.";

RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).

RN [2]

RP SEQUENCE, AND FUNCTION.

RC SPECIES=C. pallasii; TISSUE=Brain, and Pituitary;

RX MEDLINE=20114351; PubMed=10650929;

RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,

RA Chang J.P., Rivier J.E., Sherwood N.M.;

RT "Primary structure and function of three gonadotropin-releasing

hormones, including a novel form, from an ancient teleost, herring.";

RL Endocrinology 141:505-512(2000).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates

the secretion of both luteinizing and follicle-stimulating

hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GnRH family.

DR PIR; A21114; A21114.

DR InterPro; IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
 DB 8 LP 9

RESULT 65

GONL_SQUAC
 ID GONL_SQUAC STANDARD; PRT; 10 AA.
 AC P27429;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin (Gonadotropin-releasing hormone) (GnRH) (LH-RH)
 DE (luliberin).
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=92335300; PubMed=1631133;

RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,

RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;

RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in

dogfish brain provides insight into GnRH evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).

CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GnRH family.

DR PIR; A46030; A46030.

DR InterPro; IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
||
8 LP 9

Db

RESULT 66
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Labaditin.
OS Jatropa multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Jatropa.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropa
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY
SEEMS TO BE BASED ON AN INTERACTION WITH C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR
TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TV 7
||
5 TV 6

Db

RESULT 67
LPK2_LOCMI
ID LPK2_LOCMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=94094539; PubMed=7903606;
RX Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustapyrokinin II from
Locusta migratoria, another member of the FXPRL-amide peptide
family.";
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PT 6
||
4 PT 5

Db

RESULT 68
NS1_MYCTU
ID NS1_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Prasad H.K., Annappurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
the genome of strain H37Rv.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PL 3
||
4 PL 5

Db

RESULT 69
ODP2_BOVIN
ID ODP2_BOVIN STANDARD; PRT; 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
RT "Primary structure around the lipooate-attachment site on the E2
component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall

CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
 CC multiple copies of three enzymatic components: pyruvate
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
 CC lipoamide dehydrogenase (E3).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
 CC acetyldihydrolipoamide.
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
 CC LIPOYL.
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
 CC SYMMETRY.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
 DR INTERPRO: IPR003016; LIPOYL.
 DR PROSITE: PS00189; LIPOYL; PARTIAL.
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
 KW Lipoyl
 FT NON_TER 1 1
 FT BINDING 5 5 LIPOYL.
 FT NON_TER 10 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1066 MW; 889BECDD1ADD33AB1 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 TV 7
 ||
 Db 7 TV 8
 ||
 RESULT 70
 ID PVK LOCM1 STANDARD; PRT; 10 AA.
 AC P83382;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Periviscerokinin (Iom-PVK-1).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 CC NCBI_TaxID=7004;
 [1] SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RP TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=21896327; PubMed=11897380;
 RA Predel R., Gaede G.;
 RT "Identification of the abundant neuropeptide from abdominal
 RT perisymphathetic organs of locusts.";
 RL Peptides 23:621-627(2002).
 CC -!- FUNCTION: Myotropic peptide; increases the frequency of
 CC contraction of the heart and stimulates amplitude and tonus of the
 CC foregut.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
 DR GO: GO:0005576; C:extracellular; IDA.
 DR GO: GO:0005184; P:neuropeptide hormone activity; IDA.
 DR GO: GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 FP 10
 ||
 Db 7 FP 8
 ||

RESULT 71
 Q2OB COMTE STANDARD; PRT; 10 AA.
 ID P80465;
 AC
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Quinolone 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Comamonadaceae; Comamonas.
 CC NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=63;
 RX MEDLINE=96035889; PubMed=7556204;
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
 RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
 RT quinoline and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
 CC 1,2-DIHYDROQUINOLINE.
 CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-
 CC 1(2H)-one + reduced acceptor.
 CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
 CC step.
 CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
 CC TWO GAMMA CHAINS (PROBABLE).
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON_TER 10 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9DC769 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 FP 10
 ||
 Db 3 FP 4
 ||
 RESULT 72
 ID SLAP_BACTG STANDARD; PRT; 10 AA.
 AC P49325;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE S-layer protein (Surface layer protein) (Fragment).
 OS Bacillus thuringiensis (subsp. galleriae).
 CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 CC NCBI_TaxID=29338;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NRRL 4045; PubMed=2592346;
 RX MEDLINE=90078111; PubMed=2592346;
 RA Luckeich M.D., Beveridge T.J.;
 RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
 RL J. Bacteriol. 171:6656-6667(1989).
 CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
 CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
 CC PIR; A60476; A60476.
 KW Cell wall; S-layer.
 FT NON_TER 10 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PP 10
||
5 PP 6

Db

RESULT 73

TEMK_RANTE STANDARD; PRT; 10 AA.

AC P56923;
30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tempoin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 10
10 AMIDATION.
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
||
2 LP 3

Db

RESULT 74

TKL2_LOCM1 STANDARD; PRT; 10 AA.

AC P16224;
01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
10 AMIDATION.
SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PL 3
||
2 PL 3

Db

RESULT 75

TMOF_AEDAE STANDARD; PRT; 10 AA.

AC P19425;
01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (COOH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=835326;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
||
5 PP 6

Db

Search completed: November 25, 2003, 19:28:23
Job time : 3.61794 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 18.7791 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTVWFP 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4	40.0	12	Q8KZ86	Q8KZ86 acinetobact
2	4	40.0	12	Q9BZ49	Q9BZ49 homo sapien
3	4	40.0	13	Q9L8K1	Q9L8K1 enterococcu
4	4	40.0	13	Q14182	Q14182 homo sapien
5	4	40.0	15	Q40562	Q40562 nicotiana t
6	4	40.0	15	Q40563	Q40563 nicotiana t
7	4	40.0	18	Q84129	Q84129 influenzavi
8	4	40.0	19	Q9RBV1	Q9RBV1 pseudomonas
9	4	40.0	20	Q9UCAB	Q9UCAB homo sapien
10	4	40.0	20	Q9S8A8	Q9S8A8 secale cere
11	4	40.0	20	Q9PRN3	Q9PRN3 petromyzon
12	3	30.0	9	Q9P3157	P83157 anabaena sp
13	3	30.0	9	Q9TWV0	Q9TWV0 anthopleura
14	3	30.0	9	Q9S8J8	Q9S8J8 oryza sativ
15	3	30.0	9	Q935G1	Q935G1 salmonella
16	3	30.0	10	Q9R5T2	Q9R5T2 acetobacter

17	3	30.0	10	4	Q14096	Q14096 homo sapien
18	3	30.0	10	11	Q9QVF7	Q9QVF7 rattus sp.
19	3	30.0	10	11	Q8VHM9	Q8VHM9 mus musculus
20	3	30.0	10	12	Q8JV78	Q8JV78 poliovaviru
21	3	30.0	10	13	Q90ZV8	Q90ZV8 psittacus e
22	3	30.0	11	4	Q60761	Q60761 homo sapien
23	3	30.0	11	4	Q9UCR1	Q9UCR1 homo sapien
24	3	30.0	11	6	Q9GL48	Q9GL48 sus scrofa
25	3	30.0	11	10	Q9S8Z9	Q9S8Z9 psophocarpu
26	3	30.0	12	4	Q9P116	Q9P116 homo sapien
27	3	30.0	12	4	Q9NTQ2	Q9NTQ2 homo sapien
28	3	30.0	12	6	Q9TRU1	Q9TRU1 bos taurus
29	3	30.0	12	10	P82329	P82329 pisum sativ
30	3	30.0	13	4	Q14890	Q14890 homo sapien
31	3	30.0	13	4	Q9UNV6	Q9UNV6 homo sapien
32	3	30.0	13	6	Q9TRW6	Q9TRW6 bos taurus
33	3	30.0	13	10	Q42373	Q42373 solarium tub
34	3	30.0	13	11	O88176	O88176 mus musculus
35	3	30.0	14	8	Q9T2K7	Q9T2K7 chlamydomon
36	3	30.0	14	10	P82326	P82326 pisum sativ
37	3	30.0	14	11	O70599	O70599 rattus norv
38	3	30.0	14	16	Q9KE26	Q9KE26 bacillus ha
39	3	30.0	15	2	Q9R5D5	Q9R5D5 chromatium
40	3	30.0	15	6	Q9TR62	Q9TR62 oryctolaqu
41	3	30.0	15	11	Q9QV25	Q9QV25 rattus sp.
42	3	30.0	15	12	Q69353	Q69353 herpes simp
43	3	30.0	16	2	Q9R5K7	Q9R5K7 streptomyce
44	3	30.0	16	4	Q9NNZ2	Q9NNZ2 homo sapien
45	3	30.0	16	5	O18378	O18378 drosophila
46	3	30.0	16	8	P92732	P92732 feijervaya
47	3	30.0	17	2	Q8VME2	Q8VME2 pseudomonas
48	3	30.0	17	2	P97135	P97135 mycobacteri
49	3	30.0	17	4	O15276	O15276 homo sapien
50	3	30.0	17	4	Q96P96	Q96P96 homo sapien
51	3	30.0	17	6	Q9TRU8	Q9TRU8 bos taurus
52	3	30.0	17	10	P83061	P83061 spinacia ol
53	3	30.0	17	12	Q8B4C4	Q8B4C4 hepatitis b
54	3	30.0	18	2	Q9R5U2	Q9R5U2 pseudomonas
55	3	30.0	18	2	Q9R5F9	Q9R5F9 aicalligenes
56	3	30.0	18	2	Q9R4V9	Q9R4V9 campylobact
57	3	30.0	18	2	Q9EYW5	Q9EYW5 erwini ste
58	3	30.0	18	2	Q9R4C6	Q9R4C6 agrobacteri
59	3	30.0	18	4	Q96F98	Q96F98 homo sapien
60	3	30.0	18	4	Q16244	Q16244 homo sapien
61	3	30.0	18	4	Q8NF84	Q8NF84 homo sapien
62	3	30.0	18	10	Q9S915	Q9S915 triticum tu
63	3	30.0	19	2	Q9K4X0	Q9K4X0 planktothri
64	3	30.0	19	4	Q9UC80	Q9UC80 homo sapien
65	3	30.0	19	4	O8NFL2	O8NFL2 homo sapien
66	3	30.0	19	4	Q9UCX6	Q9UCX6 homo sapien
67	3	30.0	19	8	Q91687	Q91687 artemia par
68	3	30.0	19	8	Q9GI97	Q9GI97 sargassum p
69	3	30.0	19	10	Q9S8F5	Q9S8F5 beta vulgar
70	3	30.0	19	12	Q69099	Q69099 herpes simp
71	3	30.0	19	13	Q9PRT0	Q9PRT0 gallus gall
72	3	30.0	19	13	Q9PRN4	Q9PRN4 petromyzon
73	3	30.0	19	15	Q90RF8	Q90RF8 human immun
74	3	30.0	19	15	Q905E8	Q905E8 human immun
75	3	30.0	20	2	Q9R4M9	Q9R4M9 pseudomonas
76	3	30.0	20	2	Q931I1	Q931I1 vibrio harv
77	3	30.0	20	2	O53370	O53370 escherichia
78	3	30.0	20	2	O50180	O50180 pseudomonas
79	3	30.0	20	2	Q46499	Q46499 desulfovibr
80	3	30.0	20	2	Q9R5E8	Q9R5E8 bacillus sp
81	3	30.0	20	4	Q96T45	Q96T45 homo sapien
82	3	30.0	20	4	Q9UCB7	Q9UCB7 homo sapien
83	3	30.0	20	4	O3UBC8	O3UBC8 homo sapien
84	3	30.0	20	5	Q25281	Q25281 leishmania
85	3	30.0	20	7	Q8WLP7	Q8WLP7 macaca mula
86	3	30.0	20	10	Q9S8H1	Q9S8H1 hordeum vul
87	3	30.0	20	11	Q9QW31	Q9QW31 rattus sp.
88	3	30.0	20	11	Q9QVG0	Q9QVG0 rattus sp.
89	2	20.0	5	13	P83308	P83308 gallus gall

90 2 20.0 7 2 P70804
 91 2 20.0 7 2 O50556
 92 2 20.0 7 2 Q54248
 93 2 20.0 7 2 Q34028
 94 2 20.0 7 8 P92214
 95 2 20.0 7 8 P92393
 96 2 20.0 7 8 P92403
 97 2 20.0 7 8 P92427
 98 2 20.0 7 8 P92430
 99 2 20.0 7 8 P92221
 100 2 20.0 7 8 P92425

ALIGNMENTS

RESULT 1
 Q8KZ86 PRELIMINARY; PRT; 12 AA.
 ID Q8KZ86
 AC Q8KZ86;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Class I integrin DNA integrase (Fragment).
 GN INT11.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=204A;
 RA Dolzani L., Gombac F., Lagatolla C., Riccio M.L., Rossolini G.M.,
 RA Tonin E., Monti-Bragadin C.,
 RT "Carriage of class I and II integrons in Italian clinical isolates of
 RT Acinetobacter baumannii";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ313334; CAC85941.1; -.
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db 7 PLPP 10

RESULT 2
 Q9BZ49 PRELIMINARY; PRT; 12 AA.
 ID Q9BZ49
 AC Q9BZ49;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Glycophorin C (Fragment).
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
 RA Zimmerman P.A.;
 RT "The association of the glycophorin C exon 3 deletion with
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
 RT Guinea";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF342984; AAK01459.1; -.
 FT NON TER 1
 FT NON TER 12

SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;
 Query Match 40.0%; Score 4; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db 7 PLPP 10

RESULT 3
 Q9L8K1 PRELIMINARY; PRT; 13 AA.
 ID Q9L8K1
 AC Q9L8K1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Vans (Fragment).
 GN VANSB.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BM4281;
 RX MEDLINE=20307504; PubMed=10846225;
 RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
 RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
 RT resistant enterococci and characterization of two novel insertion
 RT sequences.";
 RL Microbiology 146:1469-1479(2000).
 DR EMBL; AF201896; AAF73374.1; -.
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1502 MW; 8D0E282189F9672A CRC64;

Query Match 40.0%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
 Db 7 LPPT 10

RESULT 4
 Q14182 PRELIMINARY; PRT; 13 AA.
 ID Q14182
 AC Q14182;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Deoxynucleotidyltransferase (Fragment).
 GN DNTT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87213162; PubMed=3579900;
 RA Koilwal O., Kaneda T., Morishita R.;
 RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
 RT expressed in mammalian cells";
 RL Biochem. Biophys. Res. Commun. 144:185-190(1987).
 DR EMBL; M26144; AAA74588.1; -.
 KW Transferase.
 FT NON TER 13
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 40.0%; Score 4; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 QPLP 4
Db      ||||
        8 QPLP 11

RESULT 5
Q40562      PRELIMINARY;      PRT;      15 AA.
AC Q40562;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Small ras-related protein (fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SRI;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565(1994).
DR EMBL; L16786; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1707 MW; 8AB89F924EA30CAF CRC64;

Query Match      40.0%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      ||||
        3 QPLP 6

RESULT 6
Q40563      PRELIMINARY;      PRT;      15 AA.
AC Q40563;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Small ras-related protein (fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SRI;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565(1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

Query Match      40.0%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;

QY      1 QPLP 4
Db      ||||
        8 QPLP 11

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      ||||
        4 QPLP 7

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
Q84129      PRELIMINARY;      PRT;      18 AA.
ID Q84129;
AC Q84129;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
DE 8), COOH terminus of NS1 (fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates."
RL Virology 128:512-517(1983).
DR EMBL; K00959; AAA43541.1; -.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; I.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;

Query Match      40.0%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      ||||
        12 PLPP 15

RESULT 8
Q9REV1      PRELIMINARY;      PRT;      19 AA.
ID Q9REV1;
AC Q9REV1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Integrase (fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R9; TRANSPOSON=Tn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among
RT phyloplane bacteria in Michigan apple orchards."
RL Appl. Environ. Microbiol. 65:4898-4907(1999).
DR EMBL; AF157798; AAD47998.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2065 MW; 19EF26DDCA6290F0 CRC64;

Query Match      40.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      ||||
        7 PLPP 10

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OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RT Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 20 AA; 2403 MW; AC4DAD67CC69AB0D CRC64;

Query Match 40.0%; Score 4; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
Db 17 QPLP 20

RESULT 12
P83157 PRELIMINARY; PRT; 9 AA.
ID P83157;
AC P83157;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (0CT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Iron; Metal-binding.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 6 PLP 8

RESULT 13
Q9TWV0 PRELIMINARY; PRT; 9 AA.
ID Q9TWV0;
AC Q9TWV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Autho-RPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]

RESULT 9
Q9UCA8 PRELIMINARY; PRT; 20 AA.
ID Q9UCA8;
AC Q9UCA8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Tumor-derived adhesion factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94161713; PubMed=8117260;
RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
RA Yasumitsu H., Umeda M., Miyazaki K.;
RT "Cell adhesion activity of a 30-kDa major secreted protein from human
RT bladder carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 198:1046-1053(1994).
SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0AE8D CRC64;

Query Match 40.0%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 16 PLPP 19

RESULT 10
Q9S8A8 PRELIMINARY; PRT; 20 AA.
ID Q9S8A8;
AC Q9S8A8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (fragment).
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RA Rocher A., Calero M., Soriano F., Mendez E.;
RL "Identification of major rye secalins as coeliac immunoreactive
RT proteins.";
RL Biochim. Biophys. Acta 1295:13-22(1996).
SQ SEQUENCE 20 AA; 2249 MW; 96D3DA4098B5C80 CRC64;

Query Match 40.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
Db 16 QPLP 19

RESULT 11
Q9PRN3 PRELIMINARY; PRT; 20 AA.
ID Q9PRN3;
AC Q9PRN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Melanotropin MSH-B.
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PP SEQUENCE.
RX MEDLINE=93126143; PubMed=1480510;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-Ramide),
an N-terminally protected, biologically active neuropeptide from sea
anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 1 LPP 3

RESULT 14
Q9S8J8 PRELIMINARY; PRT; 9 AA.
AC Q9S8J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORYZATENSIN=BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oxyzatensin: a novel bioactive
peptide with ileum-contracting and immunomodulating activities derived
from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q9S8J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 30.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 6 PLP 8

RESULT 15
Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCMI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
BA Baker S., Basham D., Brooks K.M., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

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RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FCDCT7776D86767 CRC64;

Query Match 30.0%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 1 PLP 3

RESULT 16
Q9R5T2 PRELIMINARY; PRT; 10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 3 LPP 5

RESULT 17
Q14096 PRELIMINARY; PRT; 10 AA.
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P450IIB6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308928;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P450IIB6 gene: use of a
cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1; -.

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SQ SEQUENCE 10 AA; 895 MW; 4181B9D87DC77767 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 3 LPP 5

RESULT 18

Q9QVF7 PRELIMINARY; PRT; 10 AA.

ID Q9QVF7
 AC Q9QVF7
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92135065; PubMed=1777418;
 RA Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
 RA Yasuda T., Koike T.;
 RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
 RT cDNA cloning and inter-species differences of beta 2-GPI in
 RT alternation of anticardiolipin binding."
 RL Int. Immunol. 3:1217-1221(1991).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1100 MW; 945681B767376EAL CRC64;

Query Match 30.0%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 |||
 Db 5 PLP 7

RESULT 19

Q8VHM9 PRELIMINARY; PRT; 10 AA.

ID Q8VHM9
 AC Q8VHM9
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Interferon receptor 2a' (Fragment).
 GN IFNAR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
 RT "The genomic structure and expression patterns of the gene encoding
 RT the second chain of the murine interleukin 10 receptor, IL-10R2."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
 RT "The organization, transcriptional regulation and chromosomal
 RT localization of the locus encoding the gene for the murine type I
 RT interferon receptor, Ifnar2."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF440786; AAL40944.1; -.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 1 LPP 3

RESULT 20

Q8JV78 PRELIMINARY; PRT; 10 AA.

ID Q8JV78
 AC Q8JV78
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USAL;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA."
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF303946; AAM97796.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 7 LPP 9

RESULT 21

Q90ZV8 PRELIMINARY; PRT; 10 AA.

ID Q90ZV8
 AC Q90ZV8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Adenylate kinase (Fragment).
 OS Psittacus erithacus (grey parrot).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.
 OX NCBI_TaxID=57247;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shapiro L.H., Dumbacher J.P.;
 RT "Adenylate kinase intron 5: a new nuclear locus for avian
 RT systematics."
 RL Auk 118:248-255(2001).
 DR EMBL; AF307895; AAK43534.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
|
|
|
Db 3 PPT 5

RESULT 22

O60761 PRELIMINARY; PRT; 11 AA.
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protein (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatsuni S., Morita K., Takeda E.,
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
|
|
|
Db 7 LPP 9

RESULT 23

O9UCR1 PRELIMINARY; PRT; 11 AA.
AC O9UCR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schifmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON TER 11
FT NON TER 11
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|
|
|
Db 3 QPL 5

RESULT 24

O9GL48 PRELIMINARY; PRT; 11 AA.
AC O9GL48;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RA Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,
RA Heslan J.-M., Soullou J.-P., Charreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319662; AAG33870.1; -.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
|
|
|
Db 2 PPT 4

RESULT 25

O9S8Z9 PRELIMINARY; PRT; 11 AA.
AC O9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE M1 peptide (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
[1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABCDD77772D1 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
|
|
|
Db 3 PTV 5

RESULT 26

O9P116 PRELIMINARY; PRT; 12 AA.
AC O9P116;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Apolipoprotein E receptor 2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Korschinek I., Gharehbaghi-Schnell E., Lang I., Binder R.B.;
 RT "Expression of Apolipoprotein E Receptor 2 in atherosclerosis";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; APL29170; AAF66440.1; -.
 KW Lipoprotein; Receptor.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1467 MW; 4E89354104044877 CRC64;

 Query Match 30.0%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 PPT 6
 Db 1 PPT 3

 RESULT 27
 Q9NTQ2 PRELIMINARY; PRT; 12 AA.
 AC Q9NTQ2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE D3402L9.1 (Mu opiate receptor (MOR1)) (Fragment).
 GN D3402L9.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Phillimore B.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; ALI32774; CAB76846.1; -.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1296 MW; 68479422BDAB1DDB CRC64;

 Query Match 30.0%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 PLP 4
 Db 10 PLP 12

 RESULT 28
 Q9TRU1 PRELIMINARY; PRT; 12 AA.
 AC Q9TRU1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 43 kDa CYANAGEN bromide fragment PEAK 7 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92132498; PubMed=1734497;

RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 of bovine kidney";
 RL Scand. J. Immunol. 35:63-69(1992).
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1257 MW; OD5C94FDE9B76AA4 CRC64;

 Query Match 30.0%; Score 3; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PTV 7
 Db 7 PTV 9

 RESULT 29
 P82329 PRELIMINARY; PRT; 12 AA.
 AC P82329;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT11) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 Adamaka I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000).
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.
 KW Chloroplast; Thylakoid membrane.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3DB862 CRC64;

 Query Match 30.0%; Score 3; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 LPP 5
 Db 9 LPP 11

 RESULT 30
 Q14890 PRELIMINARY; PRT; 13 AA.
 AC Q14890;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mucin (Fragment).
 GN MUC5AC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tracheobronchial mucosa;
 RX Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,

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RA Zouitina-Gallieque S., Pigny P., Degand P., Aubert J., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus
RT cysteine-rich domain for lip15 mucin genes.";
RL Biochem. J. 0:0-0(1994).
DR EMBL; Z34280; CAA84034.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 6 LPP 8

RESULT 31
OSUNV6 PRELIMINARY; PRT; 13 AA.
AC Q9UNV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN IMPA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigar M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF085628; AAD22141.1; -.
DR EMBL; AF085627; AAD22141.1; JOINED.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 9 PTV 11

RESULT 32
Q9TRW6 PRELIMINARY; PRT; 13 AA.
AC Q9TRW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide F3 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

RA Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro Kinase (IPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1375 MW; 2C2822494805D1B7 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 6 PTV 8

RESULT 33
Q42373 PRELIMINARY; PRT; 13 AA.
AC Q42373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Patatin class I (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]_TaxID=4113;
RP SEQUENCE FROM N.A.
RX MEDLINE=86226014; PubMed=3371864;
RA Mignery G.A., Pikaard C.S., Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RT potato.";
RL Gene 62:27-44(1988).
DR EMBL; M18882; AAA33830.1; -.
DR EMBL; M18881; AAA33829.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
DB 11 TVM 13

RESULT 34
O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;

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RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RL of a muscle-specific exon in the mouse NCAM gene.";
RT Blochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 3 PLP 5

RESULT 35
Q9T2K7 PRELIMINARY; PRT; 14 AA.
AC Q9T2K7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 18-kDa chloroplast DNA-binding iron-sulfur protein (Fragment).
OS Chlamydomonas reinhardtii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RX MEDLINE=92404720; PubMed=2562513;
RA Wu M., Nie Z.-Q., Yang J.;
RT "The 18-kD protein that binds to the chloroplast DNA replicative
RT origin is an iron-sulfur protein related to a subunit of NADH
RT dehydrogenase.";
RL Plant Cell 1:551-557(1989).
SQ SEQUENCE 14 AA; 1698 MW; 7799E02B12C200CB CRC64;

Query Match 30.0%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
Db 1 MFP 3

RESULT 36
P82326 PRELIMINARY; PRT; 14 AA.
AC P82326;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins.";

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RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 5 LPP 7

RESULT 37
O70599 PRELIMINARY; PRT; 14 AA.
AC O70599;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sauer M.;
RL Thesis (1999); University of Vienna, Inst. of Molecular Biology.
DR EMBL; AJ006455; CAA07030.1; -.
KW Kinase; Transferase.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
Db 7 PTV 9

RESULT 38
Q9KE26 PRELIMINARY; PRT; 14 AA.
AC Q9KE26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BH1032.
GN BH1032.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001510; BAB04751.1; -.
KW Hypothetical protein; Complete proteome.

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SQ SEQUENCE 14 AA; 1697 MW; A9A302145A7AE8A6 CRC64;

Query Match 30.0%; Score 3; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8
Db 8 TVM 10

RESULT 39
Q9RSD5 PRELIMINARY; PRT; 15 AA.
AC Q9RSD5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein
DE (Fragment).
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochrochromatium.
OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE.
RX MEDLINE=93146381; PubMed=1490603;
RT "Isolation and identification of granule-associated proteins relevant
RT for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
RT D."; Microbiol. Lett. 78:227-232(1992).
RL FEMS Microbiol. Lett. 78:227-232(1992).
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCFCF65B88E CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MFP 10
Db 1 MFP 3

RESULT 40
Q9TR62 PRELIMINARY; PRT; 15 AA.
AC Q9TR62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=95329112; PubMed=7605356;
RT Mezdour H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RT Atherosclerosis 113:171-178(1995).
SQ SEQUENCE 15 AA; 1761 MW; DE115BB7351F0ABC CRC64;

Query Match 30.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8
Db 9 TVM 11

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RESULT 41
Q9QV25 PRELIMINARY; PRT; 15 AA.
AC Q9QV25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sigma receptor cyclophilin-like component (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=94322640; PubMed=8046989;
RT Schuster D.I., Ehrlich G.K., Murphy R.B.;
RT "Purification and partial amino acid sequence of a 28 kDa cyclophilin-
RT like component of the rat liver sigma receptor.";
RL Life Sci. 55:151-151(1994).
SQ SEQUENCE 15 AA; 1622 MW; 95E384B4EC8D14D4 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
Db 3 PTV 5

RESULT 42
Q69353 PRELIMINARY; PRT; 15 AA.
AC Q69353;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSV-2 (333) N terminus of 17.8 kDa protein gene (0.642 mu)
DE (Fragment).
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85033906; PubMed=6092683;
RT Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,
RT Wagner E.K.;
RT "Herpes simplex virus types 1 and 2 homology in the region between
RT 0.58 and 0.68 map units.";
RL J. Virol. 52:615-623(1984).
DR EMBL; K03360; AAA45840.1; -.
FT NON TER 15
SQ SEQUENCE 15 AA; 1603 MW; 20B04D60BA4507FE CRC64;

Query Match 30.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 11 QPL 13

RESULT 43
Q9R5K7 PRELIMINARY; PRT; 16 AA.
AC Q9R5K7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 23.4-kDa chitinase (Fragment).
OS Streptomyces olivaceoviridis (Streptomyces corchorusii).

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OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1921;
 RN [1]_SEQUENCE.
 RP SEQUENCE.
 RX MEDLINE=92276319; PubMed=1592803;
 RA Romaguera A., Menge U., Breves R., Diekmann H.;
 RT "Chitinases of Streptomyces olivaceoviridis and significance of
 RT processing for multiplicity.";
 RL J. Bacteriol. 174:3450-3454 (1992).
 FT NON_TER 1
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 2014 MW; 0F732A24DC14CE01 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 MFP 10
 Db |||
 6 MFP 8

RESULT 44
 Q9NNZ2 PRELIMINARY; PRT; 16 AA.
 ID Q9NNZ2
 AC Q9NNZ2
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Integrin alpha-2 subunit (Fragment).
 GN ITGA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98421383; PubMed=9746778;
 RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
 RA Kunitzki T.J.;
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
 RT that are associated with differences in platelet alpha2 beta1
 RT density.";
 RL Blood 92:2382-2388 (1998).
 DR EMBL: AF062039; AAF77577.1; -.
 FT NON_TER 16
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLP 4
 Db |||
 10 PLP 12

RESULT 45
 O18378 PRELIMINARY; PRT; 16 AA.
 ID O18378
 AC O18378;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Hypothetical 1.5 kDa protein in ANON-37CS 5'REGION (ORF3).
 GN ANON-37CC.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88038375; PubMed=3478553;
 RA Eveleth D.D., Marsh J.L.;
 RT "Overlapping transcription units in Drosophila: sequence and structure
 RT of the Cs gene.";
 RL Mol. Gen. Genet. 209:290-298 (1987).
 DR EMBL: X05991; CAA29407.1; -.
 DR Flybase; FBgn0026744; anon-37Cc.
 KW Hypothetical protein.
 SQ SEQUENCE 16 AA; 1543 MW; F6F881ED5A799277 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PTV 7
 Db |||
 13 PTV 15

RESULT 46
 P92732 PRELIMINARY; PRT; 16 AA.
 ID P92732
 AC P92732
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NADH dehydrogenase subunit II (Fragment).
 GN ND2.
 OS Fejervarya limnocharis (Boie's wart frog).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Fejervarya.
 OX NCBI_TaxID=110108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 RT rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104 (1997).
 DR EMBL: U71324; AAB48287.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1860 MW; DD1C1017F8B19DEE CRC64;

Query Match 30.0%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 MFP 10
 Db |||
 5 MFP 7

RESULT 47
 Q8VME2 PRELIMINARY; PRT; 17 AA.
 ID Q8VME2
 AC Q8VME2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE ParC protein (Fragment).
 GN PARC.
 OS Pseudomonas putida.
 OG Plasmid pWWO.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Great A., Lambertson L., Williams P.A., Thomas C.M.;

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RT "Complete nucleotide sequence of lncp-9 plasmid pW0.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344068; CAC86875.1; -.
KW Plasmid.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C365A999 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
DB 14 QPL 16

RESULT 48
P97135
ID P97135 PRELIMINARY; PRT; 17 AA.
AC P97135;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GyxA protein (Fragment).
GN GyxA.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:H37Ra;
RX MEDLINE=95072534; PubMed=7981652;
RA Madhusudan K., Ramesh V., Nagaraja V.;
RT "Molecular cloning of gyrA and gyrB genes of Mycobacterium
tuberculosis: analysis of nucleotide sequence.";
RL Biochem. Mol. Biol. Int. 33:651-660 (1994).
DR EMBL; X78888; CAA55487.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1916 MW; EF0B750A36E365AE CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 6 LPP 8

RESULT 49
O15276
ID O15276 PRELIMINARY; PRT; 17 AA.
AC O15276;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial translation elongation factor EF-Tu (Fragment).
GN TUFM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacobs H.T., Smurthwaite L., Koshy R.;
RT "Human genomic sequences encoding mitochondrial elongation factor EF-
Tu: Evidence for post-endosymbiotic intron insertion.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11797; CAA72493.1; -.
KW Elongation factor.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 14 PLP 16

RESULT 50
Q96P96
ID Q96P96 PRELIMINARY; PRT; 17 AA.
AC Q96P96;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHP2-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401217; AAL02173.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEF CRC64;

Query Match 30.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 14 PLP 16

RESULT 51
Q9TRU8
ID Q9TRU8 PRELIMINARY; PRT; 17 AA.
AC Q9TRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell
DE growth (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92115728; PubMed=1370585;
RA Ferrara N., Winer J., Henzel W.J.;
RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
RT cell growth: identification as leukemia inhibitory factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702 (1992).
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 14 PLP 16

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Db          2 P L P 4

RESULT 52
P83061
ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative FK506-binding protein (FKBP) (peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RA Kieselbach T.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro; IPR001179; FKBP_PPIase.
KW Isomerase; Rotamase; Chloroplast.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1771 MW; E2013F998EFBF908 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 3 LPP 5

RESULT 53
Q8B4C4
ID Q8B4C4 PRELIMINARY; PRT; 17 AA.
AC Q8B4C4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Precore.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Vaishali C., Acharya S.K., Panda S.K.;
RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
RT sequence of HBV from nine patients with seronegative viral
RT hepatitis."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161158; AA012630.1; -.
SQ SEQUENCE 17 AA; 1908 MW; 0B63A9BF82802588 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 15 PTV 17

RESULT 54
Q9RSU2
ID Q9RSU2 PRELIMINARY; PRT; 18 AA.
AC Q9RSU2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 2-amino-benzoate-CoA LIGASE=E3 (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RA MEDLINE=91358327; PubMed=1885526;
RA Altenschmidt U., Oswald B., Fuchs G.;
RT "Purification and characterization of benzoate-coenzyme A ligase and
RT 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT sp."
RL J. Bacteriol. 173:5494-5501 (1991).
FT NON_TER 1
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 2061 MW; C43F879692771EF CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 12 LPP 14

RESULT 55
Q9RSF9
ID Q9RSF9 PRELIMINARY; PRT; 18 AA.
AC Q9RSF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Arsenite oxidase, AOI (Fragment).
OS Alcaligenes faecalis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=511;
RN [1]
RP SEQUENCE.
RA MEDLINE=93054722; PubMed=1331097;
RA Anderson G.L., Williams J., Hille R.;
RT "The purification and characterization of arsenite oxidase from
RT Alcaligenes faecalis, a molybdenum-containing hydroxylase."
RL J. Biol. Chem. 267:23674-23682 (1992).
FT NON_TER 1
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; 4EDDC418B71A4574 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 9 LPP 11

RESULT 56
Q9R4V9
ID Q9R4V9 PRELIMINARY; PRT; 18 AA.
AC Q9R4V9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 10 kDa heat shock- and alkaline PH-induced protein (Fragment).
OS Campylobacter jejuni.

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OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE.
RX MEDLINE=95012609; PubMed=7927682; Ching W.M.;
RA Wu Y.L., Lee L.H., Rollins D.M., Ching W.M.;
RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni;
RT characterization and immunological properties.";
RL Infect. Immun. 62:4256-4260(1994).
SQ SEQUENCE 18 AA; 2056 MW; 954FED7B84DA76C4 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db |||
4 QPL 6

RESULT 57
Q9EYW5 PRELIMINARY; PRT; 18 AA.
AC Q9EYW5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RepB.
GN REPB.
OS Erwinia stewartii.
OG Plasmid pSW800.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=66271;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu C.-Y., Liu S.-T.;
RT "Erwinia stewartii plasmid pSW800 basic replicon, repA and repB
RT genes.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF310258; AAG4776.1; -.
KW Plasmid.
SQ SEQUENCE 18 AA; 1952 MW; C8FD2873F9CAC66C CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db |||
6 QPL 8

RESULT 58
Q9R4C6 PRELIMINARY; PRT; 18 AA.
AC Q9R4C6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protocatechuate 3,4-dioxygenase type I alpha subunit (EC 1.13.11.3)
DE (Fragment).
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE.
RX MEDLINE=96337865; PubMed=8772173;
RA Hammer A., Stolz A., Knackmuss H.;
RT "Purification and characterization of a novel type of protocatechuate
RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.";

RL Arch. Microbiol. 166:92-100(1996).
SQ SEQUENCE 18 AA; 2152 MW; BFC56CABD4376D84 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db |||
2 QPL 4

RESULT 59
Q96F98 PRELIMINARY; PRT; 18 AA.
AC Q96F98;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011455; AAH11455.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2114 MW; 3A6C3E2BF620B9CD CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6
Db |||
9 PPT 11

RESULT 60
Q16244 PRELIMINARY; PRT; 18 AA.
AC Q16244;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE STS protein (Fragment).
GN STS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
RT "Characterization of the deletion breakpoints in a patient with
RT steroid sulfatase deficiency.";
RL Hum. Mutat. 4:76-78(1994).
DR EMBL; S74383; AAD14153.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db |||

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Db      2 PLP 4

RESULT 61
Q8NFB4      PRELIMINARY;      PRT;      18 AA.
ID Q8NFB4
AC Q8NFB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mutant enamelin (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kida M., Ariga T.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamelin gene mutation at exon-intron boundary.";
RL J. Dent. Res. 0:0-0(2002).
DR EMBL; AF530444; AAM97323.1; -.
FT NON_TER 1 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3B8B512 CRC64;

Query Match      30.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPP 5
      |||
Db      2 LPP 4

RESULT 62
Q9S915      PRELIMINARY;      PRT;      18 AA.
ID Q9S915
AC Q9S915;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TETRAMERIC alpha-amylase inhibitor 16 kDa subunit, CM16*
DE (Fragment).
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143804; PubMed=1736890;
RA Sanchez-Monge R., Gomez L., Barber D., Lopez-Otin C., Armentia A.,
RA Salcedo G.;
RT "Wheat and barley allergens associated with baker's asthma.
RT Glycosylated subunits of the alpha-amylase-inhibitor family have
RT enhanced IGE-binding capacity.";
RL Biochem. J. 281:401-405(1992).
FT NON_TER 1 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1988 MW; 681835D1F68C30F8 CRC64;

Query Match      30.0%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLP 4
      |||
Db      16 PLP 18

RESULT 63
Q9K4X0      PRELIMINARY;      PRT;      19 AA.
ID Q9K4X0
AC Q9K4X0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GvPC-28 protein (Fragment).
DE GvPC-28.
GN GvPC-28.
OS Planktothrix agardhii.
OC Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.
OX NCBI_TaxID=54305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CYA 137;
RC MEDLINE=20391846; PubMed=10931905;
RA Beard S.J., Davis P.A., Iglesias-Rodriguez D., Skulberg O.M.,
RA Walsby A.E.;
RT "Gas vesicle genes in Planktothrix spp. from Nordic lakes: strains
RT with weak gas vesicles possess a longer variant of gvpC.";
RL Microbiology 146:2009-2018(2000).
DR EMBL; AJ253133; CAB59522.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 1944 MW; 647F169473797D19 CRC64;

Query Match      30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PTV 7
      |||
Db      2 PTV 4

RESULT 64
Q9UC80      PRELIMINARY;      PRT;      19 AA.
ID Q9UC80
AC Q9UC80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 21.5 kDa stone matrix protein (BC 1.15.1.1) (Superoxide dismutase
DE [Mn/Fe]) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239(1994).
CC -I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -I- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
KW Oxidoreductase.
SQ SEQUENCE 19 AA; 2116 MW; A0D0DAE848EE7894 CRC64;

Query Match      30.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPP 5
      |||
Db      4 LPP 6

RESULT 65
Q8NFL2      PRELIMINARY;      PRT;      19 AA.
ID Q8NFL2

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AC Q8NPL2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Prolyl isomerase (Fragment).
 GN PIN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22095969; PubMed=12101225;
 RA Ryo A., Liou Y.C., Wulf G., Nakamura M., Lee S.W., Lu K.P.;
 RT "PIN1 Is an E2F Target Gene Essential for Neu/Ras-Induced
 RT Transformation of Mammary Epithelial Cells."
 RL Mol. Cell. Biol. 22:5281-5295(2002).
 DR EMBL; AF501321; AAM81970.1; -.
 KW Isomerase.
 FT NON TER 19 19
 SQ SEQUENCE 19 AA; 2235 MW; 1C4FC381C8A0F17F CRC64;
 Query Match 30.0%; Score 3; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LPP 5
 Db |||
 7 LPP 9
 RESULT 66
 Q9UCK6 PRELIMINARY; PRT; 19 AA.
 ID Q9UCK6
 AC Q9UCK6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Aspartylglucosaminidase beta 1 subunit (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE.
 RX MEDLINE=93111925; PubMed=1281977;
 RA Rip J.W., Coulter-Mackie M.B., Rupa C.A., Gordon B.A.;
 RT "Purification and structure of human liver aspartylglucosaminidase."
 RL Biochem. J. 288:1005-1010(1992).
 DR HSP; P20933; 1APV.
 SQ SEQUENCE 19 AA; 2127 MW; BC2F148525610300 CRC64;
 Query Match 30.0%; Score 3; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLP 4
 Db |||
 2 PLP 4
 RESULT 67
 Q31687 PRELIMINARY; PRT; 19 AA.
 ID Q31687
 AC Q31687;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN ATP8.
 OS Artemia parthenogenetica.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;

OC Artemiidae; Artemia.
 OX NCBI_TaxID=6663;
 RN [1]_TaxID=6663;
 RP SEQUENCE FROM N.A.
 RC STRAIN=La Mata;
 RX MEDLINE=94223692; PubMed=8169960;
 RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
 RT "Speciation in the artemia genus: mitochondrial DNA analysis of
 RT bisexual and parthenogenetic brine shrimps."
 RL J. Mol. Evol. 38:156-168(1994).
 DR EMBL; X67263; CAA47685.1; -.
 KW Mitochondrion.
 FT NON TER 1 1
 FT NON TER 19 19
 SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;
 Query Match 30.0%; Score 3; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLP 4
 Db |||
 6 PLP 8
 RESULT 68
 Q9GI97 PRELIMINARY; PRT; 19 AA.
 ID Q9GI97
 AC Q9GI97;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
 DE (Fragment).
 OS RBC.
 GN Sargassum polycystum.
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
 OC Sargassum.
 OX NCBI_TaxID=127578;
 RN [1]_TaxID=127578;
 RP SEQUENCE FROM N.A.
 RC STRAIN=nepl27;
 RA Phillips N.E.;
 RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
 RT (Fucales, Phaeophyceae).";
 RL Thesis (1998), University of Hawaii.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=nepl27;
 RA Phillips N.E., Smith C.M., Morden C.W.;
 RT "Testing the systematics of the genus Sargassum (Fucales,
 RT Phaeophyceae) with the Rubisco operon."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF244344; AAF98113.1; -.
 KW Chloroplast.
 FT NON TER 1 1
 SQ SEQUENCE 19 AA; 2108 MW; A02FD2E6DD68A57 CRC64;
 Query Match 30.0%; Score 3; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPT 6
 Db |||
 4 PPT 6
 RESULT 69
 Q9S8F5 PRELIMINARY; PRT; 19 AA.
 ID Q9S8F5
 AC Q9S8F5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PMP=31 kDa plasma membrane intrinsic protein (Fragment).
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=161934;
[1]
RN SEQUENCE.
RP MEDLINE=95303965; PubMed=7784509;
RA Qi X., Tai C.Y., Wasserman B.P.;
RA "Plasma membrane intrinsic proteins of Beta vulgaris L.";
RL Plant Physiol. 108:387-392(1995).
FT NON TER 1
FT NON TER 19
SQ SEQUENCE 19 AA; 2102 MW; 5BF1773684FF8D84 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 10 QPL 12

RESULT 70
Q69099
ID Q69099 PRELIMINARY; PRT; 19 AA.
AC Q69099;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Protein 32 (Fragment).
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90156509; PubMed=2154597;
RA Yei S., Chowdhury S.I., Bhat B.M., Conley A.J., Wold W.S.,
RA Batterson W.;
RA "Identification and characterization of the Herpes simplex virus type
RT 2 gene encoding the essential capsid protein ICP32/VP19c.";
RL J. Virol. 64:1124-1134(1990).
DR EMBL; M33905; AAA45846.1; -.
FT NON TER 19
FT NON TER 19
SQ SEQUENCE 19 AA; 2058 MW; 47125921CA53FA35 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 5 PLP 7

RESULT 71
Q9PRT0
ID Q9PRT0 PRELIMINARY; PRT; 19 AA.
AC Q9PRT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 23A7 antigen (Fragment).
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN SEQUENCE.
RP MEDLINE=95332492; PubMed=7608337;
RA Denburg J.L., Caldwell R.T., Warner J.M.;
RA "Developmental changes in epitope accessibility as an indicator of
RT multiple states of an immunoglobulin-like neural cell adhesion
RT molecule.";
RL J. Comp. Neurol. 354:533-550(1995).
SQ SEQUENCE 19 AA; 2051 MW; 83B67BEE484EBD03 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 16 PPT 18

RESULT 72
Q9PRN4
ID Q9PRN4 PRELIMINARY; PRT; 19 AA.
AC Q9PRN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
[1]
RN SEQUENCE.
RP MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RA "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 15 PPT 17

RESULT 73
Q9ORF8
ID Q9ORF8 PRELIMINARY; PRT; 19 AA.
AC Q9ORF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=97CG276;
RC Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obergui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Farra J.H.;
RA "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127550; AAK84913.1; -.
FT NON TER 1
FT NON TER 1

```

FT NON TER 19 19
SQ SEQUENCE 19 AA; 2304 MW; 2727D4B66AE69237 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 16 PLP 18

RESULT 74
Q905E8 PRELIMINARY; PRT; 19 AA.

AC Q905E8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=37CG314;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.,
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410452; AAL10274.1; -.
FT NON_TER 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2200 MW; 367B64CAE5069886 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 16 PLP 18

RESULT 75
Q9R4M9 PRELIMINARY; PRT; 20 AA.

AC Q9R4M9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Extracellular levansucrase (EC 2.4.1.10) (Fragment).
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE.
RX MEDLINE=95270602; PubMed=7751294;
RA Hettwer U., Gross M., Rudolph K.;
RT "Purification and characterization of an extracellular levansucrase
RT from Pseudomonas syringae pv. phaseolicola.";
RL J. Bacteriol. 177:2834-2839(1995).
SQ SEQUENCE 20 AA; 2218 MW; 9DCE15F23BEFF2B5 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
|||

Db 8 PTV 10

Search completed: November 25, 2003, 19:34:04
Job time : 19.7791 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 25.5233 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-25
Perfect score: 10
Sequence: 1 QPLPPTVMFP 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0
Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03:*

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- 21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	22	Colostrinin derive
2	10	100.0	10	22	Colostrinin peptid
3	10	100.0	10	22	Colostrinin peptid
4	10	100.0	10	23	Colostrinin consti
5	10	100.0	10	23	Colostrinin consti
6	10	100.0	10	23	Neural cell regula
7	10	100.0	15	22	Colostrinin derive
8	10	100.0	15	22	Colostrinin peptid
9	10	100.0	15	22	Colostrinin peptid

83 4 40.0 7 22 AAB50762 Human cAMP-specific
 84 4 40.0 7 22 AAB50763 Human cAMP-specific
 85 4 40.0 7 23 AAB73219 Src homology3 (SH3)
 86 4 40.0 7 23 AAB73221 Src homology3 (SH3)
 87 4 40.0 7 23 AAB73222 Src homology3 (SH3)
 88 4 40.0 7 23 AAB73225 Src homology3 (SH3)
 89 4 40.0 7 23 AAB73226 Src homology3 (SH3)
 90 4 40.0 7 23 AAB73345 Exemplary pharmaco
 91 4 40.0 7 23 AAU80708 Javelin peptide #1
 92 4 40.0 8 16 AAR71945 Human 3BPI peptide
 93 4 40.0 8 19 AAWS7875 C. felis esterase
 94 4 40.0 8 20 AAY16845 Heat shock protein
 95 4 40.0 8 22 AAE12921 Ctenocephalides fe
 96 4 40.0 8 22 AAB31509 Amino acid sequenc
 97 4 40.0 9 16 AAR7304 Plasmodium falcipa
 98 4 40.0 9 16 AAR77565 HIV-B35-50(C-48),
 99 4 40.0 9 16 AAR84612 HCV-1 derived pept
 100 4 40.0 9 20 AAY10090 T cell epitope/MHC

ALIGNMENTS

RESULT 1
 AAB72270
 ID AAB72270 standard; peptide; 10 AA.
 XX
 AC AAB72270;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 25.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US222818.
 XX
 PR 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGB-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI
 XX WPI; 2001-202804/20.
 DR
 XX
 XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPPTVMFP 10
 DB 1 QPLPPTVMFP 10
 RESULT 2
 AAB72523
 ID AAB72523 standard; Peptide; 10 AA.
 XX
 AC AAB72523;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #24.
 XX
 KW Dermatalogical; oxidative stress regulator; colostrinin.
 XX
 OS Unidentified.
 XX
 PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 XX
 PR 17-AUG-1999; 99US-0149310.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 PS Claim 6; Page 26; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPPTVMFP 10
 DB 1 QPLPPTVMFP 10
 RESULT 3
 AAB72555
 ID AAB72555 standard; Peptide; 10 AA.
 XX
 AC AAB72555;
 XX
 DT 09-MAY-2001 (first entry)
 XX

DE Colostrinin peptide #24.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22774.
XX
PR 17-AUG-1999; 99US-0149633.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
DR WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPPTVMFP 10
DB 1 QPLPPTVMFP 10
RESULT 4
AAE20252
ID AAE20252 standard; peptide; 10 AA.
XX
AC AAE20252;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #24.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 10 /note= "Optionally C-terminal amide"
XX
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
PF 17-AUG-2000; 2000WO-US22776.
XX
PR (TEXA) UNIV TEXAS SYSTEM.
PA

XX Stanton GJ, Hughes TK, Boldogh I;
PI WPI; 2002-269151/31.
XX
DR Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
XX
CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 10; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPPTVMFP 10
DB 1 QPLPPTVMFP 10
RESULT 5
AAM51059
ID AAM51059 standard; Peptide; 10 AA.
XX
AC AAM51059;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide (casein amino acids 164-173).
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 10 /note= "optional C-terminal amidation"
XX
XX
PN WO200213849-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22775.
XX
PR 17-AUG-2000; 2000WO-US22775.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX

DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 164-173. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the
 CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPLPPTVMFP 10
 Db 1 QPLPPTVMFP 10
 RESULT 6
 AAO14601
 ID AAO14601 standard; peptide; 10 AA.
 AC AAO14601;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 24.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10 /note= "Optional C-terminal amide"
 FT
 XX
 FN WO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US22777.
 XX
 PR 17-AUG-2000; 2000WO-US22777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analogue -
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPLPPTVMFP 10
 Db 1 QPLPPTVMFP 10
 RESULT 7
 AAB72279
 ID AAB72279 standard; peptide; 15 AA.
 XX
 AC AAB72279;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 34.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22818.
 XX
 PR 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGS-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 CC Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for

CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPPTVMFP 10
 Db 6 QLPPTVMFP 15

RESULT 8

AAB72531
 ID AAB72531 standard; Peptide; 15 AA.

XX AC AAB72531;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the
 cell with an oxidative stress regulator selected from colostrinin, its
 constituent peptide, analog or their combinations -

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative
 stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPPTVMFP 10
 Db 6 QLPPTVMFP 15

RESULT 9

AAB72563

ID AAB72563 standard; Peptide; 15 AA.

XX AC AAB72563;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 colostrinum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -

XX PS Claim 6; Page 22; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPPTVMFP 10
 Db 6 QLPPTVMFP 15

RESULT 10

AAB59334

ID AAB59334 standard; Peptide; 15 AA.

XX AC AAB59334;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment C-9.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

PA (REG-) REGEN THERAPEUTICS PLC.
 XX Georgiades JA;
 XX WPI; 2001-071058/08.
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 XX Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 10; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPPTVMFP 10
 |||||
 Db 6 QPLPPTVMFP 15
 |||||
 RESULT 11
 AAEE20261
 ID ARE20261 standard; peptide; 15 AA.
 XX
 AC ARE20261;
 XX
 XX 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #32.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Optionally C-terminal amide"
 XX
 XX WO200213850-A1.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I;
 XX
 XX WPI; 2002-269151/31.
 XX
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 26; 51pp; English.

XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 10; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPPTVMFP 10
 |||||
 Db 6 QPLPPTVMFP 15
 |||||
 RESULT 12
 AAAM51066
 ID AAM51066 standard; Peptide; 15 AA.
 XX
 AC AAM51066;
 XX
 XX 30-MAY-2002 (first entry)
 XX
 DE Colostrinin constituent peptide (casein amino acids 159-173).
 XX
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "optional C-terminal amidation"
 XX
 XX WO200213849-A1.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM
 XX
 XX (REG-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 XX WPI; 2002-269150/31.
 XX
 XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX
 XX Claim 1; Page 34; 54pp; English.
 XX
 XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell

CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 8 related to the invention.
 CC Colostrinin peptide 8 corresponds to position 165-175 of beta-caesin.
 XX
 XX

SQ Sequence 11 AA;

Query Match 90.0%; Score 9; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPTVMFP 10
 Db 1 PLPPTVMFP 9
 |||||

RESULT 15

AAE07202
 ID AAE07202 standard; peptide; 12 AA.

XX AC

XX AC AAE07202;

XX 06-NOV-2001 (first entry)

XX DE Modified colostrinin cyclic peptide #8.

XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
 XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 XX KW acquired immunological deficiency; neurological disorder; dementia;
 XX KW antiviral; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Gln found at the C-terminal end"

XX PN WO200155199-A1.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-GB00329.

XX PR 26-JAN-2000; 2000GB-0001825.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX XX Georgiades JA;

XX XX WPI; 2001-488775/53.

XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX

PS Example 2; Page 9; 40pp; English.

XX CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #8 related to
 CC the invention.
 XX
 XX

SQ Sequence 12 AA;

Query Match 90.0%; Score 9; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPTVMFP 10
 Db 2 PLPPTVMFP 10
 |||||

RESULT 16

AAE59333

ID AAE59333 standard; Peptide; 11 AA.

XX AC AAE59333;

XX 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment C-8.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX XX Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX

PS Claim 7; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX

SQ Sequence 11 AA;

Query Match 60.0%; Score 6; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPPT 6
 Db 1 QPLPPT 6

RESULT 17
 AAW25442
 ID AAW25442 standard; peptide; 16 AA.

XX AAW25442;
 XX
 XX
 DT 27-MAR-1998 (first entry)
 XX

DE Grb2 N-terminal SH3 domain binding peptide SEQ ID NO:227.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.
 OS Unidentified.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

PA (UNYC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;

XX WPI; 1997-424572/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 20; Page 101; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX Sequence 16 AA;

Query Match 60.0%; Score 6; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0

Qy 3 LPPTVM 8
 Db 9 LPPTVM 14

RESULT 18
 AAY41630

ID AAY41630 standard; peptide; 7 AA.

XX AAY41630;

XX 02-DEC-1999 (first entry)

XX Mammalian ion channel proline rich motif containing peptide #24.

XX SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
 KW proline rich.

XX Mus sp.

XX US5955259-A.

XX 21-SEP-1999.

XX 19-DEC-1996; 96US-0769745.

XX 19-DEC-1996; 96US-0769745.

XX (UYBR-) UNIV BRANDEIS.

XX Holmes TC, Levitan IB;

XX WPI; 1999-560490/47.

XX Identification of compounds that modulate potassium ion channel binding
 PT with protein tyrosine kinase SH3 domains

PS Disclosure; Column 8; 18pp; English.

XX A method has been developed for determining if a compound modulates the
 CC binding of a potassium ion channel to the SH3 domain of a protein
 CC tyrosine kinase by contacting the channel with a polypeptide comprising
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3
 CC binding. The method is useful for assessing the ability of a compound to
 CC modulate the formation of channel-SH3 domain complexes to improve the
 CC understanding of mechanisms of potassium channel blockage and assess the
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to
 CC AAY41644 represent mammalian ion channel peptides with proline-rich
 CC motifs.

XX Sequence 7 AA;

Query Match 50.0%; Score 5; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5

Db 1 QPLPP 5

RESULT 19
 AAB17247

ID AAB17247 standard; Peptide; 7 AA.

XX AAB17247;

XX 31-OCT-2000 (first entry)

XX SH3 antagonist peptide sequence SEQ ID NO:303.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;

KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX Synthetic.
XX WO200024782-A2.
XX 04-MAY-2000.
XX 25-OCT-1999; 99WO-US25044.
XX 23-OCT-1998; 98US-0105371.
XX 22-OCT-1999; 99US-0428082.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX Claim 39; Page 302; 608pp; English.
XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from - (L1)c-P1, - (L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or - (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAG69443
CC to AAG69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX Sequence 7 AA;
Query Match 50.0%; Score 5; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPPT 6
Db 2 PLPPT 6
RESULT 20
ABR73240
ID ABR73240 standard; Peptide; 7 AA.
XX ABR73240;
XX 05-APR-2002 (first entry)
XX Src homology3 (SH3) antagonist peptide SEQ ID NO:303.
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
XX EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
XX TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNF;
XX TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
XX MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
XX cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
XX antianaemic; anorectic; antiinfertility; haemostatic; dermatological;

KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX Homo sapiens.
XX Synthetic.
XX WO200183525-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14310.
XX 03-MAY-2000; 2000US-0563286.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX WPI; 2002-130313/17.
XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX Claim 39; Page 55; 176pp; English.
XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX Sequence 7 AA;
Query Match 50.0%; Score 5; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPPT 6
Db 2 PLPPT 6
RESULT 21
AAM00293
ID AAM00293 standard; Peptide; 8 AA.
XX AAM00293;
XX 01-OCT-2001 (first entry)
XX Human protein fragment SEQ ID NO: 837.
XX

KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX Homo sapiens.

XX WO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.

XX N-PSDB; AAH89406.

XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX

PS Disclosure; Page 344; 475pp; English.

XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.

XX Query Match 50.0%; Score 5; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
DB 1 QPLPP 5

RESULT 22

AA000294

ID AA000294 standard; Peptide; 8 AA.

XX AC AA000294;

XX 01-OCT-2001 (first entry)

DE Human protein fragment SEQ ID NO: 838.

XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX Homo sapiens.

XX WO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;
XX WPI; 2001-451871/48.

XX N-PSDB; AAH89407.

XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX

PS Disclosure; Page 345; 475pp; English.

XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.

XX Query Match 50.0%; Score 5; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
DB 1 QPLPP 5

RESULT 23

AA084971

ID AA084971 standard; protein; 9 AA.

XX AC AA084971;

XX 06-AUG-2001 (first entry)

DE Clone 1 scFv CDR L3 region binding to target antigen M.

XX Antinflammatory; antiallergic; cytostatic; antibacterial; antiviral;
KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
KW antiarthritic; dermatological; immune response; modulator; enzyme;
KW antigen M; T-cell receptor; complementary determining region; CDR.

XX Homo sapiens.

XX WO200140312-A2.

XX 07-JUN-2001.

XX 04-DEC-2000; 2000WO-GB04629.

XX 03-DEC-1999; 99GB-0028789.

XX (DIVE-) DIVERSYS LTD.

XX Holt LJ, De Wildt RMT, Tomlinson I;

XX WPI; 2001-374801/39.

XX Isolating a polypeptide of interest from a naive polypeptide repertoire
PT which has not been preselected with a specific target ligand involves
PT direct screening of naive polypeptide repertoire with the target ligand
PT

XX Example 2; Page 29; 41pp; English.

CC The invention relates to isolating, from a naive polypeptide (I)
 CC repertoire (antibody or T-cell receptor polypeptides), which has not been
 CC preselected with a specific target ligand, a polypeptide of interest (II)
 CC capable of interacting with the specific target ligand. The method
 CC involves direct screening of (I) with the target ligand in order to
 CC identify (II). The polypeptides selected by the method may be used in any
 CC process which involves ligand-polypeptide binding including in vivo
 CC therapeutic and prophylactic applications, in vitro and in vivo
 CC diagnostic applications, in vitro assay and reagent applications. Enzyme
 CC variants generated and selected by the method may be assayed for
 CC activity, either in vitro or in vivo using standard techniques. Antibody
 CC polypeptides selected by the method are used diagnostically in Western
 CC analysis and in situ protein detection. The selected antibodies are
 CC useful for preventing, suppressing or treating inflammatory states,
 CC allergic hypersensitivity, cancer, bacterial or viral infection and
 CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,
 CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and
 CC myasthenia gravis. The selected polypeptides may be used extracorporeally
 CC or in vitro selectively to kill, deplete or effectively remove a target
 CC cell population from a heterogeneous collection of cells. Sequences
 CC AA884968-979 represent complementary determining regions (CDRs) of scFv
 CC heavy and light chains binding to target antigens M and D.
 CC
 CC Sequence 9 AA;

Query Match 50.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 Db 3 QPLPP 7
 |||||

RESULT 24
 AAM00291
 ID AAM00291 standard; Peptide; 12 AA.
 AC AAM00291;
 XX
 XX 01-OCT-2001 (first entry)
 DT
 DE Human protein fragment SEQ ID NO: 835.

XX Human; single nucleotide polymorphism; SNP; paternity test;
 KW forensic test; aberrant protein expression.
 KW
 XX Homo sapiens.

XX WO200151670-A2.
 XX
 XX 19-JUL-2001.
 PD
 XX
 XX 05-JAN-2001; 2001WO-US00322.
 PF
 XX
 XX 07-JAN-2000; 2000US-0174962.
 PR

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.
 DR
 DR N-PSDB; AAH89404.

PT Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes -

XX Disclosure; Page 344; 475pp; English.

XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberos
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 12 AA;

Query Match 50.0%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 Db 5 QPLPP 9
 |||||

RESULT 25
 AAR93368
 ID AAR93368 standard; peptide; 13 AA.

XX AAR93368;

XX 24-APR-1996 (first entry)

DE PI3K protein tyrosine kinase derived peptide #3.

XX SH3 ligand; SH3 binding agent; biased phage library;
 KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KW p67; complex; chronic myelogenous leukaemia; cancer.
 XX
 OS Synthetic.

XX WO9524419-A1.

XX 14-SEP-1995.

XX 13-MAR-1995; 95WO-US03208.

XX 06-JAN-1995; 95US-0369832.

XX 11-MAR-1994; 94US-0209835.

XX (ARIA-) ARIAD PHARM INC.

XX Botfield MC, Brugge JS, Rickles RJ, Zoller MJ;

XX WPI; 1995-328231/42.

PT Identification of peptide(s) binding specifically to SH3 domains -
 PT for use in inhibiting interactions mediated by SH3 domains in
 PT treatment of e.g. osteoporosis and cancer

XX Disclosure; Fig 2; 74pp; English.

XX The sequences given in AAR93343-68 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a biased phage library
 CC which comprises six random amino acids flanking the hexapeptide
 CC RSLRPL- which was identified as a recognition sequence for the src
 CC SH3 domain. These sequences were identified using the method of the
 CC invention. The method comprises contacting the SH3 domain with a
 CC mixture of peptides under conditions permitting a ligand to bind to
 CC an SH3 domain to form a complex. Any unbound peptides are removed
 CC and the complexed peptide ligands are dissociated from the complexes.
 CC The selected peptides are enriched by re-contacting them with the
 CC SH3 domain and then candidates which bind to the SH3 domain are
 CC detected. The isolated SH3 binding peptides may be used in the
 CC diagnosis, prevention and treatment of conditions or diseases resulting
 CC from cellular processes mediated by an SH3-based interaction. Such
 CC diseases include Paget's disease. Other conditions treatable with these

CC peptides include restenosis, rheumatoid arthritis, gout and other
 CC problems in which an SH3 of neutrophil oxidase p47 and p67 complex is
 CC implicated, etc.
 XX
 SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 16; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
 |||||
 Db 5 PLPPT 9

RESULT 26
 AAW11112
 ID AAW11112 standard; peptide; 13 AA.

XX AC AAW11112;
 XX DT 25-JUN-1997 (first entry)
 XX XX

DE Src SH3 domain-binding peptide used in signal transduction modulation.

XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.
 XX XX

OS Synthetic.

XX WO9603649-A1.
 PN XX

XX PD 08-FEB-1996.

XX PF 24-JUL-1995; 95WO-US09382.

XX PR 07-JUN-1995; 95US-0483555.

XX PR 22-JUL-1994; 94US-0278865.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
 XX WPI; 1996-117151/12.

XX DR
 XX XX

PT Peptide with binding affinity for Src homology region 3 (SH3)

PT domains of proteins - useful for e.g. modulating signal transduction
 PT pathways at the cellular level, esp. protein tyrosine
 PT kinase-mediated
 XX XX

PS Claim 38; Page 87; 116pp; English.

XX AAW1098-W1124 are peptides that bind to the Src SH3 domain. The SH3
 CC binding peptides are useful in modulating signal transduction pathways
 CC at the cellular level (especially protein tyrosine kinase-mediated),
 CC modulating oncogenic protein activity, or providing compounds for the
 CC development of drugs with the ability to modulate broad classes, as
 CC well as specific classes, of proteins involved in signal transduction
 CC and also for regulating the processing, trafficking or translation of
 CC RNA. Conjugates of the peptides with detectable labels or imaging agents
 CC are useful for imaging cells, tissues and organs in which Src or
 CC Src-related proteins are expressed.

XX Sequence 13 AA;

Query Match 50.0%; Score 5; DB 17; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
 |||||
 Db 5 PLPPT 9

RESULT 27

AAE21396

ID AAE21396 standard; peptide; 13 AA.

XX AC AAE21396;
 XX XX

DT 01-JUL-2002 (first entry)

XX Escherichia coli 3-isopropylmalate dehydrogenase (IPMDH) peptide #1.

XX Protein thermostability; 3-isopropylmalate dehydrogenase; IPMDH;
 KW isocitrate dehydrogenase; ICDH; enzyme.
 XX OS Escherichia coli.
 XX PN EP1182253-A2.
 XX PD 27-FEB-2002.
 XX PF 03-JUL-2001; 2001EP-0115642.
 XX PR 04-JUL-2000; 2000JP-0201920.
 XX PR 31-MAY-2001; 2001JP-0164332.
 XX PA (AJIN) AJINOMOTO CO INC.
 XX PI Yamagishi A;
 XX WPI; 2002-294076/34.

XX Improving protein thermostability of protein by estimating amino acid
 PT sequence of ancestral protein (AP), and replacing amino acids of
 PT desired protein, which differ from those of AP with the same amino
 PT acids of AP -
 XX XX
 XX Example 4; Fig 9; 73pp; English.
 XX The invention relates to a method for improving thermostability of
 CC proteins. The method involves comparing amino acid sequences derived
 CC from two or more species which evolutionarily correspond to each other
 CC in phylogenetic tree; estimating amino acid sequence of ancestral
 CC protein and replacing amino acids of desired protein, which differ
 CC from those of ancestral protein with the same amino acids of ancestral
 CC protein. The method is used for improving thermostability of proteins
 CC preferably 3-isopropylmalate dehydrogenase (IPMDH) and isocitrate
 CC dehydrogenase (ICDH). The invention also relates to a protein having
 CC an improved thermostability and a nucleic acid encoding such protein.
 CC The present sequence is Escherichia coli IPMDH peptide.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||

Db 1 QPLPP 5

RESULT 28

ABP81159

ID ABP81159 standard; peptide; 13 AA.

XX AC ABP81159;
 XX XX

DT 27-FEB-2003 (first entry)

XX Human TPO peptide with MCH class II binding activity #112.

XX Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 XX WO200268469-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 XX (MERE) MERCK PATENT GMBH.
 PI Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX Disclosure; Page 12; 36pp; English.
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and antiallergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX Sequence 13 AA;
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 Db 7 PLPPT 11
 XX
 XX
 AC ABP81160;
 XX 27-FEB-2003 (first entry)
 DT Human TPO peptide with MCH class II binding activity #113.
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 XX WO200268469-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 XX (MERE) MERCK PATENT GMBH.
 PI Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX Disclosure; Page 12; 36pp; English.
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and antiallergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX Sequence 13 AA;
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 Db 7 PLPPT 11
 XX
 XX
 AC ABP81160;
 XX 27-FEB-2003 (first entry)
 DT Human TPO peptide with MCH class II binding activity #113.
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 XX WO200268469-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 XX (MERE) MERCK PATENT GMBH.
 PI Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX Disclosure; Page 12; 36pp; English.
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and antiallergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX Sequence 13 AA;
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 Db 5 PLPPT 9
 XX
 XX
 AC ABP81161;
 XX 27-FEB-2003 (first entry)
 DT Human TPO peptide with MCH class II binding activity #114.
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 XX WO200268469-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 XX (MERE) MERCK PATENT GMBH.
 PI Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -

XX (MERE) MERCK PATENT GMBH.
 XX Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX Disclosure; Page 12; 36pp; English.
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and antiallergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX Sequence 13 AA;
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 Db 5 PLPPT 9
 XX
 XX
 AC ABP81161;
 XX 27-FEB-2003 (first entry)
 DT Human TPO peptide with MCH class II binding activity #114.
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 XX WO200268469-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 XX (MERE) MERCK PATENT GMBH.
 PI Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -

RESULT 30

ABP81161
 ID ABP81161 standard; peptide; 13 AA.
 XX
 AC ABP81161;
 XX 27-FEB-2003 (first entry)
 DT Human TPO peptide with MCH class II binding activity #114.
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 XX WO200268469-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 XX (MERE) MERCK PATENT GMBH.
 PI Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and anti-allergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6

Db 4 PLPPT 8

RESULT 31

ABP81162

ID ABP81162 standard; peptide; 13 AA.

XX AC ABP81162;

XX DT 27-FEB-2003 (first entry)

XX DE Human TPO peptide with MCH class II binding activity #115.

XX KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

XX KW MHC class II; immunosuppressive; anti-allergic; autoimmune disease.

XX OS Homo sapiens.

XX PN WO200268469-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-EP01931.

XX PR 26-FEB-2001; 2001EP-0104702.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FU, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX PI Carr FU, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and anti-allergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

CC or less immunogenicity than any non-modified molecule with the same

CC biological activity when used in vivo. The protein is useful in

CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

CC allergies and autoimmune disease treatment. The sequences shown in

CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

CC invention.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6

Db 2 PLPPT 6

RESULT 32

ABP81163

ID ABP81163 standard; peptide; 13 AA.

XX AC ABP81163;

XX DT 27-FEB-2003 (first entry)

XX DE Human TPO peptide with MCH class II binding activity #116.

XX KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

XX KW MHC class II; immunosuppressive; anti-allergic; autoimmune disease.

XX OS Homo sapiens.

XX PN WO200268469-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-EP01931.

XX PR 26-FEB-2001; 2001EP-0104702.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FU, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and anti-allergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
| | | | |
Db 1 PLPPT 5

RESULT 33
AAY03679
ID AAY03679 standard; peptide; 14 AA.
XX AC
XX AAY03679;
XX XX
XX 07-JUN-1999 (first entry)
XX DE
XX Amino acid sequence of the malaria (M) string CTL epitope BCG.
XX CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;
KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;
KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;
KW melanoma; HIV; breast; colon; vaccination.
XX Mycobacterium tuberculosis.
XX OS
XX WO9856919-A2.
XX PN
XX 17-DEC-1998.
XX PD
XX 09-JUN-1998; 98WO-GB01681.
XX PF
XX 09-JUN-1997; 97GB-0011957.
XX PR
XX (ISIS-) ISIS INNOVATION LTD.
XX PA
XX Blanchard T, Gilbert SC, Hanke T, Hill AVS, McMichael AJ;
PI Piebanski M, Schneider J, Smith GL;
PI WPI; 1999-070325/06.
XX DR
XX N-PSDB; AAX29219.
XX XX
XX Generating CD8-positive T cell response to target antigen using
PT recombinant poxvirus - for treating or preventing malaria and HIV
PT infection, also epitope strings from Plasmodium and HIV
PT XX
PS Claim 38; Page 19; 85pp; English.
XX XX
CC The invention relates to methods and reagents for generating a
CC protective CD8+ T-cell immune response against at least one target
CC antigen. The kits of the invention comprises (i) as priming composition,
CC a source of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)]
CC epitopes of the target antigen, plus a carrier and (ii) as boosting
CC composition a source of CTL epitopes, with at least one CTL epitope the
CC same as used in (i), with this source being a non-replicating or
CC replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If
CC the source of CTL epitopes in (i) is a viral vector, then the vector in
CC (ii) is from a different virus. The kits are used to generate an immune
CC response (prophylactic or therapeutic) against pathogens or tumours,
CC specifically against malaria parasites such as P. falciparum, or HIV, and
CC also many other bacterial, viral or parasitic pathogens. The kits are
CC also used for protective response against melanoma and cancer of breast
CC or colon, and generally wherever a strong CD8+ response is protective.
CC The boosting composition may be used alone to boost a naturally primed
CC response against malaria. The specified PVV provide an excellent booster
CC effect, better than that from wild-type poxvirus, resulting in complete
CC rather than partial protection against sporozoite challenge. Also PVV are
CC safer to use than wild-type virus. Sequences AAY03661-680 represent CTL
CC peptide epitopes of the malaria (M) string.
XX XX
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
| | | | |
Db 1 PLPPT 5

RESULT 34
AAM00448
ID AAM00448 standard; Peptide; 14 AA.
XX XX
XX AAM00448;
XX AC
XX 01-OCT-2001 (first entry)
XX DT
XX Human protein fragment SEQ ID NO: 996.
XX DE
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX KW
XX Homo sapiens.
XX OS
XX WO200151670-A2.
XX PN
XX 19-JUL-2001.
XX PD
XX 05-JAN-2001; 2001WO-US00322.
XX PF
XX 07-JAN-2000; 2000US-0174962.
XX PR
XX (CURA-) CURAGEN CORP.
XX PA
XX Shimkets RA, Leach MD;
XX PI
XX WPI; 2001-451871/48.
XX DR
XX N-PSDB; AAH89565.
XX XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
PT XX
XX Disclosure; Page 389; 475pp; English.
XX PS
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.
XX XX
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
| | | | |
Db 5 QPLPP 9

RESULT 35
AAB46171
ID AAB46171 standard; peptide; 14 AA.
XX XX
XX AAB46171;
XX AC
XX 04-APR-2001 (first entry)
XX DT
XX

DE XX Bacille Calmette-Guerin universal T epitope.
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 OS
 XX Mycobacterium tuberculosis.
 XX WO200072880-A2.
 XX
 XX PD 07-DEC-2000.
 XX
 XX PF 26-MAY-2000; 2000WO-US14810.
 XX
 XX PR 28-MAY-1999; 99US-0322289.
 XX
 XX PA (NEUR-) NEURALAB LTD.
 XX
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX WPI; 2001-032104/04.
 DR
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 XX PS Disclosure; Page 28; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 XX SQ Sequence 14 AA;
 Query Match 50.0%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPP 5
 Db 5 QPLPP 9
 RESULT 36
 AAB49070
 ID AAB49070 standard; peptide; 14 AA.
 XX
 AC AAB49070;
 XX
 XX 27-MAR-2001 (first entry)
 XX
 XX BCG T-cell epitope, SEQ ID NO:6.
 DE
 XX Amyloid disease; amyloid fibril deposition; amyloid plaque;
 KW immunogenic; antibody; vaccine; Alzheimer's disease;
 KW type 2 diabetes; reactive system amyloidosis;
 KW systemic senile amyloidosis; familial amyloid cardiomyopathy;
 KW transmissible spongiform encephalopathy; Creutzfeld-Jakob disease; Kuru;
 KW haemodialysis-associated beta-2-microglobulin deposition;
 KW carrier protein; universal T-cell epitope.
 XX
 XX Mycobacterium bovis.
 OS
 XX

PN WO200072876-A2.
 XX
 XX PD 07-DEC-2000.
 XX
 XX PF 01-JUN-2000; 2000WO-US15239.
 XX
 XX PR 01-JUN-1999; 99US-0137010.
 XX
 XX PA (NEUR-) NEURALAB LTD.
 XX
 XX PI Schenk DB;
 XX WPI; 2001-070921/08.
 DR
 XX Pharmaceutical composition comprising immunogen against amyloid
 PT component such as fibril peptide or protein, or antibody against
 PT amyloid component useful for treating amyloid diseases or amyloidoses -
 XX
 XX PS Disclosure; Page 43; 140pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition for
 CC preventing or treating a disease characterised by amyloid fibril
 CC deposits (amyloid plaques) in a patient. The pharmaceutical composition
 CC comprises an agent that will induce an immune response against an amyloid
 CC component, or an antibody or antibody fragment that binds to an amyloid
 CC component. The invention also relates to a method for determining
 CC the prognosis of a patient undergoing treatment for an amyloid disorder
 CC which involves measuring a patient serum amount of immunoreactivity
 CC against a selected amyloid component. A patient serum immunoreactivity
 CC of at least four times a base line serum immunoreactivity control level
 CC indicates a prognosis of improved status with respect to the disorder.
 CC The pharmaceutical compositions of the invention are useful for treating
 CC a wide variety of disorders characterised by amyloid fibril deposition in
 CC a patient. Such disorders include Alzheimer's disease characterised by
 CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
 CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
 CC fibrils derived from transthyretin (TTR); transmissible spongiform
 CC encephalopathies (e.g. Creutzfeld-Jakob disease, Kuru) characterised by
 CC prion protein deposits; and beta-2-microglobulin deposits which form as
 CC a result of long term haemodialysis treatment. The present sequence
 CC represents a universal T-cell epitope which may be used as a
 CC carrier for an epitope derived from an amyloid plaque component in a
 CC composition of the invention.
 XX
 XX SQ Sequence 14 AA;
 Query Match 50.0%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPP 5
 Db 5 QPLPP 9
 RESULT 37
 AAW38958
 ID AAW38958 standard; peptide; 15 AA.
 XX
 AC AAW38958;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:355.
 DE
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Ab1; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX

OS Synthetic.
 PN WO9730074-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US02298.
 XX
 PR 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX
 DR WPI; 1997-424972/39.
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 PS Claim 22; Page 91; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 SQ Sequence 15 AA;
 Query Match 50.0%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PLPPT 6
 Db 9 PLPPT 13
 RESULT 38
 AAW39036
 ID AAW39036 standard; peptide; 15 AA.
 AC AAW39036;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:437.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 OS
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 PD

XX 14-FEB-1997; 97WO-US02298.
 XX
 PR 16-FEB-1996; 96US-0602999.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX
 DR WPI; 1997-424972/39.
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 PS Claim 22; Page 94; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 SQ Sequence 15 AA;
 Query Match 50.0%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPLPP 5
 Db 2 QPLPP 6
 RESULT 39
 AAG78855
 ID AAG78855 standard; Peptide; 15 AA.
 XX
 AC AAG78855;
 XX
 XX 12-DEC-2001 (first entry)
 DT
 DE Growth hormone family protein 11 peptide fragment.
 XX
 KW Growth hormone; cytostatic; virucidal; immunomodulator; antiinflammatory;
 KW haemostatic; gene therapy; malignant tumour; haemopathy; HIV infection;
 KW immunological disease; inflammation.
 XX
 OS Unidentified.
 OS
 XX WO200172832-A1.
 PN
 XX 04-OCT-2001.
 PD
 XX 26-MAR-2001; 2001WO-CN00489.
 XX
 PF 27-MAR-2000; 2000CN-0115180.
 PR
 XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX Mao Y, Xie Y;
 XX WPI; 2001-602854/68.
 XX New polypeptide for the diagnosis and treatment of malignant neoplasm,
 PT hemopathy, HIV infection, immunological diseases and inflammations,
 PT comprises protein 11 of the growth hormone family -
 XX Example 5; Page 19; 35pp; Chinese.
 XX The present invention relates to protein 11 of the growth hormone family
 CC (see AAF65179 and AAG78854). The growth hormone protein and its coding
 CC sequence are useful in the diagnosis and treatment of malignant tumours,
 CC haemopathy, HIV infection, immunological diseases and various
 CC inflammations. The present sequence is an N-terminal peptide fragment of
 CC the growth hormone protein which was used in an example from the present
 CC invention.
 XX SQ Sequence 15 AA;
 Query Match 50.0%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 DB 8 PLPPT 12
 RESULT 40
 ABG72660
 ID ABG72660 standard; Peptide; 15 AA.
 XX AC ABG72660;
 XX 26-FEB-2003 (first entry)
 DT Human K-ras 10.67 proto-oncogene protein, N-terminus.
 DE Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;
 XX development disorder; human immunodeficiency virus infection; HIV;
 KW immunological disease; inflammation.
 KW Homo sapiens.
 OS CNI352063-A.
 EN 05-JUN-2002.
 PD 02-NOV-2000; 2000CN-0127155.
 PF 02-NOV-2000; 2000CN-0127155.
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA Mao Y, Xie Y;
 PI WPI; 2002-658691/71.
 XX New human K-ras proto-oncogene protein 10.67 polypeptide for treating
 PT malignant tumors, hemopathy, development disorder, human
 PT immunodeficiency virus infection, immunological diseases and various
 PT inflammations -
 XX Example 5; Page 19 (disclosure); 33pp; Chinese.
 XX The present invention discloses a new kind of polypeptide,
 CC human K-ras proto-oncogene protein 10.67, polynucleotides encoding the
 CC polypeptide and a DNA recombination process to produce the polypeptide.
 CC The present invention also discloses applying the polypeptide in
 CC treating various diseases, such as malignant tumors, haemopathy,
 CC

CC development disorder, human immunodeficiency virus (HIV) infection,
 CC immunological diseases and various inflammations. The present invention
 CC also discloses the antagonist resisting the polypeptide and its
 CC treatment effect. The present invention also discloses application of
 CC the polynucleotides encoding human K-ras proto-oncogene protein 10.67.
 CC The present sequence represents human K-ras proto-oncogene protein
 CC 10.67, N-terminus, used in an ELISA (enzyme-linked immunosorbent assay)
 CC experiment.
 XX SQ Sequence 15 AA;
 Query Match 50.0%; Score 5; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPP 5
 DB 11 QPLPP 15
 RESULT 41
 AAW25427
 ID AAW25427 standard; peptide; 16 AA.
 XX AC AAW25427;
 XX 27-MAR-1998 (first entry)
 DT Yes SH3 domain binding peptide SEQ ID NO:213.
 DE Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abi; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 OS Unidentified.
 OS WO9730074-A1.
 EN 21-AUG-1997.
 PD 14-FEB-1997; 97WO-US02298.
 PF 16-FEB-1996; 96US-0602999.
 PR (CYTO-) CYTOGEN CORP.
 XX (UYNC-) UNIV NORTH CAROLINA.
 PA Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 DR Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 19; Page 100; 131pp; English.
 XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abi; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX Sequence 16 AA;

Query Match 50.0%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
 |||||
 Db 5 PLPPT 9

RESULT 42
 AAW25376
 ID AAW25376 standard; peptide; 16 AA.

XX AC AAW25376;

XX DT 27-MAR-1998 (first entry)

XX DE Src SH3 domain binding peptide SEQ ID NO:158.

XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.
 OS Unidentified.

XX PN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

XX PI Sparks AB, Thorn JM;

XX XX WPI; 1997-424972/39.

XX PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

XX PS Claim 16; Page 99; 131pp; English.

XX CC The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX SQ Sequence 16 AA;

Query Match 50.0%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
 |||||
 Db 5 PLPPT 9

RESULT 43
 AAW25380
 ID AAW25380 standard; peptide; 16 AA.

XX AC AAW25380;

XX DT 27-MAR-1998 (first entry)

XX DE Src SH3 domain binding peptide SEQ ID NO:147.

XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.
 OS Unidentified.

XX PN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

XX PI Sparks AB, Thorn JM;

XX XX WPI; 1997-424972/39.

XX PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

XX PS Claim 16; Page 99; 131pp; English.

XX CC The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX SQ Sequence 16 AA;

Query Match 50.0%; Score 5; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 5 PLPPT 9

RESULT 44
ABP82678
ID ABP82678 standard; Peptide; 16 AA.
XX
AC ABP82678;
DT 04-MAR-2003 (first entry)
DE
DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1351.
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US50107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Claim 1; Fig 2; 523pp; English.
XX

The present invention describes antigenic peptides (I) comprising:
(a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABP82678 to ABP82869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;
Query Match 50.0%; Score 5; DB 24; Length 16;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 10 PLPPT 14

RESULT 45
AAB39277
ID AAB39277 standard; Protein; 17 AA.
XX
AC AAB39277;
XX
DT 02-FEB-2001 (first entry)
DE
DE Gene 31 human secreted protein homologous amino acid sequence #157.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
KW ophthalmological; autoimmune disease; rheumatoid arthritis; angioedema;
KW hyperproliferative disorder; cardiovascular disorder; infection;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; chemotaxis.
XX
OS Homo sapiens.
XX
PN WO2000056754-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US06792.
XX
PR 19-MAR-1999; 99US-0125362.
PR 10-DEC-1999; 99US-0169980.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen GA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-579483/54.
XX

Isolated nucleic acid molecule encoding a human secreted protein is
used in preventing, treating or ameliorating a medical condition -
Disclosure; Page 52; 434pp; English.

The polynucleotide sequences given in AAC74223-C74279 encode the human
secreted proteins represented in AAB39179-B39226. Sequences
AAB39227-B39308 are alternative proteins encoded by the genes, and also
protein sequences with which they share homology. The proteins have
activities based on the tissues and cells in which they are expressed.
Examples of activities include: immunosuppressive; antiarthritic;
antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
fungicide; and ophthalmological. The human secreted proteins,
polynucleotides, antagonists and agonists of the invention may be useful
in the treatment, prevention, and/or diagnosis of various disease,
disorders and conditions such as autoimmune diseases e.g. rheumatoid
arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
disorders e.g. cerebral ischaemia, angioedema, nervous system disorders
e.g. Alzheimer's disease, infections caused by bacteria, viruses and

CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation, to
 CC regenerate tissues, maintain organs before transplantation, in
 CC chemotaxis and as a food additive or preservative e.g. to increase
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used
 CC during the isolation and characterisation of the genes of the invention.
 XX
 SQ Sequence 17 AA;

Query Match 50.0%; Score 5; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 |||||
 Db 1 QPLPP 5

RESULT 46
 AAE03955
 ID AAE03955 standard; peptide; 18 AA.
 AC AAE03955;

DT 09-AUG-2001 (first entry)

DE Human gene 10 encoded secreted protein fragment, SEQ ID NO:126.

XX Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnerability;
 KW cell culture; chemotaxis; food additive; gene therapy;
 KW binding partner identification.

XX Homo sapiens.

XX W0200077022-A1.

XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US15136.

XX 11-JUN-1999; 99US-0138629.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;

XX WPI; 2001-367020/38.

XX Nucleic acids encoding 50 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
 PT disease, botulism, cancers and Scimitar syndrome -
 XX

PS Disclosure; Page 566-567; 61pp; English.

XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
 CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
 CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
 CC The genes and their secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 50 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental

CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.
 XX
 SQ Sequence 18 AA;

Query Match 50.0%; Score 5; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 |||||
 Db 11 QPLPP 15

RESULT 47
 AAY31181
 ID AAY31181 standard; peptide; 19 AA.

AC AAY31181;

XX 28-OCT-1999 (first entry)

DE Ubiquitin fusion protein T cell epitope.

XX Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;
 KW immune response stimulation; vaccine; T cell; viral; infection; cancer;
 KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;
 KW pulmonary infection; respiratory infection; scaffold; anti-self; pig;
 KW steridogenesis; gamete maturation; prostate; breast; castration; TNF;
 KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;
 KW inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;
 KW fertility; sperm protein; growth rate; antibody; detection.

OS Synthetic.

XX WO9942472-A1.

XX 26-AUG-1999.

XX 26-JAN-1999; 99WO-US01588.

XX 19-FEB-1998; 98US-0026276.

XX (IGEN-) IGEN INT INC.

XX Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;

PI WPI; 1999-518582/43.

DR Epitope-containing fusion proteins used to generate a highly
 XX specific immune responses

XX Example 4; Page 42; 67pp; English.

XX This invention describes a novel fusion protein, comprising a heat shock
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner
 CC which is useful for the stimulation of a highly specific immune response

CC when administered to an animal. The protein of the invention may be
 CC post-translationally modified (e.g. by the addition of fatty acids to
 CC enhance immunogenicity). The fusion proteins of the invention can be
 CC used as vaccines to induce an immune response. When a T cell epitope is
 CC attached, they can be used for control of viral infections, bacterial
 CC infections, parasitic infection and cancer. The fusion proteins can be
 CC used in pharmaceutical compositions for the treatment of gastrointestinal
 CC diseases, pulmonary infections, respiratory infections, and HIV
 CC infections. The use of ubiquitin as a scaffold is also useful for the
 CC presentation and stimulation of anti-self immune responses, e.g.
 CC generation of anti-gonadotropin releasing hormone antibodies which result
 CC in the suppression of luteinizing hormone and follicle stimulating
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation
 CC in males and females. This type of anti-self response in humans is useful
 CC in the treatment of prostate cancer and breast cancer. In livestock, the
 CC ability to stimulate an anti-self response provides a simple alternative
 CC to physical castration. Immunocastration of pigs is a better alternative
 CC side effects associated with physical castration. Other examples of
 CC diseases and conditions treated with self proteins fused with ubiquitin
 CC are TNF and its epitopes to modulate septic shock, arthritis,
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig
 CC epsilon heavy chain for the control of allergic reactions; chorionic
 CC gonadotropin for fertility control; and sperm proteins for fertility
 CC control. A further use of the fusion proteins is as part of a vaccine to
 CC enhance growth rate and thereby the final weight of the livestock prior
 CC to shipment to market. In addition, the fusion proteins of the invention
 CC can be used to detect and identify antibodies from experimental samples.
 CC This sequence represents a T cell epitope used in the construction of
 CC a ubiquitin fusion protein described in the method of the invention.

XX Sequence 19 AA;

Query Match 50.0%; Score 5; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPP 5
 Db |||||
 6 QLPP 10

RESULT 48

AAY31165
 ID AAY31165 standard; peptide; 19 AA.

XX AC AAY31165;

XX DT 28-OCT-1999 (first entry)

XX DE Ubiquitin fusion protein MT peptide.

XX Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;
 KW immune response stimulation; vaccine; T cell; viral; infection; cancer;
 KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;
 KW pulmonary infection; respiratory infection; scaffold; anti-self; pig;
 KW steroidogenesis; gamete maturation; prostate; breast; castration; TNF;
 KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;
 KW inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;
 KW fertility; sperm protein; growth rate; antibody; detection.

XX OS Synthetic.

XX FN WO9942472-A1.

XX PD 26-AUG-1999.

XX PF 26-JAN-1999; 99WO-US01588.

XX PR 19-FEB-1998; 98US-0026276.

XX PA (IGEN-) IGEN INT INC.

XX

PI Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;
 XX WPI; 1999-518582/43.

XX PT Epitope-containing fusion proteins used to generate a highly
 XX specific immune responses

XX PS Example 1; Page 27; 67pp; English.

XX This invention describes a novel fusion protein, comprising a heat shock
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner
 CC which is useful for the stimulation of a highly specific immune response
 CC when administered to an animal. The protein of the invention may be
 CC post-translationally modified (e.g. by the addition of fatty acids to
 CC enhance immunogenicity). The fusion proteins of the invention can be
 CC used as vaccines to induce an immune response. When a T cell epitope is
 CC attached, they can be used for control of viral infections, bacterial
 CC infections, parasitic infection and cancer. The fusion proteins can be
 CC used in pharmaceutical compositions for the treatment of gastrointestinal
 CC diseases, pulmonary infections, respiratory infections, and HIV
 CC infections. The use of ubiquitin as a scaffold is also useful for the
 CC presentation and stimulation of anti-self immune responses, e.g.
 CC generation of anti-gonadotropin releasing hormone antibodies which result
 CC in the suppression of luteinizing hormone and follicle stimulating
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation
 CC in males and females. This type of anti-self response in humans is useful
 CC in the treatment of prostate cancer and breast cancer. In livestock, the
 CC ability to stimulate an anti-self response provides a simple alternative
 CC to physical castration. Immunocastration of pigs is a better alternative
 CC side effects associated with physical castration. Other examples of
 CC diseases and conditions treated with self proteins fused with ubiquitin
 CC are TNF and its epitopes to modulate septic shock, arthritis,
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig
 CC epsilon heavy chain for the control of allergic reactions; chorionic
 CC gonadotropin for fertility control; and sperm proteins for fertility
 CC control. A further use of the fusion proteins is as part of a vaccine to
 CC enhance growth rate and thereby the final weight of the livestock prior
 CC to shipment to market. In addition, the fusion proteins of the invention
 CC can be used to detect and identify antibodies from experimental samples.
 CC This sequence represents a MT peptide used in the method of the
 CC invention.

XX SQ Sequence 19 AA;

Query Match 50.0%; Score 5; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPP 5
 Db |||||
 6 QLPP 10

RESULT 49

AAB71936

ID AAB71936 standard; Peptide; 19 AA.

XX AC AAB71936;

XX DT 10-MAY-2001 (first entry)

XX DE MT peptide.

XX Immunostimulant; antiallergic; growth promoting; vaccine;
 KW heat shock fusion protein; ubiquitin; self-epitope; immunogen;
 KW male-specific peptide hormone; female-specific peptide hormone; MT.

XX OS Unidentified.

XX FN WO200112216-A1.

XX PD 22-FEB-2001.

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XX PF 14-AUG-2000; 200WO-US22121.
XX PR 13-AUG-1999; 99US-0374721.
XX PA (PROT-) PROTEINIX CO.
XX PR 13-AUG-1999; 99US-0374721.
XX PA (PROT-) PROTEINIX CO.
XX KI Kanten JH, Roberts S, Lohnas G;
XX WPI; 2001-202829/20.
XX Novel fusion proteins for stimulating immune response in animals
PT against self-antigen, has heat shock protein fused to single or a group
PT of epitope-containing segments having identical or non-identical self
PT epitopes -
XX Example 1; Page 27; 94pp; English.
XX The present sequence is given in an example illustrating an invention
XX disclosing self-epitope-containing heat shock fusion proteins. The
XX proteins comprise a heat shock protein, preferably ubiquitin, fused to a
XX single epitope-containing segment or two or more non-contiguous epitope
XX containing segments, each epitope-containing segment comprising one or
XX more identical or non-identical self-epitopes. The heat shock fusion
XX proteins are useful for stimulating an immune response in an animal,
XX especially a pig, directed towards a self-antigen, in particular a male
XX or female-specific peptide hormone. The physiological consequence is
XX substantially similar to the consequences of surgical castration. The
XX proteins are useful for identifying antibodies in experimental or
XX diagnostic samples and for reducing levels of a predetermined endogenous
XX protein, such as gonadotropin releasing hormone, tumour necrosis factor
XX or growth hormone protein. They are also useful for reducing allergic
XX response and for increasing the growth rate of an animal. The proteins
XX have a high specific immune response and do not result in detrimental
XX side-effects. The present sequence encodes a peptide sequence which is
XX inserted into a ubiquitin scaffold to test the peptide as an immunogen
XX for eliciting a targeted immune response.
XX SQ Sequence 19 AA;
XX Query Match 50.0%; Score 5; DB 22; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 71;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 QPLPP 5
XX Db 6 QPLPP 10
XX RESULT 50
XX AAW16997
XX ID AAW16997 standard; peptide; 20 AA.
XX AC AAW16997;
XX DT 27-JUN-1997 (first entry)
XX DE SRC SH3 domain-binding peptide.
XX KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
XX protein tyrosine kinase; signal transduction; RNA processing;
XX trafficking; translation.
XX OS Synthetic.
XX PN WO9603649-A1.
XX PR 08-FEB-1996.
XX XX

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PF 24-JUL-1995; 95WO-US09382.
XX 07-JUN-1995; 95US-0483555.
XX 22-JUL-1994; 94US-0278865.
XX (TYNC-) UNIV NORTH CAROLINA.
XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
XX WPI; 1996-117151/12.
XX Peptide with binding affinity for Src homology region 3 (SH3)
XX domains of proteins - useful for e.g. modulating signal transduction
XX pathways at the cellular level, esp. protein tyrosine
XX kinase-mediated
XX Example 14; Page 58; 116pp; English.
XX AAW16996-W17009 are SRC SH3-binding peptides derived from a biased
XX peptide library, exhibiting selective SH3 binding. The SH3 binding
XX peptides are useful in modulating signal transduction pathways at the
XX cellular level (especially protein tyrosine kinase-mediated), modulating
XX oncogenic protein activity, or providing compounds for the development
XX of drugs with the ability to modulate broad classes, as well as specific
XX classes, of proteins involved in signal transduction and also for
XX regulating the processing, trafficking or translation of RNA. Conjugates
XX of the peptides with detectable labels or imaging agents are useful for
XX imaging cells, tissues and organs in which Src or Src-related proteins
XX are expressed.
XX SQ Sequence 20 AA;
XX Query Match 50.0%; Score 5; DB 17; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 74;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 2 PLPPT 6
XX Db 7 PLPPT 11
XX RESULT 51
XX AAR99513
XX ID AAR99513 standard; peptide; 20 AA.
XX AC AAR99513;
XX DT 09-JAN-1997 (first entry)
XX DE T-cell epitope used in construction of chimeric immunoglobulin.
XX KW Chimera; chimeric; immunoglobulin; Ig; B-cell; T-cell; lymphocyte;
XX epitope; immune response; vaccine; pathogen; antibody; influenza;
XX measles; hepatitis; foot and mouth disease; tetanus toxoid;
XX human immunodeficiency virus; HIV; heat shock protein; M protein;
XX hen egg white lysozyme; nuclease.
XX OS Mycobacteria sp.
XX PN WO9619584-A1.
XX 27-JUN-1996.
XX 21-DEC-1995; 95WO-US16718.
XX 22-DEC-1994; 94US-0363276.
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX Bona C, Zaghouani H;
XX WPI; 1996-309598/31.
XX XX

```

PT Chimeric immunoglobulin with CDR loop substd. for T and or B cell
PT epitope - useful in vaccine composition to enhance immune response
PT to pathogens
XX
PS Disclosure; Page 19; 131pp; English.
XX
CC Chimeric immunoglobulins (Ig) having a CDR loop of the parent Ig
CC replaced with a foreign peptide sequence corresponding to a T- or B-
CC cell epitope, may be used in vaccine compositions to enhance an
CC immune response to a pathogen. Chimeric Ig comprising a B-cell
CC epitope can also be used to label B-cells, to test the ability of a
CC subject to mount a humoral response to a particular B-cell epitope
CC or to collect B-cells which recognise the epitope.. An antibody
CC comprising a chimeric Ig molecule which comprises an antigen binding
CC site may be used in diagnostic assays to detect the presence of a
CC particular target antigen, which binds to the antibody binding site.
CC Sequences of B-cell epitopes are given in AAR9503-08. Sequences of
CC T-cell epitopes are given in AAR9509-17. The term T-cell epitope
CC refers to a peptide which is associated with MHC self antigens and
CC is recognised by a T-cell and which functionally activates the T
CC cell. This peptide is an epitope of Mycobacteria heat shock
CC protein.
XX
SQ Sequence 20 AA;
Query Match 50.0%; Score 5; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPP 5
Db |||||
6 QPLPP 10
RESULT 52
AAW35439
ID AAW35439 standard; peptide; 20 AA.
XX
AC AAW35439;
XX
DT 25-MAR-2003 (updated)
DT 22-APR-1998 (first entry)
XX
DE T-cell stimulatory peptide from Mycobacterium tuberculosis 38kd antigen.
XX
XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
XX scaffold; inhibition; metastasis; wound healing; solid phase.
XX
OS Mycobacterium tuberculosis.
XX
XX WO9738011-A1.
XX
PD 16-OCT-1997.
XX
PF 03-APR-1997; 97WO-DK00146.
XX
PR 03-APR-1996; 96DK-0000398.
XX
XX (PEPR-) PEPRESEARCH AS.
XX
XX Heegaard PMH, Jakobsen PH;
XX
XX WPI; 1997-512645/47.
XX
XX Non-dendritic peptide carrier linked to a solid phase - useful as a
XX diagnostic agent and as a scaffold for production of chemical
XX derivatives
XX
XX Claim 30; Page 199; 262pp; English.
XX
XX A non-dendritic peptide carrier (A) has been developed which is coupled
XX through a linker to a solid phase, forming a complex of (A)-solid phase.
XX Where (A) comprises 10-50 amino acids capable of forming a secondary

CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence
CC represents a specifically claimed T-cell stimulatory peptide from the
CC present invention. An (A)-solid phase complex can be used as a scaffold
CC for the production of chemical derivatives, characterised by covalently
CC attaching molecules at attachment points. Alternatively (A) is used as
CC a scaffold-peptide for the incorporation into an Immunostimulating
CC Complex (Iscm) resulting in an (A)-Iscm complex which is used for the
CC chemical coupling of antigenic substances in an aqueous solution by
CC conjugation. (A) derivatised with one or more peptides having
CC fibronectin-, laminin- or vitronectin-like binding activities can be
CC used for the promotion of cell-attachment to plastic surfaces, in
CC particular to inhibit tumour growth and metastasis, and for promotion
CC of wound healing. Also a derivatised (A) can be used for the selection
CC of specifically-binding aptamers or as a diagnostic agent. Such
CC diagnostic-(A) molecules could be used to detect molecules derived from
CC or indicative of pregnancy or of a disease, such as an infectious,
CC autoimmune or cancerous disease.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 AA;
Query Match 50.0%; Score 5; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPP 5
Db |||||
6 QPLPP 10
RESULT 53
AAW12237
ID AAW12237 standard; peptide; 20 AA.
XX
AC AAW12237;
XX
DT 06-AUG-1997 (first entry)
XX
DE Heatshock protein T-cell epitope.
XX
XX B-cell epitope; gp120; hypervariable region 3 loop; envelope protein;
XX immunoglobulin; vaccine; cancer; viral infection; leukaemia; V3 loop;
XX influenza virus; target antigen; helper T-cell epitope; immune response;
XX cell-surface receptor; HIV-1; immune system; therapy.
XX
OS Mycobacterium bovis.
XX
XX WO9636357-A1.
XX
PD 21-NOV-1996.
XX
PF 13-MAY-1996; 96WO-US06756.
XX
PR 07-JUN-1995; 95US-0477424.
PR 15-MAY-1995; 95US-0441328.
XX
XX (BONA/) BONA C A.
XX (BRUM/) BRUMEANU T.
XX (DEHA/) DEHAZYA P.
XX (LEEY/) LEE Y C.
XX
XX Bona CA, Brumeanu T, Dehazy P, Lee YC;
XX WPI; 1997-011851/01.
XX
XX New methods of coupling peptide(s) to immuno-globulin(s) via
XX carbohydrate - and related conjugates, useful for treating cancer
XX and viral infections and in vaccines
XX
XX Disclosure; Page 12; 69pp; English.
XX

CC AAW12233-W12241 represent T-cell epitopes that can be used in the method
 CC of the invention. The method of the invention is for conjugating a
 CC peptide (such as this sequence) to an immunoglobulin (Ig) molecule, via
 CC a carbohydrate (CB) residue of the Ig. The method comprises
 CC enzymatically oxidising the CB residue of the Ig, then reacting this
 CC residue with an amino group of the peptide. The product of this reaction
 CC is then stabilised by reacting it with a reducing agent. The conjugate
 CC may be used as a vaccine and in diagnostic and therapeutic methods. The
 CC conjugates are used to treat cancer and viral infections, such as
 CC leukaemia and influenza viruses. The conjugates are used to obtain a
 CC ligand of the peptide using affinity purification, and to detect and
 CC quantitate the amount of a target antigen of the Ig. When the peptide is
 CC a B-cell epitope, the conjugates are used to label B-cells, and when the
 CC peptide is a helper T-cell epitope, the conjugates are used to test the
 CC ability of a subject to mount an immune response to that epitope. The
 CC conjugates are more effective in eliciting an immune response than
 CC unconjugated peptides. The conjugates increase the half-life of the
 CC peptide and also, via binding of the Fc region of the Ig to cell-surface
 CC receptor, recruit elements of the immune system to improve the overall
 CC efficiency of the immune response.
 XX Sequence 20 AA;

Query Match 50.0%; Score 5; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 6 QPLPP 10

RESULT 54
 AAW60693
 ID AAW60693 standard; peptide; 20 AA.

XX AC AAW60693;
 XX DT 22-SEP-1998 (first entry)
 XX DE Mycobacteria heat shock protein T cell epitope (residues 350-369).
 XX KW Immunisation; target antigen; epitope; inoculation; infant mammal;
 KW viral antigen; depressed humoral response; respiratory syncytial virus;
 KW rotavirus; measles virus; human immunodeficiency virus; hepatitis virus;
 KW herpes simplex virus; influenza virus; Streptococcus pneumoniae;
 KW Hemophilus influenzae; Neisseria meningitidis; Staphylococcus aureus;
 KW protozoan antigen; malaria; heat shock protein.
 XX OS Mycobacterium sp.

XX WO9822145-A1.
 XX PD 28-MAY-1998.
 XX PF 21-NOV-1997; 97WO-US21687.
 XX PR 22-NOV-1996; 96US-0755034.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX PI Bona C, Bot A;
 XX WPI; 1998-312182/27.

XX Immunisation of infant mammals - by inoculating the mammal with a
 PT nucleic acid encoding a relevant epitope of a target antigen
 XX Disclosure; Page 10; 83pp; English.

XX Sequence shown in AAW60683 to AAW60700 are epitope sequences of various
 CC viral antigens used to exemplify the method of invention of immunising
 CC an infant mammal against a target antigen. The method comprises

CC inoculating the mammal with a nucleic acid encoding a relevant epitope
 CC of a target antigen in a carrier, such that the relevant epitope is
 CC expressed in the infant mammal. The genetic immunisation of infant
 CC mammals can give rise to effective cellular (including the induction of
 CC cytotoxic T lymphocytes) and humoral immune responses against the target
 CC antigen. The methods are particularly used for treating infants with the
 CC depressed humoral responses, that have high-zone tolerances against the
 CC target antigens or have a Th2 biased immune response. The target antigen
 CC may be a viral antigen, e.g. a respiratory syncytial virus antigen, a
 CC rotavirus antigen, a measles virus antigen, a human immunodeficiency
 CC virus antigen, a hepatitis virus antigen, a hepatitis B virus antigen, a
 CC herpes simplex virus antigen or an influenza virus antigen, a bacterial
 CC antigen e.g. Streptococcus pneumoniae antigen, Hemophilus influenzae
 CC antigen, Neisseria meningitidis antigen, Staphylococcus aureus antigen
 CC or a protozoan antigen such as a malaria antigen.

XX Sequence 20 AA;

Query Match 50.0%; Score 5; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 6 QPLPP 10

RESULT 55
 ABB79926
 ID ABB79926 standard; Peptide; 20 AA.

XX AC ABB79926;
 XX DT 12-DEC-2002 (first entry)
 XX DE Mycobacterium heat shock protein T-cell epitope.
 XX KW Vaccine; genetic immunisation; gene therapy; antigen; epitope;
 KW heat shock protein; T-cell; T-lymphocyte.
 XX OS Mycobacterium sp.

XX US2002115625-A1.
 XX PD 22-AUG-2002.
 XX PF 08-MAR-2001; 2001US-0801540.
 XX PR 19-MAY-1999; 99US-0308511.

XX (BOTA/) BOT A.
 XX (BONA/) BONA C.
 XX PI Bot A, Bona C;
 XX WPI; 2002-712482/77.

XX Immunizing an infant mammal against a target antigen or inducing a
 PT cytotoxic T cell response against a pathogen in the mammal, comprises
 PT administering nucleic acid encoding relevant epitopes of pathogen
 PT associated target antigens -
 XX Disclosure; Page 4; 45pp; English.

XX The present sequence is that of a T-cell epitope from Mycobacteria
 CC heat shock protein (residues 350-369). This is a Th epitope which,
 CC in the context of MHC Class II self antigens, may be recognised by a
 CC helper T-cell and thereby promote B-cell antibody production via the
 CC Th cell. It is an example of T-cell epitopes which may be used
 CC according to the invention. The invention relates to immunising an
 CC infant mammal against a target antigen or inducing a cytotoxic T-cell
 CC response against a pathogen. The method involves inoculating the
 CC infant with a nucleic acid encoding one or more relevant epitopes of

CC one or more target antigens associated with the pathogen in a carrier,
 CC so that the relevant epitope(s) is expressed in the infant mammal.
 CC B- or T-cell epitopes may be used, and the pathogen may be a virus,
 CC bacterium, protozoan, fungus, yeast, or parasite. The method may
 CC reduce the need for subsequent boost administrations and may
 CC prevent the side-effects associated with live attenuated vaccines.
 CC Administration of multiple epitopes directed to antigens
 CC associated with more than one pathogen may provide an infant with a
 CC broader spectrum of protection, and may be a means for inducing an
 CC immune response to a variety of childhood pathogens.
 XX
 XX

SQ Sequence 20 AA;

Query Match 50.0%; Score 5; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 6 QPLPP 10

RESULT 56

AAR80055
 ID AAR80055 standard; peptide; 4 AA.

XX
 AC AAR80055;

XX DT 25-APR-1996 (first entry)

XX XX Peptidase substrate #9.

XX KW Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
 KW cerebral function.

XX OS Synthetic.

XX FN JP07227281-A.

XX PD 29-AUG-1995.

XX PF 15-FEB-1994; 94JP-0042027.

XX PR 15-FEB-1994; 94JP-0042027.

XX PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

XX PA (NIHA-) NIPPON HAM KK.

XX DR WPI; 1995-331519/43.

XX PT 140 kDa peptidase hydrolyses proline rich proteins - useful for
 PT prevention and treatment of diseases related to proline rich
 PT proteins and studies of cerebral functions

XX PS Example 4; Page 6; 7pp; Japanese.

XX CC The sequences represented by AAR80046 and AAR80048-R80059 are substrates
 CC for the novel peptidase of the invention. The peptidase hydrolyses
 CC P-P-P, P-P-P, and P-P and recognises the proline at the second residue
 CC from the N-terminal of a peptide to release the N-terminal amino acid.
 CC The enzyme's activity is stimulated with MnCl2 and inhibited with
 CC o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
 CC hydrolysis of proline containing physiologically active peptides,
 CC oligoproline and proline rich proteins in the living body, particularly
 CC in the brain of mammals. The peptidase is useful for the prevention and
 CC treatment of proline rich protein related diseases and study of cerebral
 CC functions.
 XX

SQ Sequence 4 AA;

Query Match 40.0%; Score 4; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 |||||
 Db 1 PLPP 4

RESULT 57

AA45075
 ID AA45075 standard; peptide; 5 AA.

XX AC AA45075;

XX DT 31-MAY-2000 (first entry)

XX DE Rat amelogenin N-terminal peptide.

XX KW Amelogenin; splice variant; rat; chondrogenesis; osteogenesis;
 KW chondrogenic inducing molecule; CIM; cartilage growth; osteopathic;
 KW extracellular matrix protein; tooth enamel; enamel mineralisation;
 KW ameloblast; bone regeneration; composite cell construct.
 XX

OS Rattus sp.

XX FN WO200006734-A1.

XX PD 10-FEB-2000.

XX PF 29-JUL-1999; 99WO-US17342.

XX PR 29-JUL-1998; 98US-0094489.

XX XX (NOUN) UNIV NORTHWESTERN.

XX PI Veis A, Nebgen DR;

XX DR WPI; 2000-205464/18.

XX PT Novel amelogenin polypeptides and polynucleotides, useful for enhancing
 PT bone generation in mammals and synthesizing bone matrix or articular
 PT surfaces at implant sites -
 XX

XX PS Example 1; Page 70; 79pp; English.

XX CC The present sequence is the amino terminal peptide of the secreted form
 CC of rat amelogenin protein, that corresponds to amino acids 1-5. This
 CC peptide is used to design forward PCR primer P1, to clone and sequence
 CC amelogenin protein. This peptide is highly conserved in bovine, pig
 CC and human species. The amelogenin splice variants functions as an
 CC osteogenic or chondrogenic inducing molecule (CIM), which is useful for
 CC enhancing bone or cartilage growth. It has osteopathic activity.
 CC Amelogenin belongs to the family of extracellular matrix proteins, in
 CC developing tooth enamel, that are produced by the ameloblasts and plays
 CC a role in enamel mineralisation. Chondrogenic or osteogenic inducing
 CC amelogenin molecules are useful to induce differentiation of cells to
 CC the osteogenic and chondrogenic phenotypes and can be used in a
 CC composite cell construct for bone and cartilage regeneration. The
 CC polynucleotides can be employed to produce the polypeptides by
 CC recombinant techniques.
 XX

SQ Sequence 5 AA;

Query Match 40.0%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 |||||
 Db 2 PLPP 5

RESULT 58

AAR28486
 ID AAR28486 standard; peptide; 6 AA.